

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2006, 10:38:34 ; Search time 93 Seconds

(without alignments)

2.906 Million cell updates/sec

Title: US-10-764-316-6-COPY

Perfect score: 2743

Sequence: 1 9cgggcccgtatccattgt.....aaaaaaaaaaaaaaaaaaaaa 2743

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 1733 seqs, 49269 residues

Total number of hits satisfying chosen parameters: 3466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1733 summaries

Database : estdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78.4	2.9	80	1	ACCESSION:BY799992
2	73.8	2.7	78	1	ACCESSION:AA587192
3	55.4	2.0	61	1	ACCESSION:AA079243
4	50	1.8	50	1	ACCESSION:AU103749
5	48.4	1.8	50	1	ACCESSION:AU103750
6	46.8	1.7	50	1	ACCESSION:AU103751
7	46.8	1.7	50	1	ACCESSION:AU103772
8	41.8	1.5	52	1	ACCESSION:T92783
9	39.8	1.5	46	1	ACCESSION:CF298283
10	38.6	1.4	46	1	ACCESSION:BG610636
11	38.4	1.4	43	1	ACCESSION:CV733592
12	37.6	1.4	47	1	ACCESSION:CF317896
13	37.2	1.4	44	1	ACCESSION:CF305383
14	37.2	1.4	46	1	ACCESSION:CV732719
15	37	1.3	37	1	ACCESSION:CF329026
16	37	1.3	42	1	ACCESSION:AL046183
17	37	1.3	44	1	ACCESSION:CF332388
18	36.8	1.3	43	1	ACCESSION:CV730946
19	36.8	1.3	44	1	ACCESSION:CF302212
20	36.8	1.3	46	1	ACCESSION:CF332152
21	36.8	1.3	46	1	ACCESSION:CF32463
22	36.6	1.3	43	1	ACCESSION:CV725460
23	36.6	1.3	44	1	ACCESSION:CF331239
24	36.6	1.3	45	1	ACCESSION:CF332233
25	36.6	1.3	45	1	ACCESSION:CF332233
26	36.4	1.3	38	1	ACCESSION:CV724890
27	36.4	1.3	43	1	ACCESSION:CV733486
28	36.4	1.3	44	1	ACCESSION:CF316377
29	36.2	1.3	42	1	ACCESSION:CF292085
30	36.2	1.3	42	1	ACCESSION:CV734468
31	36.2	1.3	42	1	ACCESSION:CV734501
32	36.2	1.3	44	1	ACCESSION:CV731327
33	36	1.3	37	1	ACCESSION:AJ659250

ACCESSION:CF328866	37	1	CF328866
ACCESSION:CV731657	37	1	CV731657
ACCESSION:CV730040	38	1	CV730040
ACCESSION:CF300591	39	1	CF300591
ACCESSION:CV726948	39	1	CV726948
ACCESSION:CV727347	39	1	CV727347
ACCESSION:CF309581	40	1	CF309581
ACCESSION:CV733657	41	1	CV733657
ACCESSION:CV726108	43	1	CV726108
ACCESSION:CV728159	43	1	CV728159
ACCESSION:CV734232	43	1	CV734232
ACCESSION:CV726790	44	1	CV726790
ACCESSION:CF331757	45	1	CF331757
ACCESSION:CV734230	45	1	CV734230
ACCESSION:CV729079	37	1	CV729079
ACCESSION:CV730711	37	1	CV730711
ACCESSION:CV734007	37	1	CV734007
ACCESSION:CF315184	38	1	CF315184
ACCESSION:CV727074	38	1	CV727074
ACCESSION:CV727193	38	1	CV727193
ACCESSION:CF291979	39	1	CF291979
ACCESSION:CV732133	39	1	CV732133
ACCESSION:CF301837	41	1	CF301837
ACCESSION:CV725219	41	1	CV725219
ACCESSION:CF302691	43	1	CF302691
ACCESSION:CV725096	43	1	CV725096
ACCESSION:DV573571	43	1	DV573571
ACCESSION:DV573572	43	1	DV573572
ACCESSION:CF298596	44	1	CF298596
ACCESSION:CN545689	44	1	CN545689
ACCESSION:CF344384	44	1	CF344384
ACCESSION:CF315871	35	1	CF315871
ACCESSION:CF334198	35	1	CF334198
ACCESSION:CF335633	35	1	CF335633
ACCESSION:CV725312	35	1	CV725312
ACCESSION:CV725444	35	1	CV725444
ACCESSION:CV725518	35	1	CV725518
ACCESSION:CV725797	35	1	CV725797
ACCESSION:CV726506	35	1	CV726506
ACCESSION:CV727085	35	1	CV727085
ACCESSION:CV727326	35	1	CV727326
ACCESSION:CV728725	35	1	CV728725
ACCESSION:CV728984	35	1	CV728984
ACCESSION:CV729199	35	1	CV729199
ACCESSION:CV730453	35	1	CV730453
ACCESSION:CV730547	35	1	CV730547
ACCESSION:CV731689	35	1	CV731689
ACCESSION:CV733059	35	1	CV733059
ACCESSION:CV733251	35	1	CV733251
ACCESSION:CV733296	35	1	CV733296
ACCESSION:CV733344	35	1	CV733344
ACCESSION:CV733739	35	1	CV733739
ACCESSION:CV734164	35	1	CV734164
ACCESSION:AZ623128	35	1	ACCESSION:AZ623128
ACCESSION:AZ803371	35	1	ACCESSION:AZ803371
ACCESSION:AJ791385	36	1	ACCESSION:AJ791385
ACCESSION:AL587891	36	1	ACCESSION:AL587891
ACCESSION:AM046410	36	1	ACCESSION:AM046410
ACCESSION:CF279874	36	1	ACCESSION:CF279874
ACCESSION:CF317028	36	1	ACCESSION:CF317028
ACCESSION:CF331913	36	1	ACCESSION:CF331913
ACCESSION:CF331983	36	1	ACCESSION:CF331983
ACCESSION:CF333863	36	1	ACCESSION:CF333863
ACCESSION:BE876160	36	1	ACCESSION:BE876160
ACCESSION:CV724782	36	1	ACCESSION:CV724782
ACCESSION:CV725281	36	1	ACCESSION:CV725281
ACCESSION:CV725289	36	1	ACCESSION:CV725289
ACCESSION:CV725592	36	1	ACCESSION:CV725592
ACCESSION:CV726151	36	1	ACCESSION:CV726151
ACCESSION:CV726321	36	1	ACCESSION:CV726321
ACCESSION:CV727111	36	1	ACCESSION:CV727111
ACCESSION:CV728675	36	1	ACCESSION:CV728675

C 107	35	1.3	36	1	CV728870	ACCESSION: CV728870	C 180	35	1.3	38	1	CV728809	ACCESSION: CV728809
C 108	35	1.3	36	1	CV729206	ACCESSION: CV729206	C 181	35	1.3	38	1	CV728835	ACCESSION: CV728835
C 109	35	1.3	36	1	CV730235	ACCESSION: CV730235	C 182	35	1.3	38	1	CV729857	ACCESSION: CV729857
C 110	35	1.3	36	1	CV730921	ACCESSION: CV730921	C 183	35	1.3	38	1	CV731476	ACCESSION: CV731476
C 111	35	1.3	36	1	CV730953	ACCESSION: CV730953	C 184	35	1.3	38	1	DR064343	ACCESSION: DR064343
C 112	35	1.3	36	1	CV732578	ACCESSION: CV732578	C 185	35	1.3	38	1	DM337683	ACCESSION: DM337683
C 113	35	1.3	36	1	CV732659	ACCESSION: CV732659	C 186	35	1.3	38	1	AZ785034	ACCESSION: AZ785034
C 114	35	1.3	36	1	CV733597	ACCESSION: CV733597	C 187	35	1.3	39	1	BG287495	ACCESSION: BG287495
C 115	35	1.3	36	1	CV734403	ACCESSION: CV734403	C 188	35	1.3	39	1	B1694035	ACCESSION: B1694035
C 116	35	1.3	36	1	AZ470916	ACCESSION: AZ470916	C 189	35	1.3	39	1	CF298508	ACCESSION: CF298508
C 117	35	1.3	36	1	AZ628484	ACCESSION: AZ628484	C 190	35	1.3	39	1	CF302356	ACCESSION: CF302356
C 118	35	1.3	36	1	AZ793484	ACCESSION: AZ793484	C 191	35	1.3	39	1	CF315736	ACCESSION: CF315736
C 119	35	1.3	36	1	AZ949866	ACCESSION: AZ949866	C 192	35	1.3	39	1	CF321323	ACCESSION: CF321323
C 120	35	1.3	36	1	AZ957867	ACCESSION: AZ957867	C 193	35	1.3	39	1	CF330732	ACCESSION: CF330732
C 121	35	1.3	36	1	DU814006	ACCESSION: DU814006	C 194	35	1.3	39	1	BF032623	ACCESSION: BF032623
C 122	35	1.3	36	1	DU834235	ACCESSION: DU834235	C 195	35	1.3	39	1	BE891613	ACCESSION: BE891613
C 123	35	1.3	36	1	DX046307	ACCESSION: DX046307	C 196	35	1.3	39	1	CV724457	ACCESSION: CV724457
C 124	35	1.3	37	1	BG033620	ACCESSION: BG033620	C 197	35	1.3	39	1	CV724623	ACCESSION: CV724623
C 125	35	1.3	37	1	CF291818	ACCESSION: CF291818	C 198	35	1.3	39	1	CV725192	ACCESSION: CV725192
C 126	35	1.3	37	1	CF300002	ACCESSION: CF300002	C 199	35	1.3	39	1	CV725228	ACCESSION: CV725228
C 127	35	1.3	37	1	CF300328	ACCESSION: CF300328	C 200	35	1.3	39	1	CV725383	ACCESSION: CV725383
C 128	35	1.3	37	1	CF301560	ACCESSION: CF301560	C 201	35	1.3	39	1	CV725570	ACCESSION: CV725570
C 129	35	1.3	37	1	CF301864	ACCESSION: CF301864	C 202	35	1.3	39	1	CV726046	ACCESSION: CV726046
C 130	35	1.3	37	1	CF307971	ACCESSION: CF307971	C 203	35	1.3	39	1	CV726057	ACCESSION: CV726057
C 131	35	1.3	37	1	CF316114	ACCESSION: CF316114	C 204	35	1.3	39	1	CV726327	ACCESSION: CV726327
C 132	35	1.3	37	1	CF321294	ACCESSION: CF321294	C 205	35	1.3	39	1	CV726361	ACCESSION: CV726361
C 133	35	1.3	37	1	CF326975	ACCESSION: CF326975	C 206	35	1.3	39	1	CV726728	ACCESSION: CV726728
C 134	35	1.3	37	1	CF333624	ACCESSION: CF333624	C 207	35	1.3	39	1	CV726866	ACCESSION: CV726866
C 135	35	1.3	37	1	CF336769	ACCESSION: CF336769	C 208	35	1.3	39	1	CV726936	ACCESSION: CV726936
C 136	35	1.3	37	1	CV724637	ACCESSION: CV724637	C 209	35	1.3	39	1	CV726971	ACCESSION: CV726971
C 137	35	1.3	37	1	CV725878	ACCESSION: CV725878	C 210	35	1.3	39	1	CV727002	ACCESSION: CV727002
C 138	35	1.3	37	1	CV726514	ACCESSION: CV726514	C 211	35	1.3	39	1	CV727016	ACCESSION: CV727016
C 139	35	1.3	37	1	CV726571	ACCESSION: CV726571	C 212	35	1.3	39	1	CV727114	ACCESSION: CV727114
C 140	35	1.3	37	1	CV727266	ACCESSION: CV727266	C 213	35	1.3	39	1	CV727215	ACCESSION: CV727215
C 141	35	1.3	37	1	CV727448	ACCESSION: CV727448	C 214	35	1.3	39	1	CV727351	ACCESSION: CV727351
C 142	35	1.3	37	1	CV727567	ACCESSION: CV727567	C 215	35	1.3	39	1	CV727680	ACCESSION: CV727680
C 143	35	1.3	37	1	CV727819	ACCESSION: CV727819	C 216	35	1.3	39	1	CV728240	ACCESSION: CV728240
C 144	35	1.3	37	1	CV728196	ACCESSION: CV728196	C 217	35	1.3	39	1	CV728278	ACCESSION: CV728278
C 145	35	1.3	37	1	CV728197	ACCESSION: CV728197	C 218	35	1.3	39	1	CV729217	ACCESSION: CV729217
C 146	35	1.3	37	1	CV730003	ACCESSION: CV730003	C 219	35	1.3	39	1	CV730113	ACCESSION: CV730113
C 147	35	1.3	37	1	CV730176	ACCESSION: CV730176	C 220	35	1.3	39	1	CV732729	ACCESSION: CV732729
C 148	35	1.3	37	1	CV731472	ACCESSION: CV731472	C 221	35	1.3	39	1	CV733026	ACCESSION: CV733026
C 149	35	1.3	37	1	AZ321759	ACCESSION: AZ321759	C 222	35	1.3	39	1	CV733160	ACCESSION: CV733160
C 150	35	1.3	37	1	AZ463801	ACCESSION: AZ463801	C 223	35	1.3	39	1	CV733431	ACCESSION: CV733431
C 151	35	1.3	37	1	AZ831214	ACCESSION: AZ831214	C 224	35	1.3	39	1	CV733935	ACCESSION: CV733935
C 152	35	1.3	37	1	CZ914427	ACCESSION: CZ914427	C 225	35	1.3	39	1	CV733973	ACCESSION: CV733973
C 153	35	1.3	37	1	DX071328	ACCESSION: DX071328	C 226	35	1.3	39	1	AZ633088	ACCESSION: AZ633088
C 154	35	1.3	37	1	DX072665	ACCESSION: DX072665	C 227	35	1.3	40	1	AL037510	ACCESSION: AL037510
C 155	35	1.3	37	1	DR102924T	ACCESSION: AL977144	C 228	35	1.3	40	1	AL449576	ACCESSION: AL449576
C 156	35	1.3	37	1	DR102924T	ACCESSION: AL985556	C 229	35	1.3	40	1	BG166502	ACCESSION: BG166502
C 157	35	1.3	38	1	CF291176	ACCESSION: CF291176	C 230	35	1.3	40	1	CF311814	ACCESSION: CF311814
C 158	35	1.3	38	1	CF301164	ACCESSION: CF301164	C 231	35	1.3	40	1	CF327027	ACCESSION: CF327027
C 159	35	1.3	38	1	CF301819	ACCESSION: CF301819	C 232	35	1.3	40	1	CF328199	ACCESSION: CF328199
C 160	35	1.3	38	1	CF321261	ACCESSION: CF321261	C 233	35	1.3	40	1	CF328306	ACCESSION: CF328306
C 161	35	1.3	38	1	CF328351	ACCESSION: CF328351	C 234	35	1.3	40	1	CF334545	ACCESSION: CF334545
C 162	35	1.3	38	1	CF329605	ACCESSION: CF329605	C 235	35	1.3	40	1	CV724551	ACCESSION: CV724551
C 163	35	1.3	38	1	CF329690	ACCESSION: CF329690	C 236	35	1.3	40	1	CV725014	ACCESSION: CV725014
C 164	35	1.3	38	1	CF329730	ACCESSION: CF329730	C 237	35	1.3	40	1	CV725673	ACCESSION: CV725673
C 165	35	1.3	38	1	BF525501	ACCESSION: BF525501	C 238	35	1.3	40	1	CV726807	ACCESSION: CV726807
C 166	35	1.3	38	1	BF526154	ACCESSION: BF526154	C 239	35	1.3	40	1	CV727416	ACCESSION: CV727416
C 167	35	1.3	38	1	CV724657	ACCESSION: CV724657	C 240	35	1.3	40	1	CV727587	ACCESSION: CV727587
C 168	35	1.3	38	1	CV725198	ACCESSION: CV725198	C 241	35	1.3	40	1	CV727805	ACCESSION: CV727805
C 169	35	1.3	38	1	CV725495	ACCESSION: CV725495	C 242	35	1.3	40	1	CV727843	ACCESSION: CV727843
C 170	35	1.3	38	1	CV726250	ACCESSION: CV726250	C 243	35	1.3	40	1	CV727858	ACCESSION: CV727858
C 171	35	1.3	38	1	CV726534	ACCESSION: CV726534	C 244	35	1.3	40	1	CV728325	ACCESSION: CV728325
C 172	35	1.3	38	1	CV726895	ACCESSION: CV726895	C 245	35	1.3	40	1	CV728655	ACCESSION: CV728655
C 173	35	1.3	38	1	CV726983	ACCESSION: CV726983	C 246	35	1.3	40	1	CV730371	ACCESSION: CV730371
C 174	35	1.3	38	1	CV727096	ACCESSION: CV727096	C 247	35	1.3	40	1	CV731031	ACCESSION: CV731031
C 175	35	1.3	38	1	CV727478	ACCESSION: CV727478	C 248	35	1.3	40	1	CV731319	ACCESSION: CV731319
C 176	35	1.3	38	1	CV727598	ACCESSION: CV727598	C 249	35	1.3	40	1	CV731528	ACCESSION: CV731528
C 177	35	1.3	38	1	CV727921	ACCESSION: CV727921	C 250	35	1.3	40	1	CV732353	ACCESSION: CV732353
C 178	35	1.3	38	1	CV728176	ACCESSION: CV728176	C 251	35	1.3	40	1	CV732629	ACCESSION: CV732629
C 179	35	1.3	38	1	CV728223	ACCESSION: CV728223	C 252	35	1.3	40	1	CV732676	ACCESSION: CV732676

C 253	35	1.3	40	1	CV733006	ACCESSION: CV733006	326	35	1.3	43	1	CV062138	ACCESSION: CV062138
C 254	35	1.3	40	1	CV733017	ACCESSION: CV733017	C 327	35	1.3	43	1	CV724539	ACCESSION: CV724539
C 255	35	1.3	40	1	CV733422	ACCESSION: CV733422	C 328	35	1.3	43	1	CV724959	ACCESSION: CV724959
C 256	35	1.3	40	1	CV733638	ACCESSION: CV733638	C 329	35	1.3	43	1	CV724969	ACCESSION: CV724969
C 257	35	1.3	40	1	AZ831983	ACCESSION: AZ831983	C 330	35	1.3	43	1	CV725127	ACCESSION: CV725127
C 258	35	1.3	40	1	DU835034	ACCESSION: DU835034	C 331	35	1.3	43	1	CV725506	ACCESSION: CV725506
C 259	35	1.3	40	1	AJ792759	ACCESSION: AJ792759	C 332	35	1.3	43	1	CV725680	ACCESSION: CV725680
C 260	35	1.3	41	1	CF291539	ACCESSION: CF291539	C 333	35	1.3	43	1	CV725720	ACCESSION: CV725720
C 261	35	1.3	41	1	CF318677	ACCESSION: CF318677	C 334	35	1.3	43	1	CV725822	ACCESSION: CV725822
C 262	35	1.3	41	1	CF320203	ACCESSION: CF320203	C 335	35	1.3	43	1	CV726349	ACCESSION: CV726349
C 263	35	1.3	41	1	CF330464	ACCESSION: CF330464	C 336	35	1.3	43	1	CV726594	ACCESSION: CV726594
C 264	35	1.3	41	1	CF334638	ACCESSION: CF334638	C 337	35	1.3	43	1	CV726751	ACCESSION: CV726751
C 265	35	1.3	41	1	CV725868	ACCESSION: CV725868	C 338	35	1.3	43	1	CV727328	ACCESSION: CV727328
C 266	35	1.3	41	1	CV725993	ACCESSION: CV725993	C 339	35	1.3	43	1	CV727684	ACCESSION: CV727684
C 267	35	1.3	41	1	CV726255	ACCESSION: CV726255	C 340	35	1.3	43	1	CV728681	ACCESSION: CV728681
C 268	35	1.3	41	1	CV726393	ACCESSION: CV726393	C 341	35	1.3	43	1	CV728686	ACCESSION: CV728686
C 269	35	1.3	41	1	CV726923	ACCESSION: CV726923	C 342	35	1.3	43	1	CV728737	ACCESSION: CV728737
C 270	35	1.3	41	1	CV727015	ACCESSION: CV727015	C 343	35	1.3	43	1	CV728887	ACCESSION: CV728887
C 271	35	1.3	41	1	CV727210	ACCESSION: CV727210	C 344	35	1.3	43	1	CV729000	ACCESSION: CV729000
C 272	35	1.3	41	1	CV727412	ACCESSION: CV727412	C 345	35	1.3	43	1	CV729158	ACCESSION: CV729158
C 273	35	1.3	41	1	CV727841	ACCESSION: CV727841	C 346	35	1.3	43	1	CV729970	ACCESSION: CV729970
C 274	35	1.3	41	1	CV728055	ACCESSION: CV728055	C 347	35	1.3	43	1	CV730586	ACCESSION: CV730586
C 275	35	1.3	41	1	CV728228	ACCESSION: CV728228	C 348	35	1.3	43	1	CV730813	ACCESSION: CV730813
C 276	35	1.3	41	1	CV728716	ACCESSION: CV728716	C 349	35	1.3	43	1	CV731060	ACCESSION: CV731060
C 277	35	1.3	41	1	CV728978	ACCESSION: CV728978	C 350	35	1.3	43	1	CV731475	ACCESSION: CV731475
C 278	35	1.3	41	1	CV729041	ACCESSION: CV729041	C 351	35	1.3	43	1	CV732091	ACCESSION: CV732091
C 279	35	1.3	41	1	CV731427	ACCESSION: CV731427	C 352	35	1.3	43	1	CV732291	ACCESSION: CV732291
C 280	35	1.3	41	1	CV731668	ACCESSION: CV731668	C 353	35	1.3	43	1	CV732533	ACCESSION: CV732533
C 281	35	1.3	41	1	CV732073	ACCESSION: CV732073	C 354	35	1.3	43	1	CV732664	ACCESSION: CV732664
C 282	35	1.3	41	1	CV733839	ACCESSION: CV733839	C 355	35	1.3	43	1	CV733072	ACCESSION: CV733072
C 283	35	1.3	41	1	CV734304	ACCESSION: CV734304	C 356	35	1.3	43	1	CV733143	ACCESSION: CV733143
C 284	35	1.3	41	1	AZ775066	ACCESSION: AZ775066	C 357	35	1.3	43	1	CV733227	ACCESSION: CV733227
C 285	35	1.3	41	1	AZ827008	ACCESSION: AZ827008	C 358	35	1.3	43	1	CV733316	ACCESSION: CV733316
C 286	35	1.3	41	1	DU834001	ACCESSION: DU834001	C 359	35	1.3	43	1	CV734334	ACCESSION: CV734334
C 287	35	1.3	41	1	DU834619	ACCESSION: DU834619	C 360	35	1.3	43	1	CX002408	ACCESSION: CX002408
C 288	35	1.3	41	1	DU835000	ACCESSION: DU835000	C 361	35	1.3	43	1	AZ355703	ACCESSION: AZ355703
C 289	35	1.3	41	1	DX049410	ACCESSION: DX049410	C 362	34.8	1.3	40	1	CR762707	ACCESSION: CR762707
C 290	35	1.3	42	1	AG291919	ACCESSION: AG291919	C 363	34.8	1.3	43	1	CV066153	ACCESSION: CV066153
C 291	35	1.3	42	1	BG292448	ACCESSION: BG292448	C 364	34.4	1.3	36	1	CV725617	ACCESSION: CV725617
C 292	35	1.3	42	1	CF318540	ACCESSION: CF318540	C 365	34.4	1.3	41	1	DY231188	ACCESSION: DY231188
C 293	35	1.3	42	1	CF318962	ACCESSION: CF318962	C 366	34	1.2	34	1	CJ038300	ACCESSION: CJ038300
C 294	35	1.3	42	1	CF319867	ACCESSION: CF319867	C 367	34	1.2	34	1	CV724455	ACCESSION: CV724455
C 295	35	1.3	42	1	CF320056	ACCESSION: CF320056	C 368	34	1.2	34	1	CV726231	ACCESSION: CV726231
C 296	35	1.3	42	1	CF322408	ACCESSION: CF322408	C 369	34	1.2	34	1	CV726784	ACCESSION: CV726784
C 297	35	1.3	42	1	BF3343329	ACCESSION: BF3343329	C 370	34	1.2	34	1	CV727320	ACCESSION: CV727320
C 298	35	1.3	42	1	AW334133	ACCESSION: AW334133	C 371	34	1.2	34	1	CV729064	ACCESSION: CV729064
C 299	35	1.3	42	1	CV062024	ACCESSION: CV062024	C 372	34	1.2	34	1	CV730592	ACCESSION: CV730592
C 300	35	1.3	42	1	CV725428	ACCESSION: CV725428	C 373	34	1.2	34	1	CV730644	ACCESSION: CV730644
C 301	35	1.3	42	1	CV726363	ACCESSION: CV726363	C 374	34	1.2	34	1	CV731182	ACCESSION: CV731182
C 302	35	1.3	42	1	CV726372	ACCESSION: CV726372	C 375	34	1.2	34	1	CV734338	ACCESSION: CV734338
C 303	35	1.3	42	1	CV728634	ACCESSION: CV728634	C 376	34	1.2	34	1	AZ465350	ACCESSION: AZ465350
C 304	35	1.3	42	1	CV728806	ACCESSION: CV728806	C 377	34	1.2	34	1	AZ501040	ACCESSION: AZ501040
C 305	35	1.3	42	1	CV729215	ACCESSION: CV729215	C 378	34	1.2	34	1	AZ809643	ACCESSION: AZ809643
C 306	35	1.3	42	1	CV729267	ACCESSION: CV729267	C 379	34	1.2	34	1	DU835285	ACCESSION: DU835285
C 307	35	1.3	42	1	CV731493	ACCESSION: CV731493	C 380	34	1.2	34	1	DX037933	ACCESSION: DX037933
C 308	35	1.3	42	1	CV731845	ACCESSION: CV731845	C 381	34	1.2	34	1	CV730365	ACCESSION: CV730365
C 309	35	1.3	42	1	CV732835	ACCESSION: CV732835	C 382	34	1.2	37	1	CF291807	ACCESSION: CF291807
C 310	35	1.3	42	1	CV732860	ACCESSION: CV732860	C 383	34	1.2	42	1	CF330901	ACCESSION: CF330901
C 311	35	1.3	42	1	CV733275	ACCESSION: CV733275	C 384	34	1.2	42	1	CV726166	ACCESSION: CV726166
C 312	35	1.3	42	1	CV733323	ACCESSION: CV733323	C 385	33.8	1.2	41	1	DX045841	ACCESSION: DX045841
C 313	35	1.3	42	1	CV733344	ACCESSION: CV733344	C 386	33.8	1.2	42	1	CV728107	ACCESSION: CV728107
C 314	35	1.3	42	1	CV733603	ACCESSION: CV733603	C 387	33.6	1.2	40	1	CF331029	ACCESSION: CF331029
C 315	35	1.3	42	1	CV733690	ACCESSION: CV733690	C 388	33.6	1.2	42	1	AL038483	ACCESSION: AL038483
C 316	35	1.3	42	1	CV733938	ACCESSION: CV733938	C 389	33.4	1.2	35	1	BE894837	ACCESSION: BE894837
C 317	35	1.3	42	1	CV734112	ACCESSION: CV734112	C 390	33.4	1.2	35	1	CO785671	ACCESSION: CO785671
C 318	35	1.3	42	1	CX058845	ACCESSION: CX058845	C 391	33.4	1.2	35	1	DN955388	ACCESSION: DN955388
C 319	35	1.3	42	1	DU835485	ACCESSION: DU835485	C 392	33.4	1.2	36	1	BE894682	ACCESSION: BE894682
C 320	35	1.3	43	1	AJ923543	ACCESSION: AJ923543	C 393	33.4	1.2	36	1	CV724804	ACCESSION: CV724804
C 321	35	1.3	43	1	AL587884	ACCESSION: AL587884	C 394	33.4	1.2	36	1	CZ912531	ACCESSION: CZ912531
C 322	35	1.3	43	1	BG028362	ACCESSION: BG028362	C 395	33.4	1.2	36	1	DU830895	ACCESSION: DU830895
C 323	35	1.3	43	1	BI908698	ACCESSION: BI908698	C 396	33.4	1.2	37	1	AL048768	ACCESSION: AL048768
C 324	35	1.3	43	1	CF302744	ACCESSION: CF302744	C 397	33.4	1.2	37	1	CV732356	ACCESSION: CV732356
C 325	35	1.3	43	1	CF334344	ACCESSION: CF334344	C 398	33.4	1.2	37	1	AZ824309	ACCESSION: AZ824309

C 399	33.4	1.2	37	1	DX062077	ACCESSION: DX062077	C 472	32	1.2	32	1	CF313717	ACCESSION: CF313717
C 400	33.4	1.2	38	1	CF302184	ACCESSION: CF302184	C 473	32	1.2	32	1	CF321046	ACCESSION: CF321046
C 401	33.4	1.2	38	1	CF316791	ACCESSION: CF316791	C 474	32	1.2	32	1	CF328471	ACCESSION: CF328471
C 402	33.4	1.2	38	1	AW333985	ACCESSION: AW333985	C 475	32	1.2	32	1	CF331270	ACCESSION: CF331270
C 403	33.4	1.2	38	1	DR074451	ACCESSION: DR074451	C 476	32	1.2	32	1	AW327277	ACCESSION: AW327277
C 404	33.4	1.2	38	1	AZ589726	ACCESSION: AZ589726	C 477	32	1.2	32	1	CV724815	ACCESSION: CV724815
C 405	33.4	1.2	38	1	DX060574	ACCESSION: DX060574	C 478	32	1.2	32	1	CV725190	ACCESSION: CV725190
C 406	33.4	1.2	38	1	CF319510	ACCESSION: CF319510	C 479	32	1.2	32	1	CV725571	ACCESSION: CV725571
C 407	33.4	1.2	39	1	CF0786273	ACCESSION: CF0786273	C 480	32	1.2	32	1	CV726012	ACCESSION: CV726012
C 408	33.4	1.2	39	1	CNS0040NT	ACCESSION: AL054298	C 481	32	1.2	32	1	CV726385	ACCESSION: CV726385
C 409	33.4	1.2	40	1	AL638703	ACCESSION: AL638703	C 482	32	1.2	32	1	CV727659	ACCESSION: CV727659
C 410	33.4	1.2	40	1	CF336399	ACCESSION: CF336399	C 483	32	1.2	32	1	CV728625	ACCESSION: CV728625
C 411	33.4	1.2	40	1	DV082973	ACCESSION: DV082973	C 484	32	1.2	32	1	CV729255	ACCESSION: CV729255
C 412	33.4	1.2	40	1	DX076358	ACCESSION: DX076358	C 485	32	1.2	32	1	CV732146	ACCESSION: CV732146
C 413	33.4	1.2	41	1	CF300448	ACCESSION: CF300448	C 486	32	1.2	32	1	CV732586	ACCESSION: CV732586
C 414	33.4	1.2	41	1	CF302032	ACCESSION: CF302032	C 487	32	1.2	32	1	AZ459536	ACCESSION: AZ459536
C 415	33.4	1.2	41	1	CF305364	ACCESSION: CF305364	C 488	32	1.2	32	1	AZ470832	ACCESSION: AZ470832
C 416	33.4	1.2	41	1	AV742106	ACCESSION: AV742106	C 489	32	1.2	32	1	AZ611890	ACCESSION: AZ611890
C 417	33.4	1.2	41	1	CV731029	ACCESSION: CV731029	C 490	32	1.2	32	1	AZ778018	ACCESSION: AZ778018
C 418	33.4	1.2	41	1	DX049794	ACCESSION: DX049794	C 491	32	1.2	32	1	DU835386	ACCESSION: DU835386
C 419	33.2	1.2	38	1	AL038652	ACCESSION: AL038652	C 492	32	1.2	32	1	DR85121T	ACCESSION: AL986044
C 420	33.2	1.2	39	1	CF328529	ACCESSION: CF328529	C 493	32	1.2	33	1	AL587609	ACCESSION: AL587609
C 421	33	1.2	33	1	CF291613	ACCESSION: CF291613	C 494	32	1.2	33	1	B0431798	ACCESSION: BU431798
C 422	33	1.2	33	1	CF311229	ACCESSION: CF311229	C 495	32	1.2	34	1	AZ345610	ACCESSION: AZ345610
C 423	33	1.2	33	1	CF326967	ACCESSION: CF326967	C 496	32	1.2	35	1	BF338797	ACCESSION: BF338797
C 424	33	1.2	33	1	CF328313	ACCESSION: CF328313	C 497	32	1.2	35	1	DR073823	ACCESSION: DR073823
C 425	33	1.2	33	1	CF336752	ACCESSION: CF336752	C 498	32	1.2	39	1	AM046479	ACCESSION: AM046479
C 426	33	1.2	33	1	CF337105	ACCESSION: CF337105	C 499	32	1.2	40	1	CV723737	ACCESSION: CV723737
C 427	33	1.2	33	1	CV725203	ACCESSION: CV725203	C 500	31.8	1.2	35	1	BQ590703	ACCESSION: BQ590703
C 428	33	1.2	33	1	CV725846	ACCESSION: CV725846	C 501	31.8	1.2	35	1	CV724720	ACCESSION: CV724720
C 429	33	1.2	33	1	CV725871	ACCESSION: CV725871	C 502	31.8	1.2	36	1	AZ945733	ACCESSION: AZ945733
C 430	33	1.2	33	1	CV725959	ACCESSION: CV725959	C 503	31.8	1.2	36	1	CZ919025	ACCESSION: CZ919025
C 431	33	1.2	33	1	CV726801	ACCESSION: CV726801	C 504	31.8	1.2	37	1	CF298167	ACCESSION: CF298167
C 432	33	1.2	33	1	CV726984	ACCESSION: CV726984	C 505	31.8	1.2	38	1	DN988546	ACCESSION: DN988546
C 433	33	1.2	33	1	CV732151	ACCESSION: CV732151	C 506	31.8	1.2	39	1	TA116F09P	ACCESSION: AL462533
C 434	33	1.2	33	1	CV732198	ACCESSION: CV732198	C 507	31.4	1.1	33	1	CZ908819	ACCESSION: CZ908819
C 435	33	1.2	33	1	CV732853	ACCESSION: CV732853	C 508	31.4	1.1	36	1	CF298131	ACCESSION: CF298131
C 436	33	1.2	33	1	CV733051	ACCESSION: CV733051	C 509	31.4	1.1	37	1	CF278363	ACCESSION: CF278363
C 437	33	1.2	33	1	CV734457	ACCESSION: CV734457	C 510	31.4	1.1	39	1	CA853500	ACCESSION: CA853500
C 438	33	1.2	33	1	CK013914	ACCESSION: CK013914	C 511	31.2	1.1	38	1	CF321807	ACCESSION: CF321807
C 439	33	1.2	33	1	AZ486795	ACCESSION: AZ486795	C 512	31.2	1.1	39	1	CF308197	ACCESSION: CF308197
C 440	33	1.2	33	1	AZ627839	ACCESSION: AZ627839	C 513	31	1.1	31	1	AJ659810	ACCESSION: AJ659810
C 441	33	1.2	33	1	CZ917348	ACCESSION: CZ917348	C 514	31	1.1	31	1	AJ693992	ACCESSION: AJ693992
C 442	33	1.2	33	1	DU830405	ACCESSION: DU830405	C 515	31	1.1	31	1	AM044121	ACCESSION: AM044121
C 443	33	1.2	33	1	DX033863	ACCESSION: DX033863	C 516	31	1.1	31	1	BX569502	ACCESSION: BX569502
C 444	33	1.2	34	1	AL587876	ACCESSION: AL587876	C 517	31	1.1	31	1	CF278807	ACCESSION: CF278807
C 445	33	1.2	34	1	BU431799	ACCESSION: BU431799	C 518	31	1.1	31	1	CF300345	ACCESSION: CF300345
C 446	33	1.2	34	1	CV734277	ACCESSION: CV734277	C 519	31	1.1	31	1	AZ333315	ACCESSION: AZ333315
C 447	33	1.2	36	1	BI761940	ACCESSION: BI761940	C 520	31	1.1	31	1	AZ510092	ACCESSION: AZ510092
C 448	33	1.2	38	1	AJ792257	ACCESSION: AJ792257	C 521	31	1.1	31	1	AZ623538	ACCESSION: AZ623538
C 449	33	1.2	38	1	CV064759	ACCESSION: CV064759	C 522	31	1.1	31	1	AZ627692	ACCESSION: AZ627692
C 450	33	1.2	39	1	CF327755	ACCESSION: CF327755	C 523	31	1.1	31	1	AZ778697	ACCESSION: AZ778697
C 451	32.8	1.2	37	1	CF292043	ACCESSION: CF292043	C 524	31	1.1	31	1	AZ821215	ACCESSION: AZ821215
C 452	32.4	1.2	34	1	CF302250	ACCESSION: CF302250	C 525	31	1.1	31	1	AZ826618	ACCESSION: AZ826618
C 453	32.4	1.2	34	1	CF315464	ACCESSION: CF315464	C 526	31	1.1	31	1	AZ826618	ACCESSION: AZ826618
C 454	32.4	1.2	34	1	CZ906552	ACCESSION: CZ906552	C 527	31	1.1	31	1	CZ917108	ACCESSION: CZ917108
C 455	32.4	1.2	34	1	DX054666	ACCESSION: DX054666	C 528	31	1.1	31	1	DU835031	ACCESSION: DU835031
C 456	32.4	1.2	34	1	DX058168	ACCESSION: DX058168	C 529	31	1.1	31	1	DX063750	ACCESSION: DX063750
C 457	32.4	1.2	34	1	DR41AAT	ACCESSION: AL980969	C 530	31	1.1	31	1	AV674152	ACCESSION: AV674152
C 458	32.4	1.2	36	1	AM047864	ACCESSION: AM047864	C 531	31	1.1	34	1	AW334249	ACCESSION: AW334249
C 459	32.4	1.2	38	1	CNS45543	ACCESSION: CNS45543	C 532	31	1.1	36	1	CV066718	ACCESSION: CV066718
C 460	32.2	1.2	37	1	CNS45945	ACCESSION: CNS45945	C 533	30.8	1.1	34	1	BQ587432	ACCESSION: BQ587432
C 461	32.2	1.2	38	1	AL037916	ACCESSION: AL037916	C 534	30.8	1.1	34	1	DU832879	ACCESSION: DU832879
C 462	32.2	1.2	39	1	CNS46173	ACCESSION: CNS46173	C 535	30.8	1.1	34	1	DX048708	ACCESSION: DX048708
C 463	32.2	1.2	40	1	BQ591342	ACCESSION: BQ591342	C 536	30.6	1.1	37	1	CV848473	ACCESSION: CV848473
C 464	32	1.2	32	1	AJ9233479	ACCESSION: AJ9233479	C 537	30.4	1.1	32	1	AJ791147	ACCESSION: AJ791147
C 465	32	1.2	32	1	AM044529	ACCESSION: AM044529	C 538	30.4	1.1	32	1	CF302459	ACCESSION: CF302459
C 466	32	1.2	32	1	AM044934	ACCESSION: AM044934	C 539	30.4	1.1	32	1	CNS46365	ACCESSION: CNS46365
C 467	32	1.2	32	1	AM045405	ACCESSION: AM045405	C 540	30.4	1.1	32	1	DV083947	ACCESSION: DV083947
C 468	32	1.2	32	1	CF291773	ACCESSION: CF291773	C 541	30.4	1.1	32	1	AZ314322	ACCESSION: AZ314322
C 469	32	1.2	32	1	CF299386	ACCESSION: CF299386	C 542	30.4	1.1	32	1	AZ579652	ACCESSION: AZ579652
C 470	32	1.2	32	1	CF309233	ACCESSION: CF309233	C 543	30.4	1.1	32	1	DU834670	ACCESSION: DU834670
C 471	32	1.2	32	1	CF309345	ACCESSION: CF309345	C 544	30.4	1.1	32	1	DX033610	ACCESSION: DX033610

C 545	30.4	1.1	32	1	DR1P7S	ACCESSION:AL733323	C 618	29.4	1.1	36	1	CN546685	ACCESSION:CN546685
C 546	30.4	1.1	33	1	CF334899	ACCESSION:CF334899	C 619	29.4	1.1	36	1	CV091545	ACCESSION:CV091545
C 547	30.4	1.1	34	1	AZ307192	ACCESSION:AZ307192	C 620	29.2	1.1	34	1	AL038356	ACCESSION:AL038356
C 548	30.4	1.1	35	1	CN545906	ACCESSION:CN545906	C 621	29.2	1.1	35	1	T50295	ACCESSION:T50295
C 549	30.4	1.1	36	1	CN546158	ACCESSION:CN546158	C 622	29.2	1.1	35	1	AZ351309	ACCESSION:AZ351309
C 550	30.4	1.1	36	1	CN546709	ACCESSION:CN546709	C 623	29.2	1.1	35	1	CZ914519	ACCESSION:CZ914519
C 551	30.4	1.1	36	1	DU834429	ACCESSION:DU834429	C 624	29	1.1	35	1	AM044739	ACCESSION:AM044739
C 552	30.4	1.1	37	1	CN545897	ACCESSION:CN545897	C 625	29	1.1	29	1	AM048584	ACCESSION:AM048584
C 553	30.4	1.1	37	1	DN988462	ACCESSION:DN988462	C 626	29	1.1	29	1	CF279536	ACCESSION:CF279536
C 554	30.4	1.1	38	1	CN546437	ACCESSION:CN546437	C 627	29	1.1	29	1	CF299920	ACCESSION:CF299920
C 555	30.4	1.1	38	1	CN546551	ACCESSION:CN546551	C 628	29	1.1	29	1	CF312601	ACCESSION:CF312601
C 556	30.4	1.1	38	1	CN546633	ACCESSION:CN546633	C 629	29	1.1	29	1	CF312601	ACCESSION:CF312601
C 557	30.2	1.1	36	1	CZ916174	ACCESSION:CZ916174	C 630	29	1.1	29	1	CN545237	ACCESSION:CN545237
C 558	30	1.1	30	1	AL038650	ACCESSION:AL038650	C 631	29	1.1	29	1	CN546188	ACCESSION:CN546188
C 559	30	1.1	30	1	AM044444	ACCESSION:AM044444	C 632	29	1.1	29	1	CN546382	ACCESSION:CN546382
C 560	30	1.1	30	1	BG666435	ACCESSION:BG666435	C 633	29	1.1	29	1	CN546438	ACCESSION:CN546438
C 561	30	1.1	30	1	CF280699	ACCESSION:CF280699	C 634	29	1.1	29	1	CN546557	ACCESSION:CN546557
C 562	30	1.1	30	1	CF292086	ACCESSION:CF292086	C 635	29	1.1	29	1	CV999708	ACCESSION:CV999708
C 563	30	1.1	30	1	CF299555	ACCESSION:CF299555	C 636	29	1.1	29	1	DR073120	ACCESSION:DR073120
C 564	30	1.1	30	1	CF312417	ACCESSION:CF312417	C 637	29	1.1	29	1	AZ389966	ACCESSION:AZ389966
C 565	30	1.1	30	1	CF322226	ACCESSION:CF322226	C 638	29	1.1	29	1	AZ414283	ACCESSION:AZ414283
C 566	30	1.1	30	1	CF327835	ACCESSION:CF327835	C 639	29	1.1	29	1	AZ451930	ACCESSION:AZ451930
C 567	30	1.1	30	1	CF336555	ACCESSION:CF336555	C 640	29	1.1	29	1	AZ468402	ACCESSION:AZ468402
C 568	30	1.1	30	1	CN545913	ACCESSION:CN545913	C 641	29	1.1	29	1	AZ486793	ACCESSION:AZ486793
C 569	30	1.1	30	1	CN546459	ACCESSION:CN546459	C 642	29	1.1	29	1	AZ661709	ACCESSION:AZ661709
C 570	30	1.1	30	1	CN546474	ACCESSION:CN546474	C 643	29	1.1	29	1	AZ784208	ACCESSION:AZ784208
C 571	30	1.1	30	1	CN546789	ACCESSION:CN546789	C 644	29	1.1	29	1	AZ806470	ACCESSION:AZ806470
C 572	30	1.1	30	1	CV728764	ACCESSION:CV728764	C 645	29	1.1	29	1	AZ812242	ACCESSION:AZ812242
C 573	30	1.1	30	1	CX014987	ACCESSION:CX014987	C 646	29	1.1	29	1	AZ868731	ACCESSION:AZ868731
C 574	30	1.1	30	1	DR073060	ACCESSION:DR073060	C 647	29	1.1	29	1	CZ919318	ACCESSION:CZ919318
C 575	30	1.1	30	1	AZ357603	ACCESSION:AZ357603	C 648	29	1.1	29	1	DU833998	ACCESSION:DU833998
C 576	30	1.1	30	1	AZ455741	ACCESSION:AZ455741	C 649	29	1.1	29	1	DU835145	ACCESSION:DU835145
C 577	30	1.1	30	1	AZ481739	ACCESSION:AZ481739	C 650	29	1.1	29	1	AG193759	ACCESSION:AG193759
C 578	30	1.1	30	1	AZ582114	ACCESSION:AZ582114	C 651	29	1.1	30	1	TA334G09Q	ACCESSION:TA334G09Q
C 579	30	1.1	30	1	CZ917652	ACCESSION:CZ917652	C 652	29	1.1	30	1	BG865511	ACCESSION:BG865511
C 580	30	1.1	30	1	CZ919796	ACCESSION:CZ919796	C 653	29	1.1	30	1	CN545845	ACCESSION:CN545845
C 581	30	1.1	30	1	CW020481	ACCESSION:CW020481	C 654	29	1.1	31	1	CZ514262	ACCESSION:CZ514262
C 582	30	1.1	30	1	DU835531	ACCESSION:DU835531	C 655	29	1.1	32	1	CN546517	ACCESSION:CN546517
C 583	30	1.1	31	1	AG191161	ACCESSION:AG191161	C 656	29	1.1	32	1	DN955775	ACCESSION:DN955775
C 584	30	1.1	31	1	BG292912	ACCESSION:BG292912	C 657	29	1.1	34	1	BU431802	ACCESSION:BU431802
C 585	30	1.1	31	1	CN545579	ACCESSION:CN545579	C 658	29	1.1	35	1	CV064432	ACCESSION:CV064432
C 586	30	1.1	31	1	CN545867	ACCESSION:CN545867	C 659	29	1.1	35	1	AM044046	ACCESSION:AM044046
C 587	30	1.1	31	1	CN545921	ACCESSION:CN545921	C 660	28.8	1.0	32	1	CF318239	ACCESSION:CF318239
C 588	30	1.1	31	1	CN546024	ACCESSION:CN546024	C 661	28.8	1.0	32	1	AZ627842	ACCESSION:AZ627842
C 589	30	1.1	31	1	CN546130	ACCESSION:CN546130	C 662	28.8	1.0	34	1	AJ800678	ACCESSION:AJ800678
C 590	30	1.1	31	1	AZ597046	ACCESSION:AZ597046	C 663	28.8	1.0	36	1	AM043639	ACCESSION:AM043639
C 591	30	1.1	31	1	CZ917966	ACCESSION:CZ917966	C 664	28.4	1.0	30	1	CN546288	ACCESSION:CN546288
C 592	30	1.1	32	1	AZ400441	ACCESSION:AZ400441	C 665	28.4	1.0	30	1	AZ443322	ACCESSION:AZ443322
C 593	30	1.1	33	1	AU013658	ACCESSION:AU013658	C 666	28.4	1.0	30	1	AZ458127	ACCESSION:AZ458127
C 594	30	1.1	33	1	DN955605	ACCESSION:DN955605	C 667	28.4	1.0	30	1	CZ917310	ACCESSION:CZ917310
C 595	30	1.1	35	1	CV066327	ACCESSION:CV066327	C 668	28.4	1.0	30	1	DU833997	ACCESSION:DU833997
C 596	29.8	1.1	33	1	CN545607	ACCESSION:CN545607	C 669	28.4	1.0	32	1	CN546007	ACCESSION:CN546007
C 597	29.8	1.1	33	1	DX050853	ACCESSION:DX050853	C 670	28.4	1.0	33	1	CN546531	ACCESSION:CN546531
C 598	29.8	1.1	37	1	CF301193	ACCESSION:CF301193	C 671	28.4	1.0	33	1	CV725332	ACCESSION:CV725332
C 599	29.6	1.1	36	1	CN546175	ACCESSION:CN546175	C 672	28.4	1.0	34	1	BG531309	ACCESSION:BG531309
C 600	29.6	1.1	37	1	AL587823	ACCESSION:AL587823	C 673	28.4	1.0	34	1	BG612023	ACCESSION:BG612023
C 601	29.4	1.1	31	1	BQ591372	ACCESSION:BQ591372	C 674	28.4	1.0	35	1	CN546161	ACCESSION:CN546161
C 602	29.4	1.1	31	1	CD577356	ACCESSION:CD577356	C 675	28.4	1.0	35	1	CN546416	ACCESSION:CN546416
C 603	29.4	1.1	31	1	CN545785	ACCESSION:CN545785	C 676	28.4	1.0	35	1	CN546519	ACCESSION:CN546519
C 604	29.4	1.1	31	1	CN546374	ACCESSION:CN546374	C 677	28.2	1.0	33	1	AJ791259	ACCESSION:AJ791259
C 605	29.4	1.1	31	1	AZ486763	ACCESSION:AZ486763	C 678	28.2	1.0	33	1	CF335736	ACCESSION:CF335736
C 606	29.4	1.1	31	1	AZ785111	ACCESSION:AZ785111	C 679	28.2	1.0	33	1	CZ919845	ACCESSION:CZ919845
C 607	29.4	1.1	31	1	DU835198	ACCESSION:DU835198	C 680	28.2	1.0	33	1	DR85L9T	ACCESSION:DR85L9T
C 608	29.4	1.1	31	1	DX033882	ACCESSION:DX033882	C 681	28.2	1.0	34	1	CN973659	ACCESSION:CN973659
C 609	29.4	1.1	32	1	AL038680	ACCESSION:AL038680	C 682	28.2	1.0	35	1	AJ746854	ACCESSION:AJ746854
C 610	29.4	1.1	34	1	CN545857	ACCESSION:CN545857	C 683	28	1.0	28	1	AJ666435	ACCESSION:AJ666435
C 611	29.4	1.1	34	1	CN546360	ACCESSION:CN546360	C 684	28	1.0	28	1	AM043789	ACCESSION:AM043789
C 612	29.4	1.1	34	1	CN546656	ACCESSION:CN546656	C 685	28	1.0	28	1	AM043903	ACCESSION:AM043903
C 613	29.4	1.1	35	1	CN545982	ACCESSION:CN545982	C 686	28	1.0	28	1	AM043968	ACCESSION:AM043968
C 614	29.4	1.1	35	1	CN546734	ACCESSION:CN546734	C 687	28	1.0	28	1	AM044512	ACCESSION:AM044512
C 615	29.4	1.1	36	1	AL036993	ACCESSION:AL036993	C 688	28	1.0	28	1	CF282351	ACCESSION:CF282351
C 616	29.4	1.1	36	1	CN545377	ACCESSION:CN545377	C 689	28	1.0	28	1	CF321885	ACCESSION:CF321885
C 617	29.4	1.1	36	1	CN546215	ACCESSION:CN546215	C 690	28	1.0	28	1	CF330748	ACCESSION:CF330748

691	28	1.0	28	1	CF330938	ACCESSION:CF330938	C 764	27	1.0	27	1	DR072930	ACCESSION:DR072930
C 692	28	1.0	28	1	CN546364	ACCESSION:CN546364	C 765	27	1.0	27	1	AZ344642	ACCESSION:AZ344642
C 693	28	1.0	28	1	CN546703	ACCESSION:CN546703	C 766	27	1.0	27	1	AZ401672	ACCESSION:AZ401672
C 694	28	1.0	28	1	DR073098	ACCESSION:DR073098	C 767	27	1.0	27	1	AZ486791	ACCESSION:AZ486791
C 695	28	1.0	28	1	AZ399637	ACCESSION:AZ399637	C 768	27	1.0	27	1	AZ511894	ACCESSION:AZ511894
C 696	28	1.0	28	1	AZ401766	ACCESSION:AZ401766	C 769	27	1.0	27	1	AZ580921	ACCESSION:AZ580921
C 697	28	1.0	28	1	AZ471744	ACCESSION:AZ471744	C 770	27	1.0	27	1	AZ616094	ACCESSION:AZ616094
C 698	28	1.0	28	1	AZ493138	ACCESSION:AZ493138	C 771	27	1.0	27	1	AZ623186	ACCESSION:AZ623186
C 699	28	1.0	28	1	AZ553365	ACCESSION:AZ553365	C 772	27	1.0	27	1	AZ627847	ACCESSION:AZ627847
C 700	28	1.0	28	1	AZ785035	ACCESSION:AZ785035	C 773	27	1.0	27	1	AZ809295	ACCESSION:AZ809295
C 701	28	1.0	28	1	AZ824519	ACCESSION:AZ824519	C 774	27	1.0	27	1	AZ917070	ACCESSION:AZ917070
C 702	28	1.0	28	1	AZ833425	ACCESSION:AZ833425	C 775	27	1.0	27	1	DX046035	ACCESSION:DX046035
C 703	28	1.0	28	1	AZ866569	ACCESSION:AZ866569	C 776	27	1.0	27	1	DX056021	ACCESSION:DX056021
C 704	28	1.0	28	1	CZ912316	ACCESSION:CZ912316	C 777	27	1.0	27	1	AG829428	ACCESSION:AG829428
C 705	28	1.0	28	1	CZ913960	ACCESSION:CZ913960	C 778	27	1.0	27	1	TA355806P	ACCESSION:TA355806P
C 706	28	1.0	28	1	DU828712	ACCESSION:DU828712	C 779	27	1.0	28	1	AL048439	ACCESSION:AL048439
C 707	28	1.0	28	1	DU835260	ACCESSION:DU835260	C 780	27	1.0	28	1	CF322082	ACCESSION:CF322082
C 708	28	1.0	28	1	DU835584	ACCESSION:DU835584	C 781	27	1.0	28	1	CF337400	ACCESSION:CF337400
C 709	28	1.0	28	1	DX072153	ACCESSION:DX072153	C 782	27	1.0	28	1	CN545498	ACCESSION:CN545498
C 710	28	1.0	28	1	TA291A01Q	ACCESSION:AL486613	C 783	27	1.0	28	1	CN546292	ACCESSION:CN546292
C 711	28	1.0	28	1	TA379D11P	ACCESSION:AL497637	C 784	27	1.0	28	1	CN546304	ACCESSION:CN546304
C 712	28	1.0	29	1	CN545883	ACCESSION:CN545883	C 785	27	1.0	28	1	DN988459	ACCESSION:DN988459
C 713	28	1.0	29	1	CZ912823	ACCESSION:CZ912823	C 786	27	1.0	28	1	CZ918534	ACCESSION:CZ918534
C 714	28	1.0	29	1	CZ914240	ACCESSION:CZ914240	C 787	27	1.0	32	1	CA853459	ACCESSION:CA853459
C 715	28	1.0	30	1	CN545968	ACCESSION:CN545968	C 788	27	1.0	32	1	R16114	ACCESSION:R16114
C 716	28	1.0	30	1	CN546523	ACCESSION:CN546523	C 789	26.8	1.0	30	1	CZ913832	ACCESSION:CZ913832
C 717	28	1.0	30	1	CZ919540	ACCESSION:CZ919540	C 790	26.8	1.0	32	1	CZ913296	ACCESSION:CZ913296
C 718	28	1.0	31	1	AW245279	ACCESSION:AW245279	C 791	26.8	1.0	32	1	CV733741	ACCESSION:CV733741
C 719	28	1.0	31	1	CV057897	ACCESSION:CV057897	C 792	26.6	1.0	33	1	CF300359	ACCESSION:CF300359
C 720	28	1.0	32	1	AM046790	ACCESSION:AM046790	C 793	26.4	1.0	28	1	CF307749	ACCESSION:CF307749
C 721	28	1.0	32	1	CD577661	ACCESSION:CD577661	C 794	26.4	1.0	28	1	AW332443	ACCESSION:AW332443
C 722	28	1.0	32	1	A2397471	ACCESSION:A2397471	C 795	26.4	1.0	28	1	CN545659	ACCESSION:CN545659
C 723	28	1.0	33	1	AV743346	ACCESSION:AV743346	C 796	26.4	1.0	28	1	CK001046	ACCESSION:CK001046
C 724	27.8	1.0	31	1	AW249485	ACCESSION:AW249485	C 797	26.4	1.0	28	1	DR062845	ACCESSION:DR062845
C 725	27.8	1.0	31	1	CX014884	ACCESSION:CX014884	C 798	26.4	1.0	28	1	AZ514352	ACCESSION:AZ514352
C 726	27.8	1.0	33	1	CV727574	ACCESSION:CV727574	C 799	26.4	1.0	28	1	AZ824574	ACCESSION:AZ824574
C 727	27.6	1.0	34	1	AJ656734	ACCESSION:AJ656734	C 800	26.4	1.0	28	1	CZ916890	ACCESSION:CZ916890
C 728	27.6	1.0	34	1	BQ594010	ACCESSION:BQ594010	C 801	26.4	1.0	28	1	TA29A09P	ACCESSION:TA29A09P
C 729	27.4	1.0	29	1	BQ590537	ACCESSION:BQ590537	C 802	26.4	1.0	29	1	CF328476	ACCESSION:CF328476
C 730	27.4	1.0	29	1	CN545226	ACCESSION:CN545226	C 803	26.2	1.0	31	1	CF328476	ACCESSION:CF328476
C 731	27.4	1.0	29	1	CN545618	ACCESSION:CN545618	C 804	26.2	1.0	31	1	CF297930	ACCESSION:CF297930
C 732	27.4	1.0	29	1	CN546518	ACCESSION:CN546518	C 805	26.2	1.0	32	1	AZ451251	ACCESSION:AZ451251
C 733	27.4	1.0	29	1	AZ825156	ACCESSION:AZ825156	C 806	26	0.9	26	1	AM043187	ACCESSION:AM043187
C 734	27.4	1.0	29	1	CZ914157	ACCESSION:CZ914157	C 807	26	0.9	26	1	AM045920	ACCESSION:AM045920
C 735	27.4	1.0	29	1	DU834266	ACCESSION:DU834266	C 808	26	0.9	26	1	AM045920	ACCESSION:AM045920
C 736	27.4	1.0	30	1	AL038672	ACCESSION:AL038672	C 809	26	0.9	26	1	AM045959	ACCESSION:AM045959
C 737	27.4	1.0	30	1	DU677300	ACCESSION:DU677300	C 810	26	0.9	26	1	AM047208	ACCESSION:AM047208
C 738	27.4	1.0	30	1	CN546316	ACCESSION:CN546316	C 811	26	0.9	26	1	CF278359	ACCESSION:CF278359
C 739	27.4	1.0	30	1	DR31A15T	ACCESSION:AL987581	C 812	26	0.9	26	1	CF282426	ACCESSION:CF282426
C 740	27.4	1.0	33	1	CN545916	ACCESSION:CN545916	C 813	26	0.9	26	1	CF297087	ACCESSION:CF297087
C 741	27.4	1.0	33	1	AZ759842	ACCESSION:AZ759842	C 814	26	0.9	26	1	CF297087	ACCESSION:CF297087
C 742	27.4	1.0	34	1	DN988790	ACCESSION:DN988790	C 815	26	0.9	26	1	CF302874	ACCESSION:CF302874
C 743	27.2	1.0	32	1	CF298526	ACCESSION:CF298526	C 816	26	0.9	26	1	CF311369	ACCESSION:CF311369
C 744	27.2	1.0	32	1	CF334956	ACCESSION:CF334956	C 817	26	0.9	26	1	CF311439	ACCESSION:CF311439
C 745	27.2	1.0	32	1	AW250841	ACCESSION:AW250841	C 818	26	0.9	26	1	AW327613	ACCESSION:AW327613
C 746	27.2	1.0	32	1	CZ467504	ACCESSION:CZ467504	C 819	26	0.9	26	1	CN545213	ACCESSION:CN545213
C 747	27	1.0	27	1	AM048211	ACCESSION:AM048211	C 820	26	0.9	26	1	CN545225	ACCESSION:CN545225
C 748	27	1.0	27	1	CF291968	ACCESSION:CF291968	C 821	26	0.9	26	1	CN545546	ACCESSION:CN545546
C 749	27	1.0	27	1	CF329725	ACCESSION:CF329725	C 822	26	0.9	26	1	CN545888	ACCESSION:CN545888
C 750	27	1.0	27	1	CF330557	ACCESSION:CF330557	C 823	26	0.9	26	1	CN546608	ACCESSION:CN546608
C 751	27	1.0	27	1	CF335229	ACCESSION:CF335229	C 824	26	0.9	26	1	CN546649	ACCESSION:CN546649
C 752	27	1.0	27	1	AW327923	ACCESSION:AW327923	C 825	26	0.9	26	1	DN953783	ACCESSION:DN953783
C 753	27	1.0	27	1	CN545326	ACCESSION:CN545326	C 826	26	0.9	26	1	DN955188	ACCESSION:DN955188
C 754	27	1.0	27	1	CN545492	ACCESSION:CN545492	C 827	26	0.9	26	1	DR073125	ACCESSION:DR073125
C 755	27	1.0	27	1	CN545530	ACCESSION:CN545530	C 828	26	0.9	26	1	AZ359871	ACCESSION:AZ359871
C 756	27	1.0	27	1	CN545597	ACCESSION:CN545597	C 829	26	0.9	26	1	AZ376664	ACCESSION:AZ376664
C 757	27	1.0	27	1	CN545938	ACCESSION:CN545938	C 830	26	0.9	26	1	AZ389765	ACCESSION:AZ389765
C 758	27	1.0	27	1	CN545962	ACCESSION:CN545962	C 831	26	0.9	26	1	AZ414673	ACCESSION:AZ414673
C 759	27	1.0	27	1	CN546052	ACCESSION:CN546052	C 832	26	0.9	26	1	AZ593300	ACCESSION:AZ593300
C 760	27	1.0	27	1	CN546271	ACCESSION:CN546271	C 833	26	0.9	26	1	AZ612722	ACCESSION:AZ612722
C 761	27	1.0	27	1	CN546337	ACCESSION:CN546337	C 834	26	0.9	26	1	AZ624441	ACCESSION:AZ624441
C 762	27	1.0	27	1	CN546559	ACCESSION:CN546559	C 835	26	0.9	26	1	AZ627846	ACCESSION:AZ627846
C 763	27	1.0	27	1	CN546574	ACCESSION:CN546574	C 836	26	0.9	26	1	AZ652515	ACCESSION:AZ652515

C 837	26	0.9	26	1	AZ800453	ACCSSION:AZ800453	C 910	25	0.9	26	1	AL587774	ACCSSION:AL587774
C 838	26	0.9	26	1	AZ963974	ACCSSION:AZ963974	C 911	25	0.9	26	1	AM048107	ACCSSION:AM048107
C 839	26	0.9	26	1	CZ490199	ACCSSION:CZ490199	C 912	25	0.9	26	1	CF296851	ACCSSION:CF296851
C 840	26	0.9	26	1	CZ910095	ACCSSION:CZ910095	C 913	25	0.9	26	1	CN545723	ACCSSION:CN545723
C 841	26	0.9	26	1	DUB32827	ACCSSION:DUB32827	C 914	25	0.9	27	1	AJ789548	ACCSSION:AJ789548
C 842	26	0.9	26	1	DUB35360	ACCSSION:DUB35360	C 915	25	0.9	31	1	TA444G08P	ACCSSION:TA444G08P
C 843	26	0.9	26	1	DX034224	ACCSSION:DX034224	C 916	24.8	0.9	28	1	CZ469056	ACCSSION:CZ469056
C 844	26	0.9	26	1	TA324D07P	ACCSSION:TA324D07P	C 917	24.4	0.9	26	1	AM042970	ACCSSION:AM042970
C 845	26	0.9	27	1	CN545777	ACCSSION:CN545777	C 918	24.4	0.9	26	1	CR546444	ACCSSION:CR546444
C 846	26	0.9	27	1	CN545880	ACCSSION:CN545880	C 919	24.4	0.9	26	1	AZ355083	ACCSSION:AZ355083
C 847	26	0.9	27	1	TA257B07P	ACCSSION:TA257B07P	C 920	24.4	0.9	26	1	AZ623156	ACCSSION:AZ623156
C 848	26	0.9	27	1	TA257B07P	ACCSSION:TA257B07P	C 921	24.4	0.9	26	1	AZ635695	ACCSSION:AZ635695
C 849	26	0.9	29	1	AJ658314	ACCSSION:AJ658314	C 922	24.4	0.9	26	1	CZ917641	ACCSSION:CZ917641
C 850	26	0.9	30	1	AZ819924	ACCSSION:AZ819924	C 923	24.4	0.9	26	1	CZ919575	ACCSSION:CZ919575
C 851	26	0.9	30	1	CN545889	ACCSSION:CN545889	C 924	24.4	0.9	26	1	AG201580	ACCSSION:AG201580
C 852	26	0.9	30	1	AZ962183	ACCSSION:AZ962183	C 925	24.4	0.9	27	1	DT471186	ACCSSION:DT471186
C 853	26	0.9	31	1	AM044314	ACCSSION:AM044314	C 926	24.4	0.9	27	1	N52529	ACCSSION:N52529
C 854	26	0.9	32	1	CD577496	ACCSSION:CD577496	C 927	24.4	0.9	27	1	AZ862643	ACCSSION:AZ862643
C 855	25.8	0.9	29	1	BQ583967	ACCSSION:BQ583967	C 928	24.4	0.9	28	1	CF299294	ACCSSION:CF299294
C 856	25.8	0.9	29	1	CN545957	ACCSSION:CN545957	C 929	24.4	0.9	28	1	T52836	ACCSSION:T52836
C 857	25.6	0.9	32	1	R59306	ACCSSION:R59306	C 930	24.4	0.9	28	1	AZ481286	ACCSSION:AZ481286
C 858	25.6	0.9	32	1	AZ326012	ACCSSION:AZ326012	C 931	24.4	0.9	29	1	CF299155	ACCSSION:CF299155
C 859	25.6	0.9	32	1	CZ915120	ACCSSION:CZ915120	C 932	24.2	0.9	29	1	DR073498	ACCSSION:DR073498
C 860	25.6	0.9	32	1	CZ918635	ACCSSION:CZ918635	C 933	24.2	0.9	29	1	CL693162	ACCSSION:CL693162
C 861	25.4	0.9	27	1	AZ434285	ACCSSION:AZ434285	C 934	24.2	0.9	29	1	TA378G07P	ACCSSION:TA378G07P
C 862	25.4	0.9	27	1	AZ458228	ACCSSION:AZ458228	C 935	24	0.9	24	1	AJ921827	ACCSSION:AJ921827
C 863	25.4	0.9	27	1	AZ941721	ACCSSION:AZ941721	C 936	24	0.9	24	1	AM043978	ACCSSION:AM043978
C 864	25.4	0.9	27	1	AZ970621	ACCSSION:AZ970621	C 937	24	0.9	24	1	AM045511	ACCSSION:AM045511
C 865	25.4	0.9	27	1	DX070376	ACCSSION:DX070376	C 938	24	0.9	24	1	AM046329	ACCSSION:AM046329
C 866	25.4	0.9	28	1	R37697	ACCSSION:R37697	C 939	24	0.9	24	1	AM048042	ACCSSION:AM048042
C 867	25.4	0.9	28	1	T56352	ACCSSION:T56352	C 940	24	0.9	24	1	BG670391	ACCSSION:BG670391
C 868	25.4	0.9	28	1	AZ836072	ACCSSION:AZ836072	C 941	24	0.9	24	1	BS554611	ACCSSION:BS554611
C 869	25.2	0.9	30	1	CF299716	ACCSSION:CF299716	C 942	24	0.9	24	1	CF276855	ACCSSION:CF276855
C 870	25.2	0.9	30	1	CZ919253	ACCSSION:CZ919253	C 943	24	0.9	24	1	CF301561	ACCSSION:CF301561
C 871	25.2	0.9	31	1	DX082113	ACCSSION:DX082113	C 944	24	0.9	24	1	CF320862	ACCSSION:CF320862
C 872	25.2	0.9	31	1	CZ918715	ACCSSION:CZ918715	C 945	24	0.9	24	1	CN545449	ACCSSION:CN545449
C 873	25	0.9	25	1	CF291048	ACCSSION:CF291048	C 946	24	0.9	24	1	CN545307	ACCSSION:CN545307
C 874	25	0.9	25	1	CF291646	ACCSSION:CF291646	C 947	24	0.9	24	1	CN545657	ACCSSION:CN545657
C 875	25	0.9	25	1	CF299288	ACCSSION:CF299288	C 948	24	0.9	24	1	CN545784	ACCSSION:CN545784
C 876	25	0.9	25	1	CF300333	ACCSSION:CF300333	C 949	24	0.9	24	1	CN546689	ACCSSION:CN546689
C 877	25	0.9	25	1	CF316323	ACCSSION:CF316323	C 950	24	0.9	24	1	DR073080	ACCSSION:DR073080
C 878	25	0.9	25	1	CF317714	ACCSSION:CF317714	C 951	24	0.9	24	1	DR074082	ACCSSION:DR074082
C 879	25	0.9	25	1	CF319073	ACCSSION:CF319073	C 952	24	0.9	24	1	AZ328848	ACCSSION:AZ328848
C 880	25	0.9	25	1	CF330786	ACCSSION:CF330786	C 953	24	0.9	24	1	AZ363562	ACCSSION:AZ363562
C 881	25	0.9	25	1	CN545505	ACCSSION:CN545505	C 954	24	0.9	24	1	AZ386491	ACCSSION:AZ386491
C 882	25	0.9	25	1	CN546041	ACCSSION:CN546041	C 955	24	0.9	24	1	AZ390642	ACCSSION:AZ390642
C 883	25	0.9	25	1	CN546397	ACCSSION:CN546397	C 956	24	0.9	24	1	AZ459280	ACCSSION:AZ459280
C 884	25	0.9	25	1	CN546477	ACCSSION:CN546477	C 957	24	0.9	24	1	AZ644621	ACCSSION:AZ644621
C 885	25	0.9	25	1	CN546728	ACCSSION:CN546728	C 958	24	0.9	24	1	AZ834990	ACCSSION:AZ834990
C 886	25	0.9	25	1	CV999835	ACCSSION:CV999835	C 959	24	0.9	24	1	AZ970038	ACCSSION:AZ970038
C 887	25	0.9	25	1	DR073093	ACCSSION:DR073093	C 960	24	0.9	24	1	AZ984490	ACCSSION:AZ984490
C 888	25	0.9	25	1	DR073104	ACCSSION:DR073104	C 961	24	0.9	24	1	AZ993423	ACCSSION:AZ993423
C 889	25	0.9	25	1	DR073105	ACCSSION:DR073105	C 962	24	0.9	24	1	DUB29467	ACCSSION:DUB29467
C 890	25	0.9	25	1	DR073133	ACCSSION:DR073133	C 963	24	0.9	24	1	DUB30197	ACCSSION:DUB30197
C 891	25	0.9	25	1	L32039	ACCSSION:L32039	C 964	24	0.9	24	1	DX047568	ACCSSION:DX047568
C 892	25	0.9	25	1	AZ344725	ACCSSION:AZ344725	C 965	24	0.9	24	1	DX053980	ACCSSION:DX053980
C 893	25	0.9	25	1	AZ350777	ACCSSION:AZ350777	C 966	24	0.9	24	1	DX072040	ACCSSION:DX072040
C 894	25	0.9	25	1	AZ389458	ACCSSION:AZ389458	C 967	24	0.9	24	1	DX080492	ACCSSION:DX080492
C 895	25	0.9	25	1	AZ609234	ACCSSION:AZ609234	C 968	24	0.9	24	1	DX082296	ACCSSION:DX082296
C 896	25	0.9	25	1	AZ623157	ACCSSION:AZ623157	C 969	24	0.9	24	1	DX082296	ACCSSION:DX082296
C 897	25	0.9	25	1	AZ788646	ACCSSION:AZ788646	C 970	24	0.9	24	1	TA169D12P	ACCSSION:TA169D12P
C 898	25	0.9	25	1	AZ949287	ACCSSION:AZ949287	C 971	24	0.9	24	1	TA27B08Q	ACCSSION:TA27B08Q
C 899	25	0.9	25	1	AZ980407	ACCSSION:AZ980407	C 972	24	0.9	24	1	TA354C06P	ACCSSION:TA354C06P
C 900	25	0.9	25	1	CZ914066	ACCSSION:CZ914066	C 973	24	0.9	24	1	TA371F11P	ACCSSION:TA371F11P
C 901	25	0.9	25	1	CZ918479	ACCSSION:CZ918479	C 974	24	0.9	24	1	TA95B08P	ACCSSION:TA95B08P
C 902	25	0.9	25	1	DUB29648	ACCSSION:DUB29648	C 975	24	0.9	25	1	AL587648	ACCSSION:AL587648
C 903	25	0.9	25	1	DUB32111	ACCSSION:DUB32111	C 976	24	0.9	25	1	CF317007	ACCSSION:CF317007
C 904	25	0.9	25	1	DUB34405	ACCSSION:DUB34405	C 977	24	0.9	25	1	CF638767	ACCSSION:CF638767
C 905	25	0.9	25	1	DUB34424	ACCSSION:DUB34424	C 978	24	0.9	25	1	N33150	ACCSSION:N33150
C 906	25	0.9	25	1	DUB34577	ACCSSION:DUB34577	C 979	24	0.9	25	1	AZ381039	ACCSSION:AZ381039
C 907	25	0.9	25	1	DX075967	ACCSSION:DX075967	C 980	24	0.9	26	1	CF639306	ACCSSION:CF639306
C 908	25	0.9	25	1	TA324E10P	ACCSSION:TA324E10P	C 981	24	0.9	27	1	R31539	ACCSSION:R31539
C 909	25	0.9	26	1	AL038686	ACCSSION:AL038686	C 982	24	0.9	28	1	AZ358038	ACCSSION:AZ358038

c 983	23.8	0.9	27	1	CF299084	ACCESSION:CF299084	c1056	23	0.8	27	1	N34459	ACCESSION:N34459
c 984	23.8	0.9	27	1	CF318113	ACCESSION:CF318113	c1057	23	0.8	28	1	AJ922998	ACCESSION:AJ922998
c 985	23.8	0.9	27	1	R59382	ACCESSION:R59382	1058	23	0.8	28	1	DX072773	ACCESSION:DX072773
c 986	23.8	0.9	28	1	C2914142	ACCESSION:C2914142	c1059	22.8	0.8	26	1	BM658913	ACCESSION:BM658913
c 987	23.8	0.9	28	1	DX071727	ACCESSION:DX071727	c1060	22.8	0.8	26	1	BM658913	ACCESSION:BM658913
c 988	23.4	0.9	25	1	A2404078	ACCESSION:A2404078	c1061	22.8	0.8	26	1	BM658913	ACCESSION:BM658913
c 989	23.4	0.9	25	1	DUB333936	ACCESSION:DUB333936	c1062	22.8	0.8	27	1	CM020478	ACCESSION:CM020478
c 990	23.4	0.9	25	1	DUB34323	ACCESSION:DUB34323	c1063	22.8	0.8	27	1	C2908520	ACCESSION:C2908520
c 991	23.4	0.9	26	1	CF299646	ACCESSION:CF299646	c1064	22.8	0.8	28	1	CV091538	ACCESSION:CV091538
c 992	23.4	0.9	26	1	A2316353	ACCESSION:A2316353	c1065	22.4	0.8	28	1	TA327D04P	ACCESSION:TA327D04P
c 993	23.4	0.9	28	1	AL587582	ACCESSION:AL587582	c1066	22.4	0.8	24	1	CF281313	ACCESSION:CF281313
c 994	23.4	0.9	28	1	AU257468	ACCESSION:AU257468	c1067	22.4	0.8	24	1	AW247159	ACCESSION:AW247159
c 995	23.4	0.9	29	1	DR064440	ACCESSION:DR064440	c1068	22.4	0.8	24	1	A2438069	ACCESSION:A2438069
c 996	23.4	0.9	29	1	DR072912	ACCESSION:DR072912	c1069	22.4	0.8	24	1	A2458112	ACCESSION:A2458112
c 997	23.4	0.9	29	1	T67079	ACCESSION:T67079	c1070	22.4	0.8	24	1	A2607198	ACCESSION:A2607198
c 998	23.2	0.8	28	1	AA852828	ACCESSION:AA852828	c1071	22.4	0.8	24	1	AZ621257	ACCESSION:AZ621257
c 999	23.2	0.8	29	1	CF314795	ACCESSION:CF314795	c1072	22.4	0.8	24	1	DUB35497	ACCESSION:DUB35497
c1000	23.2	0.8	29	1	DR074680	ACCESSION:DR074680	c1073	22.4	0.8	24	1	DX045709	ACCESSION:DX045709
c1001	23.2	0.8	29	1	A2827060	ACCESSION:A2827060	c1074	22.4	0.8	27	1	N27663	ACCESSION:N27663
c1002	23.2	0.8	29	1	C2171125	ACCESSION:C2171125	1075	22.4	0.8	27	1	CF310745	ACCESSION:CF310745
c1003	23	0.8	23	1	AJ695799	ACCESSION:AJ695799	1076	22.4	0.8	28	1	AL039138	ACCESSION:AL039138
c1004	23	0.8	23	1	AJ747297	ACCESSION:AJ747297	c1077	22.2	0.8	28	1	DX082097	ACCESSION:DX082097
c1005	23	0.8	23	1	AM044732	ACCESSION:AM044732	c1078	22.2	0.8	27	1	CF298133	ACCESSION:CF298133
c1006	23	0.8	23	1	AM047142	ACCESSION:AM047142	c1079	22.2	0.8	27	1	CF328811	ACCESSION:CF328811
c1007	23	0.8	23	1	CF279238	ACCESSION:CF279238	c1080	22.2	0.8	27	1	CF333518	ACCESSION:CF333518
c1008	23	0.8	23	1	CF297943	ACCESSION:CF297943	c1081	22.2	0.8	27	1	N89936	ACCESSION:N89936
c1009	23	0.8	23	1	CF310501	ACCESSION:CF310501	1082	22	0.8	27	1	CL654516	ACCESSION:CL654516
c1010	23	0.8	23	1	CF319212	ACCESSION:CF319212	c1083	22	0.8	22	1	AJ747407	ACCESSION:AJ747407
c1011	23	0.8	23	1	CF322953	ACCESSION:CF322953	c1084	22	0.8	22	1	CF299342	ACCESSION:CF299342
c1012	23	0.8	23	1	CF329042	ACCESSION:CF329042	c1085	22	0.8	22	1	CF300133	ACCESSION:CF300133
c1013	23	0.8	23	1	CF334657	ACCESSION:CF334657	c1086	22	0.8	22	1	CF310366	ACCESSION:CF310366
c1014	23	0.8	23	1	CM545940	ACCESSION:CM545940	1087	22	0.8	22	1	CF311269	ACCESSION:CF311269
c1015	23	0.8	23	1	CM546520	ACCESSION:CM546520	1088	22	0.8	22	1	CF311713	ACCESSION:CF311713
c1016	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1089	22	0.8	22	1	CF312498	ACCESSION:CF312498
c1017	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1090	22	0.8	22	1	CF330679	ACCESSION:CF330679
c1018	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1091	22	0.8	22	1	CF333430	ACCESSION:CF333430
c1019	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1092	22	0.8	22	1	CF334781	ACCESSION:CF334781
c1020	23	0.8	23	1	CM577495	ACCESSION:CM577495	1093	22	0.8	22	1	CF336250	ACCESSION:CF336250
c1021	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1094	22	0.8	22	1	CF337580	ACCESSION:CF337580
c1022	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1095	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1023	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1096	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1024	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1097	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1025	23	0.8	23	1	CM577495	ACCESSION:CM577495	1098	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1026	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1100	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1027	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1101	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1028	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1102	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1029	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1103	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1030	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1104	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1031	23	0.8	23	1	CM577495	ACCESSION:CM577495	1105	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1032	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1106	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1033	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1107	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1034	23	0.8	23	1	CM577495	ACCESSION:CM577495	1108	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1035	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1109	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1036	23	0.8	23	1	CM577495	ACCESSION:CM577495	1110	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1037	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1111	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1038	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1112	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1039	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1113	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1040	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1114	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1041	23	0.8	23	1	CM577495	ACCESSION:CM577495	1115	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1042	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1116	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1043	23	0.8	23	1	CM577495	ACCESSION:CM577495	1117	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1044	23	0.8	23	1	CM577495	ACCESSION:CM577495	1118	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1045	23	0.8	23	1	CM577495	ACCESSION:CM577495	1119	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1046	23	0.8	23	1	CM577495	ACCESSION:CM577495	1120	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1047	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1121	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1048	23	0.8	23	1	CM577495	ACCESSION:CM577495	1122	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1049	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1123	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1050	23	0.8	23	1	CM577495	ACCESSION:CM577495	1124	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1051	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1125	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1052	23	0.8	23	1	CM577495	ACCESSION:CM577495	1126	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1053	23	0.8	23	1	CM577495	ACCESSION:CM577495	c1127	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1054	23	0.8	23	1	CM577495	ACCESSION:CM577495	1128	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1055	23	0.8	23	1	CM577495	ACCESSION:CM577495	1129	22	0.8	22	1	CF338524	ACCESSION:CF338524

c1129	22	0.8	22	1	AZ843514	ACCSSION:AZ843514	1202	21	0.8	21	1	CF338057	ACCSSION:CF338057
c1130	22	0.8	22	1	AZ946102	ACCSSION:AZ946102	c1203	21	0.8	21	1	CF338522	ACCSSION:CF338522
c1131	22	0.8	22	1	DUB34428	ACCSSION:DUB34428	c1204	21	0.8	21	1	CN546489	ACCSSION:CN546489
c1132	22	0.8	22	1	DUB35320	ACCSSION:DUB35320	c1205	21	0.8	21	1	CN546504	ACCSSION:CN546504
c1133	22	0.8	22	1	DX033920	ACCSSION:DX033920	c1206	21	0.8	21	1	CN546595	ACCSSION:CN546595
c1134	22	0.8	22	1	DX046124	ACCSSION:DX046124	c1207	21	0.8	21	1	COT79794	ACCSSION:COT79794
c1135	22	0.8	22	1	DX056961	ACCSSION:DX056961	c1208	21	0.8	21	1	DR063419	ACCSSION:DR063419
c1136	22	0.8	22	1	DX069868	ACCSSION:DX069868	c1209	21	0.8	21	1	DR072918	ACCSSION:DR072918
c1137	22	0.8	22	1	DX080494	ACCSSION:DX080494	c1210	21	0.8	21	1	AZ348593	ACCSSION:AZ348593
c1138	22	0.8	22	1	AG194579	ACCSSION:AG194579	c1211	21	0.8	21	1	AZ350611	ACCSSION:AZ350611
c1139	22	0.8	22	1	TA131B09P	ACCSSION:AL464164	c1212	21	0.8	21	1	AZ386711	ACCSSION:AZ386711
c1140	22	0.8	22	1	TA329F10P	ACCSSION:AL492691	c1213	21	0.8	21	1	AZ386794	ACCSSION:AZ386794
c1141	22	0.8	22	1	TA35C12Q	ACCSSION:AL44256	c1214	21	0.8	21	1	AZ389287	ACCSSION:AZ389287
c1142	22	0.8	22	1	TA380A07P	ACCSSION:AL497713	c1215	21	0.8	21	1	AZ389687	ACCSSION:AZ389687
c1143	22	0.8	23	1	CF329694	ACCSSION:CF329694	c1216	21	0.8	21	1	AZ406936	ACCSSION:AZ406936
c1144	22	0.8	23	1	CF332379	ACCSSION:CF332379	c1217	21	0.8	21	1	AZ412739	ACCSSION:AZ412739
c1145	22	0.8	23	1	DT495201	ACCSSION:DT495201	c1218	21	0.8	21	1	AZ412931	ACCSSION:AZ412931
c1146	22	0.8	23	1	AZ425710	ACCSSION:AZ425710	c1219	21	0.8	21	1	AZ415029	ACCSSION:AZ415029
c1147	22	0.8	23	1	AZ801003	ACCSSION:AZ801003	c1220	21	0.8	21	1	AZ465890	ACCSSION:AZ465890
c1148	22	0.8	24	1	CAB53764	ACCSSION:CAB53764	c1221	21	0.8	21	1	AZ611116	ACCSSION:AZ611116
c1149	22	0.8	24	1	CF312319	ACCSSION:CF312319	c1222	21	0.8	21	1	AZ611423	ACCSSION:AZ611423
c1150	22	0.8	24	1	AZ812579	ACCSSION:AZ812579	c1223	21	0.8	21	1	AZ615628	ACCSSION:AZ615628
c1151	22	0.8	25	1	N59260	ACCSSION:N59260	c1224	21	0.8	21	1	AZ627843	ACCSSION:AZ627843
c1152	22	0.8	25	1	CZ914626	ACCSSION:CZ914626	c1225	21	0.8	21	1	AZ627845	ACCSSION:AZ627845
c1153	22	0.8	25	1	CZ916641	ACCSSION:CZ916641	c1226	21	0.8	21	1	AZ657727	ACCSSION:AZ657727
c1154	22	0.8	25	1	TA154D03P	ACCSSION:AL472971	c1227	21	0.8	21	1	AZ766952	ACCSSION:AZ766952
c1155	22	0.8	27	1	AM046273	ACCSSION:AM046273	c1228	21	0.8	21	1	AZ769976	ACCSSION:AZ769976
c1156	22	0.8	27	1	CZ914111	ACCSSION:CZ914111	c1229	21	0.8	21	1	AZ793486	ACCSSION:AZ793486
c1157	21.8	0.8	25	1	CF319499	ACCSSION:CF319499	c1230	21	0.8	21	1	AZ799327	ACCSSION:AZ799327
c1158	21.8	0.8	25	1	AW249476	ACCSSION:AW249476	c1231	21	0.8	21	1	AZ810054	ACCSSION:AZ810054
c1159	21.8	0.8	25	1	DN954014	ACCSSION:DN954014	c1232	21	0.8	21	1	AZ815424	ACCSSION:AZ815424
c1160	21.8	0.8	25	1	CF30737	ACCSSION:CF30737	c1233	21	0.8	21	1	AZ819181	ACCSSION:AZ819181
c1161	21.8	0.8	25	1	AZ442170	ACCSSION:AZ442170	c1234	21	0.8	21	1	AZ832198	ACCSSION:AZ832198
c1162	21.8	0.8	25	1	DX053323	ACCSSION:DX053323	c1235	21	0.8	21	1	AZ843603	ACCSSION:AZ843603
c1163	21.8	0.8	26	1	CF337311	ACCSSION:CF337311	c1236	21	0.8	21	1	AZ960063	ACCSSION:AZ960063
c1164	21.4	0.8	23	1	CF334077	ACCSSION:CF334077	c1237	21	0.8	21	1	BH000837	ACCSSION:BH000837
c1165	21.4	0.8	23	1	DR072900	ACCSSION:DR072900	c1238	21	0.8	21	1	DUB28985	ACCSSION:DUB28985
c1166	21.4	0.8	23	1	DT501689	ACCSSION:DT501689	c1239	21	0.8	21	1	DUB30099	ACCSSION:DUB30099
c1167	21.4	0.8	23	1	AZ382013	ACCSSION:AZ382013	c1240	21	0.8	21	1	DUB32906	ACCSSION:DUB32906
c1168	21.4	0.8	23	1	AZ486853	ACCSSION:AZ486853	c1241	21	0.8	21	1	DUB34573	ACCSSION:DUB34573
c1169	21.4	0.8	23	1	AZ627841	ACCSSION:AZ627841	c1242	21	0.8	21	1	DUB35098	ACCSSION:DUB35098
c1170	21.4	0.8	23	1	AZ645254	ACCSSION:AZ645254	c1243	21	0.8	21	1	DX046130	ACCSSION:DX046130
c1171	21.4	0.8	23	1	CL693171	ACCSSION:CL693171	c1244	21	0.8	21	1	DX050095	ACCSSION:DX050095
c1172	21.4	0.8	23	1	DUB28758	ACCSSION:DUB28758	c1245	21	0.8	21	1	DX056929	ACCSSION:DX056929
c1173	21.4	0.8	23	1	TA55C06P	ACCSSION:AL455778	c1246	21	0.8	21	1	DX059939	ACCSSION:DX059939
c1174	21.4	0.8	24	1	CD743368	ACCSSION:CD743368	c1247	21	0.8	21	1	DX075742	ACCSSION:DX075742
c1175	21.4	0.8	24	1	CF292725	ACCSSION:CF292725	c1248	21	0.8	21	1	DX082155	ACCSSION:DX082155
c1176	21.4	0.8	24	1	AZ404871	ACCSSION:AZ404871	c1249	21	0.8	21	1	DX082624	ACCSSION:DX082624
c1177	21.4	0.8	24	1	AZ486788	ACCSSION:AZ486788	c1250	21	0.8	22	1	AL038477	ACCSSION:AL038477
c1178	21.4	0.8	25	1	AU265663	ACCSSION:AU265663	c1251	21	0.8	22	1	CF282024	ACCSSION:CF282024
c1179	21.4	0.8	25	1	AV737092	ACCSSION:AV737092	c1252	21	0.8	22	1	COT78290	ACCSSION:COT78290
c1180	21.4	0.8	25	1	CG726337	ACCSSION:CG726337	c1253	21	0.8	22	1	AZ304806	ACCSSION:AZ304806
c1181	21.4	0.8	26	1	AG194089	ACCSSION:AG194089	c1254	21	0.8	22	1	AZ374487	ACCSSION:AZ374487
c1182	21.2	0.8	26	1	AM043942	ACCSSION:AM043942	c1255	21	0.8	22	1	AZ505769	ACCSSION:AZ505769
c1183	21.2	0.8	26	1	CF280688	ACCSSION:CF280688	c1256	21	0.8	22	1	AZ823875	ACCSSION:AZ823875
c1184	21.2	0.8	26	1	AW333508	ACCSSION:AW333508	c1257	21	0.8	23	1	AL048776	ACCSSION:AL048776
c1185	21.2	0.8	26	1	AZ358846	ACCSSION:AZ358846	c1258	21	0.8	23	1	DT503381	ACCSSION:DT503381
c1186	21.2	0.8	26	1	CZ917639	ACCSSION:CZ917639	c1259	21	0.8	26	1	AL037096	ACCSSION:AL037096
c1187	21	0.8	21	1	AJ658282	ACCSSION:AJ658282	c1260	21	0.8	26	1	TA321G11P	ACCSSION:AL492311
c1188	21	0.8	21	1	AJ666203	ACCSSION:AJ666203	c1261	20.8	0.8	24	1	AZ626101	ACCSSION:AZ626101
c1189	21	0.8	21	1	AL048777	ACCSSION:AL048777	c1262	20.8	0.8	24	1	AZ627850	ACCSSION:AZ627850
c1190	21	0.8	21	1	AM047262	ACCSSION:AM047262	c1263	20.8	0.8	24	1	CL693181	ACCSSION:CL693181
c1191	21	0.8	21	1	CF282216	ACCSSION:CF282216	c1264	20.8	0.8	24	1	DUB29360	ACCSSION:DUB29360
c1192	21	0.8	21	1	CF292703	ACCSSION:CF292703	c1265	20.8	0.8	25	1	AZ476141	ACCSSION:AZ476141
c1193	21	0.8	21	1	CF295642	ACCSSION:CF295642	c1266	20.8	0.8	25	1	CZ910207	ACCSSION:CZ910207
c1194	21	0.8	21	1	CF297615	ACCSSION:CF297615	c1267	20.8	0.8	25	1	CZ917081	ACCSSION:CZ917081
c1195	21	0.8	21	1	CF298322	ACCSSION:CF298322	c1268	20.8	0.8	26	1	AZ437459	ACCSSION:AZ437459
c1196	21	0.8	21	1	CF300809	ACCSSION:CF300809	c1269	20.4	0.7	22	1	CF298427	ACCSSION:CF298427
c1197	21	0.8	21	1	CF312715	ACCSSION:CF312715	c1270	20.4	0.7	22	1	DT494457	ACCSSION:DT494457
c1198	21	0.8	21	1	CF316073	ACCSSION:CF316073	c1271	20.4	0.7	22	1	DT497428	ACCSSION:DT497428
c1199	21	0.8	21	1	CF326952	ACCSSION:CF326952	c1272	20.4	0.7	22	1	DT502811	ACCSSION:DT502811
c1200	21	0.8	21	1	CF327391	ACCSSION:CF327391	c1273	20.4	0.7	22	1	BH000233	ACCSSION:BH000233
c1201	21	0.8	21	1	CF332956	ACCSSION:CF332956	c1274	20.4	0.7	22	1	DUB35072	ACCSSION:DUB35072

1275	20.4	0.7	22	1	DX060105	ACCESSION:DX060105
1276	20.4	0.7	22	1	TX030G05P	ACCESSION:AL497183
1277	20.4	0.7	23	1	AL038397	ACCESSION:AL038397
1278	20.4	0.7	23	1	AL038592	ACCESSION:AL038592
1279	20.4	0.7	23	1	AL038609	ACCESSION:AL038609
1280	20.4	0.7	23	1	AL038688	ACCESSION:AL038688
c1281	20.4	0.7	23	1	BX559898	ACCESSION:BX559898
c1282	20.4	0.7	23	1	CF279593	ACCESSION:CF279593
1283	20.4	0.7	23	1	DT496947	ACCESSION:DT496947
1284	20.4	0.7	23	1	AL048765	ACCESSION:AL048765
1285	20.4	0.7	24	1	CF326993	ACCESSION:CF326993
1286	20.4	0.7	24	1	DT496307	ACCESSION:DT496307
c1287	20.4	0.7	25	1	CF310471	ACCESSION:CF310471
1288	20.4	0.7	25	1	DX046299	ACCESSION:DX046299
c1289	20.2	0.7	25	1	CF300714	ACCESSION:CF300714
1290	20.2	0.7	25	1	A2427752	ACCESSION:A2427752
1291	20.2	0.7	25	1	A2867155	ACCESSION:A2867155
1292	20.2	0.7	25	1	TA12F02Q	ACCESSION:AL451366
c1293	20	0.7	20	1	AJ666402	ACCESSION:AJ666402
1294	20	0.7	20	1	AL038427	ACCESSION:AL038427
1295	20	0.7	20	1	AL038429	ACCESSION:AL038429
1296	20	0.7	20	1	AL038570	ACCESSION:AL038570
1297	20	0.7	20	1	AL038750	ACCESSION:AL038750
1298	20	0.7	20	1	CF280913	ACCESSION:CF280913
1299	20	0.7	20	1	CF282035	ACCESSION:CF282035
1300	20	0.7	20	1	CF282414	ACCESSION:CF282414
c1301	20	0.7	20	1	CF299822	ACCESSION:CF299822
1302	20	0.7	20	1	CF301720	ACCESSION:CF301720
1303	20	0.7	20	1	CF302027	ACCESSION:CF302027
1304	20	0.7	20	1	CF310604	ACCESSION:CF310604
1305	20	0.7	20	1	CF313067	ACCESSION:CF313067
c1306	20	0.7	20	1	CF313569	ACCESSION:CF313569
c1307	20	0.7	20	1	CF319133	ACCESSION:CF319133
1308	20	0.7	20	1	CF321721	ACCESSION:CF321721
1309	20	0.7	20	1	CF328565	ACCESSION:CF328565
c1310	20	0.7	20	1	CF333173	ACCESSION:CF333173
c1311	20	0.7	20	1	CF334170	ACCESSION:CF334170
c1312	20	0.7	20	1	CF336525	ACCESSION:CF336525
c1313	20	0.7	20	1	CF337494	ACCESSION:CF337494
c1314	20	0.7	20	1	AW334823	ACCESSION:AW334823
c1315	20	0.7	20	1	CN545446	ACCESSION:CN545446
c1316	20	0.7	20	1	CN545501	ACCESSION:CN545501
1317	20	0.7	20	1	DN953318	ACCESSION:DN953318
c1318	20	0.7	20	1	DN954281	ACCESSION:DN954281
1319	20	0.7	20	1	DN954289	ACCESSION:DN954289
1320	20	0.7	20	1	DR065440	ACCESSION:DR065440
c1321	20	0.7	20	1	DR073089	ACCESSION:DR073089
c1322	20	0.7	20	1	DR073130	ACCESSION:DR073130
1323	20	0.7	20	1	DT493556	ACCESSION:DT493556
c1324	20	0.7	20	1	T50573	ACCESSION:T50573
c1325	20	0.7	20	1	A2307671	ACCESSION:A2307671
c1326	20	0.7	20	1	A2333980	ACCESSION:A2333980
1327	20	0.7	20	1	A2341530	ACCESSION:A2341530
1328	20	0.7	20	1	A2343031	ACCESSION:A2343031
1329	20	0.7	20	1	A2351273	ACCESSION:A2351273
1330	20	0.7	20	1	A2357623	ACCESSION:A2357623
c1331	20	0.7	20	1	A2369734	ACCESSION:A2369734
1332	20	0.7	20	1	A2386573	ACCESSION:A2386573
1333	20	0.7	20	1	A2396481	ACCESSION:A2396481
1334	20	0.7	20	1	A2442328	ACCESSION:A2442328
c1335	20	0.7	20	1	A2463331	ACCESSION:A2463331
c1336	20	0.7	20	1	A2477734	ACCESSION:A2477734
c1337	20	0.7	20	1	A2479464	ACCESSION:A2479464
c1338	20	0.7	20	1	A2486784	ACCESSION:A2486784
c1339	20	0.7	20	1	A2498625	ACCESSION:A2498625
1340	20	0.7	20	1	A2514729	ACCESSION:A2514729
1341	20	0.7	20	1	A2581208	ACCESSION:A2581208
1342	20	0.7	20	1	A2588011	ACCESSION:A2588011
1343	20	0.7	20	1	A2607328	ACCESSION:A2607328
c1344	20	0.7	20	1	A2623155	ACCESSION:A2623155
c1345	20	0.7	20	1	A2623214	ACCESSION:A2623214
1346	20	0.7	20	1	A2643992	ACCESSION:A2643992
c1347	20	0.7	20	1	A2645829	ACCESSION:A2645829

1348	20	0.7	20	1	AZ650271	ACCESSION:AZ650271
1349	20	0.7	20	1	AZ760838	ACCESSION:AZ760838
1350	20	0.7	20	1	AZ764504	ACCESSION:AZ764504
c1351	20	0.7	20	1	AZ765211	ACCESSION:AZ765211
1352	20	0.7	20	1	AZ772091	ACCESSION:AZ772091
c1353	20	0.7	20	1	AZ779425	ACCESSION:AZ779425
1354	20	0.7	20	1	AZ784041	ACCESSION:AZ784041
c1355	20	0.7	20	1	AZ793467	ACCESSION:AZ793467
c1356	20	0.7	20	1	AZ798529	ACCESSION:AZ798529
1357	20	0.7	20	1	AZ805163	ACCESSION:AZ805163
1358	20	0.7	20	1	AZ806521	ACCESSION:AZ806521
1359	20	0.7	20	1	AZ806585	ACCESSION:AZ806585
1360	20	0.7	20	1	AZ809306	ACCESSION:AZ809306
1361	20	0.7	20	1	AZ810986	ACCESSION:AZ810986
1362	20	0.7	20	1	AZ813908	ACCESSION:AZ813908
1363	20	0.7	20	1	AZ817323	ACCESSION:AZ817323
1364	20	0.7	20	1	AZ817414	ACCESSION:AZ817414
1365	20	0.7	20	1	AZ817467	ACCESSION:AZ817467
1366	20	0.7	20	1	AZ817608	ACCESSION:AZ817608
c1367	20	0.7	20	1	AZ818489	ACCESSION:AZ818489
c1368	20	0.7	20	1	AZ818816	ACCESSION:AZ818816
1369	20	0.7	20	1	AZ837491	ACCESSION:AZ837491
1370	20	0.7	20	1	AZ841342	ACCESSION:AZ841342
c1371	20	0.7	20	1	AZ841558	ACCESSION:AZ841558
1372	20	0.7	20	1	AZ858052	ACCESSION:AZ858052
1373	20	0.7	20	1	AZ858419	ACCESSION:AZ858419
1374	20	0.7	20	1	AZ936914	ACCESSION:AZ936914
c1375	20	0.7	20	1	AZ949180	ACCESSION:AZ949180
1376	20	0.7	20	1	AZ963973	ACCESSION:AZ963973
1377	20	0.7	20	1	CW979138	ACCESSION:CW979138
c1378	20	0.7	20	1	DU834188	ACCESSION:DU834188
1379	20	0.7	20	1	DU835125	ACCESSION:DU835125
1380	20	0.7	20	1	DX045751	ACCESSION:DX045751
1381	20	0.7	20	1	DX055580	ACCESSION:DX055580
c1382	20	0.7	20	1	DX070282	ACCESSION:DX070282
1383	20	0.7	21	1	EX556606	ACCESSION:EX556606
c1384	20	0.7	21	1	CF276638	ACCESSION:CF276638
1385	20	0.7	21	1	CF311914	ACCESSION:CF311914
c1386	20	0.7	21	1	CF318152	ACCESSION:CF318152
c1387	20	0.7	21	1	CK000923	ACCESSION:CK000923
1388	20	0.7	21	1	DT496709	ACCESSION:DT496709
1389	20	0.7	21	1	AZ461824	ACCESSION:AZ461824
1390	20	0.7	21	1	AZ493766	ACCESSION:AZ493766
c1391	20	0.7	21	1	DX056270	ACCESSION:DX056270
1392	20	0.7	21	1	DX081159	ACCESSION:DX081159
1393	20	0.7	21	1	CF310486	ACCESSION:CF310486
1394	20	0.7	22	1	DR073660	ACCESSION:DR073660
c1395	20	0.7	23	1	AL587621	ACCESSION:AL587621
1396	20	0.7	23	1	AZ315640	ACCESSION:AZ315640
1397	20	0.7	23	1	AZ621676	ACCESSION:AZ621676
1398	20	0.7	23	1	AZ817623	ACCESSION:AZ817623
c1399	20	0.7	23	1	DX064291	ACCESSION:DX064291
c1400	20	0.7	24	1	AJ668301	ACCESSION:AJ668301
1401	20	0.7	25	1	AJ663467	ACCESSION:AJ663467
c1402	20	0.7	25	1	DX071965	ACCESSION:DX071965
c1403	19.8	0.7	23	1	EX568055	ACCESSION:EX568055
c1404	19.8	0.7	23	1	CF297907	ACCESSION:CF297907
c1405	19.8	0.7	23	1	CF314322	ACCESSION:CF314322
c1406	19.8	0.7	23	1	CF318266	ACCESSION:CF318266
c1407	19.8	0.7	23	1	AW334124	ACCESSION:AW334124
1408	19.8	0.7	23	1	AZ447220	ACCESSION:AZ447220
1409	19.8	0.7	23	1	AZ662734	ACCESSION:AZ662734
1410	19.4	0.7	21	1	AL038582	ACCESSION:AL038582
1411	19.4	0.7	21	1	AL038627	ACCESSION:AL038627
1412	19.4	0.7	21	1	AL038839	ACCESSION:AL038839
c1413	19.4	0.7	21	1	EX548564	ACCESSION:EX548564
c1414	19.4	0.7	21	1	CF276747	ACCESSION:CF276747
c1415	19.4	0.7	21	1	CF296213	ACCESSION:CF296213
c1416	19.4	0.7	21	1	CF302218	ACCESSION:CF302218
c1417	19.4	0.7	21	1	CF314260	ACCESSION:CF314260
1418	19.4	0.7	21	1	DR073305	ACCESSION:DR073305
c1419	19.4	0.7	21	1	AZ317208	ACCESSION:AZ317208
c1420	19.4	0.7	21	1	AZ486776	ACCESSION:AZ486776

1348	20	0.7	20	1	AZ650271	ACCESSION:AZ650271
1349	20	0.7	20	1	AZ760838	ACCESSION:AZ760838
1350	20	0.7	20	1	AZ764504	ACCESSION:AZ764504
c1351	20	0.7	20	1	AZ765211	ACCESSION:AZ765211
1352	20	0.7	20	1	AZ772091	ACCESSION:AZ772091
c1353	20	0.7	20	1	AZ779425	ACCESSION:AZ779425
1354	20	0.7	20	1	AZ784041	ACCESSION:AZ784041
c1355	20	0.7	20	1	AZ793467	ACCESSION:AZ793467
c1356	20	0.7	20	1	AZ798529	ACCESSION:AZ798529
1357	20	0.7	20	1	AZ805163	ACCESSION:AZ805163
1358	20	0.7	20	1	AZ806521	ACCESSION:AZ806521
1359	20	0.7	20	1	AZ806585	ACCESSION:AZ806585
1360	20	0.7	20	1	AZ809306	ACCESSION:AZ809306
1361	20	0.7	20	1	AZ810986	ACCESSION:AZ810986
1362	20	0.7	20	1	AZ813908	ACCESSION:AZ813908
1363	20	0.7	20	1	AZ817323	ACCESSION:AZ817323
1364	20	0.7	20	1	AZ817414	ACCESSION:AZ817414
1365	20	0.7	20	1	AZ817467	ACCESSION:AZ817467
1366	20	0.7	20	1	AZ817608	ACCESSION:AZ817608
c1367	20	0.7	20	1	AZ818489	ACCESSION:AZ818489
c1368	20	0.7	20	1	AZ818816	ACCESSION:AZ818816
1369	20	0.7	20	1	AZ837491	ACCESSION:AZ837491
1370	20	0.7	20	1	AZ841342	ACCESSION:AZ841342
c1371	20	0.7	20	1	AZ841558	ACCESSION:AZ841558
1372	20	0.7	20	1	AZ858052	ACCESSION:AZ858052
1373	20	0.7	20	1	AZ858419	ACCESSION:AZ858419
1374	20	0.7	20	1	AZ936914	ACCESSION:AZ936914
c1375	20	0.7	20	1	AZ949180	ACCESSION:AZ949180
1376	20	0.7	20	1	AZ963973	ACCESSION:AZ963973
1377	20	0.7	20	1		

C1421	19.4	0.7	21	1	AZ792613	ACCSSION:AZ792613	1494	19	0.7	19	1	AZ450180	ACCSSION:AZ450180
1422	19.4	0.7	21	1	AZ822825	ACCSSION:AZ822825	C1495	19	0.7	19	1	AZ453930	ACCSSION:AZ453930
1423	19.4	0.7	21	1	AZ853429	ACCSSION:AZ853429	1496	19	0.7	19	1	AZ460906	ACCSSION:AZ460906
1424	19.4	0.7	21	1	CL693165	ACCSSION:CL693165	C1497	19	0.7	19	1	AZ471494	ACCSSION:AZ471494
C1425	19.4	0.7	21	1	DUB28988	ACCSSION:DUB28988	C1498	19	0.7	19	1	AZ476576	ACCSSION:AZ476576
1426	19.4	0.7	22	1	AL038142	ACCSSION:AL038142	C1499	19	0.7	19	1	AZ486786	ACCSSION:AZ486786
C1427	19.4	0.7	22	1	BX556059	ACCSSION:BX556059	C1500	19	0.7	19	1	AZ490652	ACCSSION:AZ490652
1428	19.4	0.7	22	1	CL693160	ACCSSION:CL693160	1501	19	0.7	19	1	AZ508040	ACCSSION:AZ508040
C1429	19.4	0.7	23	1	AJ666332	ACCSSION:AJ666332	1502	19	0.7	19	1	AZ579119	ACCSSION:AZ579119
1430	19.4	0.7	23	1	AL048745	ACCSSION:AL048745	1503	19	0.7	19	1	AZ583970	ACCSSION:AZ583970
C1431	19.4	0.7	23	1	CF333801	ACCSSION:CF333801	1504	19	0.7	19	1	AZ585865	ACCSSION:AZ585865
1432	19.2	0.7	24	1	AM043222	ACCSSION:AM043222	1505	19	0.7	19	1	AZ593210	ACCSSION:AZ593210
C1433	19.2	0.7	24	1	AZ304870	ACCSSION:AZ304870	C1506	19	0.7	19	1	AZ616154	ACCSSION:AZ616154
1434	19.2	0.7	24	1	AZ308553	ACCSSION:AZ308553	C1507	19	0.7	19	1	AZ627844	ACCSSION:AZ627844
1435	19.2	0.7	24	1	AZ448207	ACCSSION:AZ448207	1508	19	0.7	19	1	AZ631701	ACCSSION:AZ631701
C1436	19.2	0.7	24	1	AZ814559	ACCSSION:AZ814559	1509	19	0.7	19	1	AZ633821	ACCSSION:AZ633821
C1437	19.2	0.7	24	1	AJ668179	ACCSSION:AJ668179	1510	19	0.7	19	1	AZ643659	ACCSSION:AZ643659
C1438	19	0.7	19	1	AJ669138	ACCSSION:AJ669138	C1511	19	0.7	19	1	AZ644698	ACCSSION:AZ644698
1440	19	0.7	19	1	BQ588729	ACCSSION:BQ588729	1512	19	0.7	19	1	AZ648335	ACCSSION:AZ648335
C1441	19	0.7	19	1	CB174047	ACCSSION:CB174047	C1513	19	0.7	19	1	AZ649888	ACCSSION:AZ649888
C1442	19	0.7	19	1	CF279008	ACCSSION:CF279008	1514	19	0.7	19	1	AZ764497	ACCSSION:AZ764497
C1443	19	0.7	19	1	CF291089	ACCSSION:CF291089	1515	19	0.7	19	1	AZ764522	ACCSSION:AZ764522
1444	19	0.7	19	1	CF291090	ACCSSION:CF291090	1516	19	0.7	19	1	AZ764534	ACCSSION:AZ764534
C1445	19	0.7	19	1	CF295598	ACCSSION:CF295598	1517	19	0.7	19	1	AZ770387	ACCSSION:AZ770387
C1446	19	0.7	19	1	CF302327	ACCSSION:CF302327	1518	19	0.7	19	1	AZ778858	ACCSSION:AZ778858
C1447	19	0.7	19	1	CF304589	ACCSSION:CF304589	1519	19	0.7	19	1	AZ779901	ACCSSION:AZ779901
C1448	19	0.7	19	1	CF309801	ACCSSION:CF309801	1520	19	0.7	19	1	AZ781876	ACCSSION:AZ781876
1449	19	0.7	19	1	CF309943	ACCSSION:CF309943	C1521	19	0.7	19	1	AZ787634	ACCSSION:AZ787634
C1450	19	0.7	19	1	CF311496	ACCSSION:CF311496	1522	19	0.7	19	1	AZ788058	ACCSSION:AZ788058
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ALIGNMENTS

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VERSION BY799992.1 GI:73472467
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SOURCE Homo sapiens (human)
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Hominidae; Homo.
REFERENCE 1 (bases 1 to 80)
AUTHORS Choy, K., Wang, C., Ogura, A., Lau, T., Rogers, M., Ikeo, K.,
Gojobori, T., Lam, D. and Pang, C.
TITLE Comparative annotation of 15,809 ESTs identified from pooled early
gestation human eyes
JOURNAL Unpublished (2005)
COMMENT Contact: Kw Choy
National Institute of Genetics, Center for Information Biology and
DBJ
Yatai111, Mishima, 411-8540, Japan
Tel: 852-2632-3099
Email: richardchoy@cuhk.edu.hk
This sequence is assembled via IDEA. This clone was obtained from
National Institute of Genetics and Chinese University of HongKong.
Location/Qualifiers
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/clone="HEMeye2033G10_072.abl"
/tissue_type="eye"
/clone_lib="Homo sapiens eye"

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Query Match 2.9%; Score 78.4; DB 1; Length 80;
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Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 ATCAGTAAAGATCATAAGCAGTCATCGAGATCTCTTGGCTGTGGTGTCTATGATCCGAG 60
QY 929 AAAGACAAAATTCAGTGAA 948
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 AAAGACAAAATTCAGTGAA 80

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RESULT 2

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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source

source

source

source

source

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source

source

source

source

source

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source

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source

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1 (bases 1 to 61)
AUTHORS    Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
            Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
            Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
            Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
            Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
            Trevasakis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
            and Marra, M.
TITLE      Generation and analysis of 280,000 human expressed sequence tags
JOURNAL    Genome Res. 6 (9), 807-828 (1996)
PUBMED     8899549
COMMENT    Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
place of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.

This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2176 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..61
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3920485"
/db_xref="taxon:9606"
/clone="IMAGE:530973"
/dev_stage="Ntera-2/RA neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene neuroepithelium (#937231)"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. NT2
cells (Ntera-2/cl.d1) induced with Retinoic Acid for 24
hours. Average insert size: 1.5 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGGCAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

Query Match      2.0%; Score 55.4; DB 1; Length 61;
Best Local Similarity 91.8%; Pred.No. 13;
Matches 56; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2647 TAGCCCTCCACTTTGCTGTTCTTTACTGCTCGAATAAGAGCCCTAAGTTTCTGA 2706
Db 61 TAGCTTCCANTTTGTTGTTCTTACCTTTACTGCTCGAATAAGAGCCCTAAGTTTCTGA 2

Oy 2707 C 2707
Db 1 C 1

RESULT 4
AU103749
LOCUS      AU103749 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP06290, mRNA sequence.
ACCESSION AU103749
VERSION    AU103749.1 GI:13553270
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS    Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
            Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
            Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL    EMBO Rep. 2 (5), 388-393 (2001)
PUBMED     11375929
COMMENT    Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Tel: 81-3-5449-5343
            Fax: 81-3-5449-5416
            Email: yusuzuki@igc.jp
            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
            Sugano, S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
            Location/Qualifiers
            1..50
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="HEP06290"
            /clone_lib="Sugano Homo sapiens cDNA library"

Query Match      1.8%; Score 50; DB 1; Length 50;
Best Local Similarity 100.0%; Pred.No. 25;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 139 AGACTCGAGACCACGCTCTCTCTCGGAGAGGAGCGGCGACCTCGCGCTTT 188
Db 1 AGACTCGAGACCACGCTCTCTCTCGGAGAGGAGCGGCGACCTCGCGCTTT 50

RESULT 5
AU103750
LOCUS      AU103750 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP06361, mRNA sequence.
ACCESSION AU103750
VERSION    AU103750.1 GI:13553271
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS    Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
            Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
            Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL    EMBO Rep. 2 (5), 388-393 (2001)
PUBMED     11375929
COMMENT    Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Tel: 81-3-5449-5343
            Fax: 81-3-5449-5416
            Email: yusuzuki@igc.jp
            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
            Sugano, S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
            Location/Qualifiers
            1..50
            /organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP06361"
/clone_lib="Sugano Homo sapiens cDNA library"

Query Match      1.8%; Score 48.4; DB 1; Length 50;
Best Local Similarity 98.0%; Pred. No. 32;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 139 AGACTCGAGACCAACGCTCTCTCTCGGGAAGGAGGCGGCACCTCGCGTTT 188
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Db 1 AGACTCGAGACCAACGCTCTCTCTCGGGAAGGAGGCGGCACCTCGCGTTT 50

RESULT 6
LOCUS AU103751 50 bp mRNA linear EST 28-JAN-2004
DEFINITION AU103751 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP06548, mRNA sequence.
ACCESSION AU103751
VERSION AU103751.1 GI:13553272
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Tel: 81-3-5449-5343
Fax: 81-3-5449-5416
Email: ysuzuki@hgc.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP13405"
/clone_lib="Sugano Homo sapiens cDNA library"

Query Match      1.7%; Score 46.8; DB 1; Length 50;
Best Local Similarity 96.0%; Pred. No. 40;
Matches 48; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCGTTATCCATTGTGTTGTTCCGCCAGCTAGCGCTGGCCCTCCCGCTT 55
|||||
Db 1 CCGTTATCCATTGTGTTGTTTCGTTCAGTTAGGCTGGCCCTCCCGCTT 50

RESULT 8
LOCUS T92783 52 bp mRNA linear EST 22-MAR-1995
DEFINITION Ye27h02.s1 Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:118995 3', similar to gb:S38729 LUPUS KU AUTOANTIGEN PROTEIN
P70 (HUMAN);, mRNA sequence.
ACCESSION T92783
VERSION T92783.1 GI:724696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 52)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le.N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevasaki,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL

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ACCESSION	CV733592	1	GI:55440563		
VERSION	EST.				
KEYWORDS	Oryza sativa (japonica cultivar-group)				
SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoidae; Oryzaceae; Oryza.				
REFERENCE	1 (bases 1 to 43)				
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.				
TITLE	Large-scale Sequencing Analysis of Rice ESTs				
COMMENT	Unpublished (2003) Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Gyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.				
FEATURES	Location/Qualifiers				
source	1..43				
	/organism="Oryza sativa (japonica cultivar-group)"				
	/mol_type="mRNA"				
	/cultivar="Nackdong"				
	/db_xref="taxon:39947"				
	/clone="FLO--08-J04"				
	/tissue_type="flower"				
	/lab_host="E.coli SOUR"				
	/clone_lib="Rice flower lambda phage cDNA library (FLO)"				
	/note="Vector: pBlueScript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."				
	Query Match 1.4%; Score 38.4; DB 1; Length 43;				
	Best Local Similarity 97.5%; Pred. No. 1.2e+02;				
	Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Oy	2704 GTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743				
Dd	43 GTAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4				
RESULT 12					
CF317896/c					
LOCUS	CF317896	47 bp	mRNA	linear	EST 15-AUG-2003
DEFINITION	HD--07-M03.g1 OHSDACL-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--07-M03, mRNA sequence.				
ACCESSION	CF317896				
VERSION	CF317896				
KEYWORDS	EST.				
SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Oryza sativa (japonica cultivar-group)				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoidae; Oryzaceae; Oryza.				
REFERENCE	1 (bases 1 to 47)				
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.				
TITLE	Large-scale Sequencing Analysis of Rice ESTs				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Gyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.				
FEATURES	Location/Qualifiers				
source	1..47				
	/organism="Oryza sativa (japonica cultivar-group)"				
	/mol_type="mRNA"				

RESULT 14
CV732719/c
LOCUS
DEFINITION
FLO--07-F03.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-F03, mRNA sequence.

ACCESSION
CV732719
VERSION
CV732719.1 GI:55438841
KEYWORDS
EST.

SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 46)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
source
1. .46
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-F03"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 1.4%; Score 37.2; DB 1; Length 46;
Matches 39; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2702 TTGTACTTAAAAA 1
Db 46 TTATAAAAAA 5

RESULT 15
CF329026/c
LOCUS
DEFINITION
NACL--04-D06.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-D06, mRNA sequence.

ACCESSION
CF329026
VERSION
CF329026.1 GI:33806289
KEYWORDS
EST.

SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
source
1. .37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="NACL--04-D06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match
Best Local Similarity 1.3%; Score 37; DB 1; Length 37;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2707 CTAAAAA 1
Db 37 CTA 1

RESULT 16
AL046183/c
LOCUS
DEFINITION
DKFZp434C127.s1 434 (synonym: htes3) Homo sapiens cDNA clone

ACCESSION
AL046183
VERSION
AL046183.1 GI:49682657
KEYWORDS
EST.

SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 42)
Koehler,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehler, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1. .42
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434C127"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site 1: NotI; Site 2: SalI"

Query Match
Best Local Similarity 1.3%; Score 37; DB 1; Length 42;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 GTACTAAAAA 1
Db 41 GTNNNNAAAAA 2

RESULT 17
CF323286/c
LOCUS
DEFINITION
NACL--08-002.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-002, mRNA


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Db      43 TTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 23
CF331239/c
LOCUS   NACL--07-E14.bl Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--07-E14, mRNA
sequence.
ACCESSION CF331239
VERSION   1
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 44)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
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    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice callus plasmid cDNA library (NACL)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."

Query Match      1.3%; Score 36.6; DB 1; Length 44;
Best Local Similarity 90.7%; Pred. NO. 1.6e+02;
Matches 39; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2701 TTTGTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
         |||||
Db      44 TCTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 25
CV729880/c
LOCUS   FLO--03-C10.bl Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--03-C10, mRNA
sequence.
ACCESSION CV729880
VERSION   1
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 45)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
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    /tissue_type="flower"
    /lab_host="E.coli SOLR"
    /clone_lib="Rice flower lambda phage cDNA library (FLO)"
    /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
    end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 36.6; DB 1; Length 45;
Best Local Similarity 90.7%; Pred. NO. 1.6e+02;
Matches 39; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db      43 TTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 24
CF332233/c
LOCUS   NACL--08-K14.bl Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--08-K14, mRNA
sequence.
ACCESSION CF332233
VERSION   1
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 45)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.

```

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
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    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="NACL--08-K14"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice callus plasmid cDNA library (NACL)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."

Query Match      1.3%; Score 36.6; DB 1; Length 45;
Best Local Similarity 90.7%; Pred. NO. 1.6e+02;
Matches 39; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2701 TTTGTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
         |||||
Db      44 TTTATAGATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 25
CV729880/c
LOCUS   FLO--03-C10.bl Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--03-C10, mRNA
sequence.
ACCESSION CV729880
VERSION   1
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 45)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
    source
    1..45
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="FLO--03-C10"
    /tissue_type="flower"
    /lab_host="E.coli SOLR"
    /clone_lib="Rice flower lambda phage cDNA library (FLO)"
    /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
    end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 36.6; DB 1; Length 45;
Best Local Similarity 90.7%; Pred. NO. 1.6e+02;
Matches 39; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site1: EcoRI; Site2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
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Query Match 1.3%; Score 36.2; DB 1; Length 42;
 Best Local Similarity 92.7%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 38; Conservative 0

Qy 2703 TGTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 41 TTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 32
 DY231327
 LOCUS EST02078 Bmp Bombyx mori cDNA clone BmpG_G14_2005-10-17_WD-051017
 DEFINITION 5', mRNA sequence.
 ACCESSION DY231327
 VERSION DY231327.1 GI:86465455
 KEYWORDS Bombyx mori (domestic silkworm)
 SOURCE Bombyx mori

ORGANISM Bombyx mori
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 Bombycoidea; Bombycidae; Bombyx.
 REFERENCE 1 (bases 1 to 44)
 AUTHORS Zhang, Y. Z., Xu, J., Chen, J., Wang, D., Nie, Z. M., Lv, Z. B., Jiang, C. Y.,
 Liu, L. L., Song, L., He, P. A., Chen, F. and Wu, X. F.

TITLE The full-length cDNA library construction of silkworm pupae (Bombyx mori) and large-scale sequencing
 JOURNAL Unpublished (2006)
 COMMENT Contact: Yaozhao, Zhang
 Biochemistry Laboratory, the college of life science
 Zhejiang Sci-Tech University
 2th Street, Xiahsa High Education area, Hangzhou City, 310018, P.
 R. China

Tel: 86 571 86843194
 Fax: 86 571 86843198
 Email: yaozhao@chinagen.com
 Seq primer: M13 Forward
 High quality sequence stop: 44
 POLYA=Yes.

FEATURES

source
 1..44
 /location/Qualifiers
 /organism="Bombyx mori"
 /mol_type="mRNA"
 /strain="Qingsong-Haoyue"
 /db_xref="taxon:7091"
 /clone="BmpG_G14_2005-10-17_WD-051017"
 /sex="male and female"
 /tissue_type="whole pupae body but for the skin"
 /dev_stage="metaphase"
 /clone_lib="Bmp"

/note="Vector: pHelix; Site 1: Hind II; The synthesis of double-stranded cDNA from mRNA was based on the method described by Gubler and Hoffman. The obtained cDNA were ligated into the plasmid vector pHelix and subsequently the ligation product was transformed into E.coli competent cells TGI. At last, the recombinant clones were screened by blue-white plaques."

Query Match 1.3%; Score 36.2; DB 1; Length 44;
 Best Local Similarity 92.7%; Pred. No. 1.7e+02; Mismatches 38; Conservative 0; Indels 0; Gaps 0;

Qy 2703 TGTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 4 TATAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 44

RESULT 33

AJ659250
 LOCUS AJ659250 KN277 Sus scrofa cDNA clone C0005215_D15, mRNA sequence.
 DEFINITION AJ659250
 ACCESSION AJ659250
 VERSION AJ659250.1 GI:49343381
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa

Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.

REFERENCE

1 (bases 1 to 37)
 Anderson, S. I., Finlayson, H. A. and Archibald, A. L.
 Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
 Unpublished (2004)

JOURNAL

COMMENT Contact: Anderson SI

Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13 Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts.

Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

source
 1..37
 /location/Qualifiers
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="C0005215_D15"
 /tissue_type="embryo"
 /clone_lib="KN277"
 /note="Vector: pBluescriptII(SK+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

Query Match 1.3%; Score 36; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 36; Conservative 0

Qy 2708 TAAAAA
 |||
 Db 1 TAAAAA

RESULT 34

CF328866/c
 LOCUS CF328866
 DEFINITION CF328866.1 GI:33805974
 sativa (japonica cultivar-group) cDNA clone NACL--03-P15, mRNA sequence.
 ACCESSION CF328866
 VERSION CF328866.1
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 37)
 Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
 Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.

AUTHORS

Unpublished (2003)

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-03-P15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 36; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAA 2743

Db 36 TAAA 1

RESULT 35

CV731657/c

LOCUS
DEFINITION
FLO--05-M14.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--05-M14, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--05-M14"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 36; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAA 2743
Db 36 TAAA 1

RESULT 36

CV730040/c

LOCUS

DEFINITION

FLO--03-G05.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--03-G05, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--03-G05"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAA 2743

Db 38 TAAA 3

RESULT 37

CF300591/c

LOCUS

DEFINITION

7LEAF--05-C03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-C03, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 40)

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1. .40
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="ABF--03-N04"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 1.3%; Score 36; DB 1; Length 40;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2708 TAAAAA..... 43 bp mRNA linear EST 05-NOV-2004

DB 36 TAAAAA..... 43 bp mRNA linear EST 05-NOV-2004

RESULT 41

CV733657/c

LOCUS

DEFINITION FLO--08-K18.g1 Rice flower lambda phage cDNA library (FLO) Oryza

sativa (japonica cultivar-group) cDNA clone FLO--08-K18, mRNA

sequence.

CV733657

Accession . CV733657.1 GI:55440691

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 41)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1. .41

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="FLO--08-K18"

/tissue_type="flower"

/lab_host="E.coli SOLR"

/clone_lib="Rice flower lambda phage cDNA library (FLO)"

/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'

end with EcoRI and 3' end with XhoI site."

Query Match

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2708 TAAAAA..... 43 bp mRNA linear EST 04-NOV-2004

DB

41 TAAAAA..... 43 bp mRNA linear EST 04-NOV-2004

RESULT 42

CV726108/c

LOCUS

DEFINITION

CV726108

Accession

Version

Keywords

Source

Organism

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 43)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1. .43

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--03-J05"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA

library (14Salt)"

/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs.

cDNA was inserted into lambda Uni-ZAP XR vector at 5' end

with EcoRI and 3' end with XhoI site."

Query Match

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2708 TAAAAA..... 43 bp mRNA linear EST 05-NOV-2004

DB

42 TAAAAA..... 43 bp mRNA linear EST 05-NOV-2004

RESULT 43

CV728159/c

LOCUS

```

DEFINITION 14Salt--06-L11.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--06-L11, mRNA sequence.
ACCESSION CV728159
VERSION CV728159.1 GI:55430428
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. 43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--06-L11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 36; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAA... 2743
Db 41 TAAAAA... 6

RESULT 44
CV734232/c
LOCUS FLO--09-102.g1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--09-102, mRNA
sequence.
ACCESSION CV734232
VERSION CV734232.1 GI:55441811
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

```

```

Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. 43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-102"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 36; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAA... 2743
Db 43 TAAAAA... 8

RESULT 45
CV726790/c
LOCUS CV726790 44 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--04-J20.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--04-J20, mRNA sequence.
ACCESSION CV726790
VERSION CV726790.1 GI:55414414
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 44)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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1. 44
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--04-J20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 36; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAA... 2743

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Db      44 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9
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RESULT 46
LOCUS   CF331757/c
DEFINITION NACL--08-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-A04, mRNA sequence.
ACCESSION CF331757
VERSION   CF331757.1 GI:33811741
KEYWORDS EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 45)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /clone="FLO--09-I01"
                     /tissue_type="flower"
                     /lab_host="E.coli SOLR"
                     /clone_lib="Rice flower lambda phage cDNA library (FLO)"
                     /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
                     XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
                     end with EcoRI and 3' end with XhoI site."
Query Match          1.3%; Score 36; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB      43 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8
|||||

RESULT 48
LOCUS   CV729079/c
DEFINITION FLO--01-L18.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-L18, mRNA sequence.
ACCESSION CV729079
VERSION   CV729079.1 GI:55432121
KEYWORDS EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 37)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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                     /lab_host="E.coli SOLR"
                     /clone_lib="Rice flower lambda phage cDNA library (FLO)"
                     /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
                     XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
                     end with EcoRI and 3' end with XhoI site."
Query Match          1.3%; Score 35.4; DB 1; Length 37;
Best Local Similarity 97.3%; Pred. No. 1.7e+02;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db      44 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9
|||||
RESULT 46
LOCUS   CF331757/c
DEFINITION NACL--08-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-A04, mRNA sequence.
ACCESSION CF331757
VERSION   CF331757.1 GI:33811741
KEYWORDS EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 45)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
Query Match          1.3%; Score 36; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB      41 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6
|||||

RESULT 47
LOCUS   CV734230/c
DEFINITION FLO--09-I01.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--09-I01, mRNA sequence.
ACCESSION CV734230
VERSION   CV734230.1 GI:55441807
KEYWORDS EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 45)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)

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/db_xref="taxon:39947"
/clone="14ROOT--02-K03"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      1.3%; Score 35.4; DB 1; Length 39;
Best Local Similarity 97.3%; Pred. No. 1.8e+02;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2704 GTACTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
      |||||
Db 37 GTACTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 55
CV732133/c
LOCUS
DEFINITION
FLO--06-H15.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-H15, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--06-H15"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35.4; DB 1; Length 39;
Best Local Similarity 97.3%; Pred. No. 1.8e+02;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAA
      |||||
Db 38 CCAAAAA

RESULT 56
CF301837/c
LOCUS
DEFINITION
7LEAF--06-N13.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-N13, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      1.3%; Score 35.4; DB 1; Length 41;
Best Local Similarity 97.3%; Pred. No. 1.8e+02;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAA
      |||||
Db 41 CAAAA

RESULT 57
CV725219/c
LOCUS
DEFINITION
14Salt--02-D04.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--02-D04, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--06-N13"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      1.3%; Score 35.4; DB 1; Length 41;
Best Local Similarity 97.3%; Pred. No. 1.8e+02;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAA
      |||||
Db 41 CAAAA

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 /db_xref="taxon:39947"
 /clone="14Salt--02-D04"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
 1.3%; Score 35.4; DB 1; Length 41;
 Best Local Similarity 97.3%; Pred. No. 1.8e+02;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAA 2743
 DB 41 CCAA 5

Query Match 1.3%; Score 35.4; DB 1; Length 41;
 Best Local Similarity 97.3%; Pred. No. 1.8e+02;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 58
 CV732097/c
 LOCUS
 DEFINITION
 FLO--06-G18.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-G18, mRNA sequence.
 CV732097
 CV732097.1 GI:55437821
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 41)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
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 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 Location/Qualifiers
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--06-G18"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
 1.3%; Score 35.4; DB 1; Length 41;
 Best Local Similarity 97.3%; Pred. No. 1.8e+02;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAA 2743
 DB 41 CAAA 5

Query Match 1.3%; Score 35.4; DB 1; Length 41;
 Best Local Similarity 97.3%; Pred. No. 1.8e+02;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 58
 CV732097/c
 LOCUS
 DEFINITION
 FLO--06-G18.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-G18, mRNA sequence.
 CV732097
 CV732097.1 GI:55437821
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 41)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
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 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 Location/Qualifiers
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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 /clone="FLO--06-G18"
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 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
 1.3%; Score 35.4; DB 1; Length 41;
 Best Local Similarity 97.3%; Pred. No. 1.8e+02;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAA 2743
 DB 41 CAAA 5

RESULT 59
 CF302691/c
 LOCUS
 DEFINITION
 7LEAF--08-H12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--08-H12, mRNA sequence.
 CF302691
 CF302691.1 GI:33674452
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 43)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 Location/Qualifiers
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 /organism="Oryza sativa (japonica cultivar-group)"
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 /clone="7LEAF--08-H12"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
 1.3%; Score 35.4; DB 1; Length 43;
 Best Local Similarity 97.3%; Pred. No. 1.9e+02;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAA 2743
 DB 43 CAAA 7

RESULT 60
 CV725096/c
 LOCUS
 DEFINITION
 14Salt--02-A01.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--02-A01, mRNA sequence.
 CV725096
 CV725096.1 GI:55412720
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 43)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@agbio

FEATURES

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1. ...43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt-02-A01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="vector: plusscript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360UM/m-2sec-1) for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

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Query Match 1.3%; Score 35.4; DB 1; Length 43;
Best Local Similarity 97.3%; Pred. No. 1.9e+02;
Matches 36: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

[illegible]

db 39 CC

RESULT 61	DV573571/c	DV573571	43 bp	mrna	linear	EST 04-NOV-2005
LOCUS						
DEFINITION	0058P0042B11.3' library 58 - normalized (50 mix pooled juveniles + adults) - male <i>Taeniopygia guttata</i> cdna clone 0058P0042B11.3', similar to prohibitin, mRNA sequence.					

REFERENCE	1 (bases 1 to 43)
AUTHORS	Wada,K., Howard,J.T., McConnell,P., Lints,T., Rivas,M.V., Whitney,O., Horita,H., Patterson,M.A., White,S., Zhao,S., Sakaquchi,H., Hagiwara,M., Shiraki,T., Hirozane-Kishikawa,T., Skene,P., Hayashizaki,Y., Carninci,P. and Jarvis,E.D.
TITLE	A molecular neuroethological approach for identifying and characterizing a melody of behaviorally regulated genes
JOURNAL	Unpublished (2005)
COMMENT	Other ESTs: 0058P00422.x0 B11 Contact: Kazuhiro Wada and Erich Jarvis Erich D. Jarvis Lab Duke University Medical Center - Department of Neurobiology Box 3209 Bryan Research Building, Durham, NC 27710, USA Tel: 919 681-1681 Email: wada@neuro.duke.edu and jarvis@neuro.duke.edu Plate: 0058P0042 row: B column: 11 POLVA=NO.

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FEATURES      Location/Qualifiers
1. .43
/organism="Taeniopygia guttata"
/mol_type="mRNA"
/db_xref="taxon:59729"
/clone="0058P0042B11"
/sex="male"
/tissue_type="brain"
/dev_stage="adult and juvenile"
/clone_lib="library 58 - normalized (50 mix pooled
juveniles + adults) - male"
/notes="Organ: Brain; Vector: pFLC-1; Site 1: ECoRI
Site 2: BamHI. The library was constructed as desc

```

Carninci, P. (2003) in *DNA Microarrays: A Molecular Cloning Manual*, eds. Bowtell, D. & Sambrook, J. (Cold Spring Harbor, NY), pp. 647-670.

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Query Match      1.3%; Score 35.4; DB 1; Length 43;
Best Local Similarity 97.3%; Pred. No. 1.9e+02;
Matches 36: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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[illegible]

RESULT 62	DV573572/c	DV573572	43 bp	mRNA	linear	EST 04-NOV-2005
LOCUS						
DEFINITION						0058P0042B11.5' library 58 - normalized [50 mix pooled juveniles + adults] - male Taeniopygia guttata cDNA clone 0058P0042B11.5' similar to prohibitin, mRNA sequence.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 43)
Wada, K., Howard, J.T., McConnell, P., Linse, T., Rivas, M.V.,
Whitney, O., Horita, H., Patterson, M.A., White, S., Zhao, S.,
Sakaguchi, H., Hagiwara, M., Shiraki, T., Hirozane-Kishikawa, T.,
Skene, P., Hayashizaki, Y., Carninci, P. and Jarvis, E.D.
A molecular neuroethological approach for identifying and
characterizing a melody of behaviorally regulated genes
Unpublished (2005)
Other ESTs: 0058P00422.y0.B11
Contact: Kazuhiro Wada and Erich Jarvis
Erich D. Jarvis Lab
Duke University Medical Center - Department of Neurobiology
Box 3209 Bryan Research Building, Durham, NC 27710, USA
Tel: 919 681-1681
Email: wada@neuro.duke.edu and jarvis@neuro.duke.edu

FEATURES
SOURCE

```
. Location/Qualifiers
1..43
 /organism="Taeniopygia guttata"
 /mol_type="mRNA"
 /db_xref="taxon:59729"
 /clone="0058P0042B11"
 /sex="male"
 /tissue_type="brain"
 /dev_stage="adult and juvenile"
 /clone_lib="library S8 - normalized (50 mix pooled
 juveniles + adults) - male"
 /note="Organ: brain; Vector: pFUC-1; Site_1: EcoRI;
 Site_2: BamHI; The library was constructed as described by
 Carninci, P. (2003) in DNA Microarrays: A Molecular
 Cloning Manual, eds. Bowtell, D. & Sambrook, J. (Cold
 Spring Harbor, NY), pp. 647-670.
 TAG TISSUE=whole brain
 TAG_SEQID=accnctacacacactaacacca"
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Query Match	1.3%	Score 35.4;	DB 1;	Length 43;
Best Local Similarity	97.3%;	Pred. No. 1.9e+02;		
Matches 36:	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Qy	2707	CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2743
pb	43	C CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	7

[illegible]


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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ATUMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonic acid Carboxyl
methyltransferase overexpression line."

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Query Match      1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||||||
DB 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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```

RESULT 69
CV725312/c
LOCUS
DEFINITION
14Salt--02-F09.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
CV725312 GI:55412936
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

```

FEATURES
    source
        1..35
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="14Salt--02-F09"
            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli SOLR"
            /clone_lib="Salt treated rice leaf lambda phage cDNA
            library (14Salt)"
            /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
            XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
            cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
            with EcoRI and 3' end with XhoI site."

```

```

Query Match      1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||||||
DB 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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```

Query Match      1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||||||
DB 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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```

RESULT 70
CV725444/c
LOCUS
DEFINITION
14Salt--02-I15.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
CV725444 GI:55413068
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

```

```

DEFINITION
14Salt--02-I15.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
CV725444 GI:55413068
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

```

FEATURES
    source
        1..35
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="14Salt--02-I15"
            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli SOLR"
            /clone_lib="Salt treated rice leaf lambda phage cDNA
            library (14Salt)"
            /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
            XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
            cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
            with EcoRI and 3' end with XhoI site."

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```

Query Match      1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||||||
DB 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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```

RESULT 71
CV725518/c
LOCUS
DEFINITION
14Salt--02-K09.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
CV725518 GI:55413142
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```



```

Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. 35
/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/db_xref="taxon:39947"
/db_xref="taxon:39947"
/clone="14Salt--02-K09"
/tissue_type="leaf"
/dev stages="14 days after germination"
/lab host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 72
CV725797/c
LOCUS
DEFINITION
14Salt--03-B16.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-B16, mRNA sequence.
ACCESSION
CV725797.1 GI:55413421
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. 35
/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/db_xref="taxon:39947"
/db_xref="taxon:39947"
/clone="14Salt--04-B02"
/tissue_type="leaf"
/dev stages="14 days after germination"
/lab host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 74
CV727085/c
LOCUS
DEFINITION
14Salt--05-A23.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-A23, mRNA sequence.
ACCESSION
CV727085.1 GI:55414709
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

```

REFERENCE 1 (bases 1 to 35)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..35
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
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 Db 35 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 75
 CV727326/c
 LOCUS
 DEFINITION 35 bp mRNA linear EST 04-NOV-2004
 14Salt--05-G17.g1 Salt treated rice leaf lambda phage cDNA library
 14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 CV727326
 CV727326.1 GI:55414950
 EST.

ORYZA SATIVA (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 35)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..35
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--05-G17"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"

/lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 76

CV728725/c
 LOCUS
 DEFINITION 35 bp mRNA linear EST 05-NOV-2004
 FLO--01-D10.b1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--01-D10, mRNA
 sequence.
 CV728725
 CV728725.1 GI:55431423
 EST.

ORYZA SATIVA (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 35)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..35
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--01-D10"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 77

CV728984/c
 LOCUS
 DEFINITION 35 bp mRNA linear EST 05-NOV-2004
 FLO--01-J11.g1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--01-J11, mRNA
 sequence.
 CV728984

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CV728984.1 GI:55431928
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 35)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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1..35
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-J11"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 78
CV729199/c
LOCUS
DEFINITION
FLO--01-O16.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-O16, mRNA
sequence.
ACCESSION
CV729199.1 GI:55432357
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 35)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
source
1..35
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-O16"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 79
CV730453/c
LOCUS
DEFINITION
FLO--04-A02.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--04-A02, mRNA
sequence.
ACCESSION
CV730453.1 GI:55434657
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 35)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
source
1..35
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="FLO--04-A02"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 80
CV730547/c
LOCUS
DEFINITION
FLO--04-C08.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--04-C08, mRNA
sequence.

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/db_xref="taxon:39947"
/clone="FLO--01-O16"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 79
CV730453/c
LOCUS
DEFINITION
FLO--04-A02.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--04-A02, mRNA
sequence.
ACCESSION
CV730453.1 GI:55434657
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 35)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="FLO--04-A02"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 80
CV730547/c
LOCUS
DEFINITION
FLO--04-C08.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--04-C08, mRNA
sequence.

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sativa (japonica cultivar-group) cDNA clone FLO--08-M15, mRNA
sequence.
CV733739
CV733739.1 GI:55440852
EST.
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 35)
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="FLO--08-M15"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 87
CV734164/c
LOCUS
DEFINITION
sativa (japonica cultivar-group) cDNA clone FLO--09-G11, mRNA
sequence.
CV734164
CV734164.1 GI:55441677
EST.
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 35)
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="FLO--09-G11"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 87
CV734164/c
LOCUS
DEFINITION
sativa (japonica cultivar-group) cDNA clone FLO--09-G11, mRNA
sequence.
CV734164
CV734164.1 GI:55441677
EST.
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 35)
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
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Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-G11"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 88
AZ623128/c
LOCUS
DEFINITION
IM0460002R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0460D02 R, genomic survey sequence.
AZ623128
AZ623128.1 GI:11745318
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 35)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: D column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 35.
FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0460D02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nb; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-G11"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 88
AZ623128/c
LOCUS
DEFINITION
IM0460002R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0460D02 R, genomic survey sequence.
AZ623128
AZ623128.1 GI:11745318
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 35)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: D column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 35.
FEATURES
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Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0460D02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nb; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were

```

ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 89
AZ803371/c
LOCUS
DEFINITION 2M0063C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ803371
VERSION AZ803371.1 GI:12955694
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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```

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

```

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0063 row: C column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 35.

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FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0063C15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were

```

ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||||||
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 90
AJ791385/c
LOCUS
DEFINITION AJ791385 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018.2.08_j14, mRNA sequence.
ACCESSION AJ791385
VERSION AJ791385.1 GI:51061705
KEYWORDS EST.
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Antirrhinum majus

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```

REFERENCE
1 (bases 1 to 36)
AUTHORS Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
TITLE Characterization of Antirrhinum Petal Development and
Identification of target Genes of the Class B MADS Box Gene
DEFICIENS
JOURNAL Plant Cell 16 (12), 3197-3215 (2004)
PUBMED 15539471
COMMENT Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforshung
Carl-von-Linne Weg 10, D-50829, Germany.

```

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FEATURES
source
1..36
/organism="Antirrhinum majus"
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/db_xref="taxon:4151"
/clone="018.2.08_j14"
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/clone_lib="Antirrhinum majus whole plant"

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Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

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RESULT 91
AL587891/c
LOCUS
DEFINITION AL587891 BP Chicken Brain Library Gallus gallus cDNA clone
R05064H03, mRNA sequence.
ACCESSION AL587891
VERSION AL587891.1 GI:13192925
KEYWORDS EST.

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SOURCE	Gallus gallus (chicken)
ORGANISM	Gallus gallus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
AUTHORS	1 (bases 1 to 36)
TITLE	Murray, F.
JOURNAL	BP Chicken Brain Library
COMMENT	Unpublished (2001) Contact: Frazer Murray Dept. Genomics and Bioinformatics Roelin Institute Roelin, Midlothian, EH25 9PS, UK Tel: +44 (0)131 527 4200 Fax: +44 (0)131 440 0434 Email: frazer.murray@bbsrc.ac.uk GCGGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clonetechn (*6854-1)
FEATURES	Seq primer: M13P. Location/Qualifiers 1..36 /organism="Gallus gallus" /mol_type="mRNA" /db_xref="taxon:9031" /clone="ROS064H03" /tissue_type="Brain" /dev_stage="Unknown" /lab_host="DH10B" /clone_lib="BP Chicken Brain Library" /note="vector: pSPOR1; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clonetechn (*6854-1)"
source	
Query Match	1.3%; Score 35; DB 1; Length 36;
Best Local Similarity	100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db	36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2
RESULT 92	
AM046410/c	
LOCUS	AM046410 Schistosoma mansoni 36 bp mRNA linear EST 20-SEP-2005
DEFINITION	AM046410 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmIC13d11.glk, mRNA sequence.
ACCESSION	AM046410
VERSION	AM046410.1 GI:75970489
KEYWORDS	EST.
SOURCE	Schistosoma mansoni
ORGANISM	Schistosoma mansoni
REFERENCE	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeida; Schistosomatoidea; Schistosomatidae; Schistosoma.
AUTHORS	1 (bases 1 to 36)
TITLE	Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C. Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
JOURNAL	Unpublished (2005)
COMMENT	Contact: Ivens AC Pathogen Microarrays Group Wellcome Trust Sanger Institute Hinxton, CB10 1SA, UNITED KINGDOM.
FEATURES	Location/Qualifiers 1..36 /organism="Schistosoma mansoni" /mol_type="mRNA" /db_xref="taxon:6183" /clone="SmIC13d11.glk" /dev stage="lung schistosomulum"
source	

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ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-06-J02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20uM) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 95
CF331913/c
LOCUS
DEFINITION      NACL--08-D12.b1 Rice callus.plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--08-D12, mRNA
sequence.
ACCESSION      CF331913.1 GI:33812047
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20uM) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CF331913
NACL--08-D12.b1 Rice callus.plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--08-D12, mRNA
sequence.
CF331913
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/mol_type="mRNA"

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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 96
CF331983/c
LOCUS
DEFINITION      NACL--08-F01.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--08-F01, mRNA
sequence.
ACCESSION      CF331983
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--08-F01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 97
CF333863/c
LOCUS
DEFINITION      NACL--08-F01.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--08-F01, mRNA
sequence.
ACCESSION      CF333863
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

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DEFINITION  JMT--02-022.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
              library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-022, mRNA sequence.
CF333863
VERSION      CF333863.1 GI:33816032
SOURCE      EST.
ORGANISM    Oryza sativa (japonica cultivar-group)
              Oryza sativa (japonica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
              clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 36)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Gyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
     1..36
     /organism="Oryza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:39947"
     /clone="JMT--02-022"
     /tissue_type="leaf"
     /dev_stage="14 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
     cDNA library (JMT)"
     /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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     prepared from Arabidopsis Jasmonate Carboxyl
     methyltransferase overexpression line."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db   1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 98
BE876160
LOCUS      BE876160.1 GI:10324936
DEFINITION Homo sapiens (human)
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
              NIH-MGC http://mgs.nci.nih.gov/.
              National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgabbs@mail.nih.gov
              Tissue Procurement: DCTD/DTF/Gazdar
              cDNA Library prepared by: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db   1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 98
BE876160
LOCUS      BE876160.1 GI:10324936
DEFINITION Homo sapiens (human)
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
              NIH-MGC http://mgs.nci.nih.gov/.
              National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgabbs@mail.nih.gov
              Tissue Procurement: DCTD/DTF/Gazdar
              cDNA Library prepared by: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be

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found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM9667 row: f column: 16
 High quality sequence stop: 36.

FEATURES

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     Location/Qualifiers
     1..36
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="IMAGE:388015"
     /tissue_type="large cell carcinoma, undifferentiated"
     /lab_host="DH10B (phage-resistant)"
     /clone_lib="NIH_MGC_69"
     /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
     Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
     Average insert size 1.1 kb. Library constructed by Life
     Technologies."

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Query Match 1.3%; Score 35; DB 1; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db   1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

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RESULT 99

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CV724782/c
LOCUS      CV724782/c
DEFINITION 36 bp mRNA linear EST 04-NOV-2004
              14Salt--01-I19.g1 Salt treated rice leaf lambda phage cDNA library
              14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
              14Salt--01-I19, mRNA sequence.

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ACCESSION   CV724782
VERSION     CV724782.1 GI:55412406
KEYWORDS    Oryza sativa (japonica cultivar-group)
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
              clade; Ehrhartoideae; Oryzeae; Oryza.
              1 (bases 1 to 36)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Gyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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FEATURES

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     Location/Qualifiers
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     /organism="Oryza sativa (japonica cultivar-group)"
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     /cultivar="Nackdong"
     /db_xref="taxon:39947"
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     /tissue_type="leaf"
     /dev_stage="14 days after germination"
     /lab_host="E.coli SOLR"
     /clone_lib="Salt treated rice leaf lambda phage cDNA
     library (14Salt)"
     /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
     XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
     cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
     with EcoRI and 3' end with XhoI site."

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Query Match 1.3%; Score 35; DB 1; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 100
CV725281/c
LOCUS CV725281 36 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--02-E17.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-E17, mRNA sequence.
ACCESSION CV725281
VERSION CV725281.1 GI:55412905
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 36)
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="14Salt--02-E17"
/tissue_type="leaf"
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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 101
CV725289/c
LOCUS CV725289 36 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--02-E21.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-E21, mRNA sequence.
ACCESSION CV725289
VERSION CV725289.1 GI:55412913
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 36)
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/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-E21"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 102
CV725592/c
LOCUS CV725592 36 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--02-M04.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-M04, mRNA sequence.
ACCESSION CV725592
VERSION CV725592.1 GI:55413216
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 36)
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 103
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LOCUS CV725592 36 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--02-M04.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-M04, mRNA sequence.
ACCESSION CV725592
VERSION CV725592.1 GI:55413216
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 36)
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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<p>/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"</p> <p>/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."</p>		<p>1.3%; Score 35; DB 1; Length 36;</p> <p>Best Local Similarity 100.0%; Pred. No. 1.0e+02;</p> <p>Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>
Qy	2709	AA 2743
Db	36	AA 2
<p>RESULT 103</p> <p>CV726151/c</p> <p>LOCUS</p> <p>DEFINITION</p> <p>ORYZA SATIVA (JAPONICA CULTIVAR-GROUP) CDNA CLONE</p> <p>ACCSSION</p> <p>VERSION</p> <p>KEYWORDS</p> <p>SOURCE</p> <p>ORGANISM</p> <p>REFERENCE</p> <p>AUTHORS</p> <p>TITLE</p> <p>JOURNAL</p> <p>COMMENT</p>		
<p>CV726151 36 bp mRNA linear EST 04-NOV-2004</p> <p>14Salt--03-K07.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) CDNA clone</p> <p>14Salt--03-K07, mRNA sequence.</p> <p>CV726151</p> <p>CV726151.1 GI:55413775</p> <p>EST.</p> <p>Oryza sativa (japonica cultivar-group)</p> <p>Oryza sativa (japonica cultivar-group)</p> <p>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.</p> <p>1 (bases 1 to 36)</p> <p>Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.</p> <p>Large-scale Sequencing Analysis of Rice ESTs</p> <p>Unpublished (2003)</p> <p>Contact: Nahm B.H.</p> <p>Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University</p> <p>Yongin, Kyeonggi, Korea</p> <p>Tel: 82 31 330 6193</p> <p>Fax: 82 31 321 6355</p> <p>Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.</p>		
<p>FEATURES</p> <p>source</p> <p>1..36</p> <p>/organism="Oryza sativa (japonica cultivar-group)"</p> <p>/mol_type="mRNA"</p> <p>/cultivar="Nackdong"</p> <p>/db_xref="taxon:39947"</p> <p>/clone="14Salt--03-K07"</p> <p>/tissue_type="leaf"</p> <p>/dev_stage="14 days after germination"</p> <p>/lab_host="E.coli SOLR"</p> <p>/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"</p> <p>/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."</p>		
<p>Query Match</p> <p>Best Local Similarity 100.0%; Pred. No. 1.0e+02;</p> <p>Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>		<p>1.3%; Score 35; DB 1; Length 36;</p> <p>Best Local Similarity 100.0%; Pred. No. 1.0e+02;</p> <p>Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>
Qy	2709	AA 2743
Db	36	AA 2
<p>RESULT 104</p> <p>CV726321/c</p> <p>LOCUS</p> <p>DEFINITION</p> <p>ORYZA SATIVA (JAPONICA CULTIVAR-GROUP) CDNA CLONE</p> <p>ACCSSION</p> <p>VERSION</p> <p>KEYWORDS</p> <p>SOURCE</p> <p>ORGANISM</p> <p>REFERENCE</p> <p>AUTHORS</p> <p>TITLE</p> <p>JOURNAL</p> <p>COMMENT</p>		
<p>CV726321 36 bp mRNA linear EST 04-NOV-2004</p> <p>14Salt--03-008.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) CDNA clone</p>		

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FEATURES
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/dev_stages="14 days after germination"
/lab_host="E.coli SOLR"
/library="14Salt"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 1.3%; Score 35; DB 1; Length 36;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 106
CV728675/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-C05, mRNA
sequence.
ACCESSION
CV728675
VERSION
1..36
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 1.3%; Score 35; DB 1; Length 36;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 107
CV728870/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-G18, mRNA
sequence.
ACCESSION
CV728870
VERSION
1..36
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match
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Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 108
CV729206/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-G21, mRNA
sequence.
ACCESSION
CV729206
VERSION
1..36
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
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/mol_type="mRNA"
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/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 1.3%; Score 35; DB 1; Length 36;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

```

```

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
Location/Qualifiers
1. .36
/organism="Oryza sativa (japonica cultivar-group)"
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/clone="FLO--01-021"
/tissue_type="flower"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 109
CV730235/c
LOCUS
DEFINITION
FLO--03-K22.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--03-K22, mRNA
sequence.
CV730235
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
Location/Qualifiers
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/organism="Oryza sativa (japonica cultivar-group)"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 111
CV730953/c
LOCUS
DEFINITION
FLO--04-M03.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--04-M03, mRNA
sequence.
CV730953
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
Location/Qualifiers
1. .36
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 111
CV730953/c
LOCUS
DEFINITION
FLO--04-M03.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--04-M03, mRNA
sequence.
CV730953
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
Location/Qualifiers
1. .36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

```


of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

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1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
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Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 112

CV732578/c
LOCUS
DEFINITION
FLO--07-B22.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-B22, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source
1..36
/organism="Oryza sativa (japonica cultivar-group)"
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 113

CV732659/c
LOCUS
DEFINITION
FLO--07-D18.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-D18, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 114

CV733597/c
LOCUS
DEFINITION
FLO--08-J07.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-J07, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..36
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO-08-J07"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/notes="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 115
CV734403/C

LOCUS FLO-09-M02.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO-09-M02, mRNA
sequence.
CV734403
CV734403.1 GI:55442165

ACCESSION Oryza sativa (japonica cultivar-group)
VERSION Oryza sativa (japonica cultivar-group)
KEYWORDS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
SOURCE 1 (bases 1 to 36)
ORGANISM Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

REFERENCE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..36
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO-09-M02"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 116
AZ470916/C

LOCUS 1M0285523F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clome UUGC1M0285E23 F, genomic survey sequence.

ACCESSION AZ470916
VERSION AZ470916.1 GI:10629041
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 36)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 595 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0285 row: E column: 23
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 36.

FEATURES

source

1..36
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0285E23"
/sex="Male"
/lab_host="E. Coli strain Xli0-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli Xli0-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AA 2743
 |||||
 Db 36 AA 2

RESULT 117
 AZ628484/c 36 bp DNA linear GSS 13-DEC-2000
 LOCUS
 DEFINITION 1M0480808R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0480808 R, genomic survey sequence.

ACCESSION
 VERSION AZ628484.1 GI:11750674
 KEYWORDS
 SOURCE GSS.
 Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 36)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0480 row: B column: 08
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 36.

FEATURES
 source

1. .36
 /location=Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0480808"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.3%; Score 35; DB 1; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AA 2743
 |||||
 Db 36 AA 2

RESULT 118
 AZ793484/c

LOCUS
 DEFINITION 2M0046G15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0046G15 R, genomic survey sequence.

ACCESSION
 VERSION AZ793484.1 GI:12938483
 KEYWORDS
 SOURCE GSS.
 Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 36)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0046 row: G column: 15
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 36.

FEATURES
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 /mol_type="genomic DNA"
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 /db_xref="taxon:10090"
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.3%; Score 35; DB 1; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db      36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 119
AZ949866/c
LOCUS   2M0213H10R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION
ACCESSION AZ949866
VERSION   AZ949866.1 GI:13821093
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
TITLE    Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL  Unpublished (2000)
COMMENT  Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0213 row: H column: 10
          Seq primer: CACACAGGAAACGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 36.
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              /db_xref="taxon:10090"
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              /sex="Female"
              /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUGC2M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (female) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred.No.1.8e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db      36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 120
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LOCUS   2M0224G19R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION
ACCESSION AZ957867
VERSION   AZ957867.1 GI:13829094
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
TITLE    Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL  Unpublished (2000)
COMMENT  Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0224 row: G column: 19
          Seq primer: CACACAGGAAACGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 36.
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              /sex="Female"
              /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUGC2M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (female) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred.No.1.8e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

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Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 121
LOCUS C2914006 36 bp DNA linear GSS 08-AUG-2005
DEFINITION 4013005B08.2EL_x1 4013 - RescueMu Grid O Zea mays genomic, genomic survey sequence.
ACCESSION C2914006
VERSION C2914006.1 GI:71930364
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 36)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013005 row: B column: 08
Class: transposon-tagged.
Location/Qualifiers
1..36
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/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 122
LOCUS DUB834235 36 bp DNA linear GSS 22-DEC-2005
DEFINITION KRS013L23F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS013L23, genomic survey sequence.
ACCESSION DUB834235
VERSION DUB834235.1 GI:83870831

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 123
LOCUS DX046307/c
DEFINITION KBrB047024F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB047024, genomic survey sequence.
ACCESSION DX046307
VERSION DX046307.1 GI:84740604
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 36)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis Sau3AI BAC clone KBrS013L23
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..36
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
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/db_xref="taxon:51351"
/clone="KBrS013L23"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa subsp. pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 123
LOCUS DX046307/c
DEFINITION KBrB047024F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB047024, genomic survey sequence.
ACCESSION DX046307
VERSION DX046307.1 GI:84740604
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 36)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr

```

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB047024
Seq primer: T7
Class: BAC ends.
Location/Qualifiers

FEATURES

source

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1. .36
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/mol_type="genomic DNA"
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/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 124
BG033620
LOCUS 37 bp mRNA linear EST 24-JAN-2001
DEFINITION 602301748F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4403554 5',
mRNA sequence.
ACCESSION BG033620
VERSION BG033620.1 GI:12426095
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE 1 (bases 1 to 37)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10113 row: 0 column: 11
High quality sequence stop: 37.

FEATURES

source

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1. .37
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4403554"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;  
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.383 Kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH_MGC Library."
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Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 125

CF291818/c

LOCUS

DEFINITION

CF291818 37 bp mRNA linear EST 14-AUG-2003

14ROOT--02-G14.b1 Rice root plasmid cDNA library (14ROOT) Oryza

sativa (japonica cultivar-group) cDNA clone 14ROOT--02-G14, mRNA

sequence.

ACCESSION CF291818

VERSION CF291818.1 GI:33660851

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; BPP

clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 37)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .37

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ROOT--02-G14"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 37;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 126

CF300002

LOCUS

DEFINITION

CF300002 37 bp mRNA linear EST 15-AUG-2003

7LEAF--04-D21.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa (japonica cultivar-group) cDNA clone 7LEAF--04-D21, mRNA

sequence.

ACCESSION CF300002

VERSION CF300002.1 GI:33671763

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; BPP

clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 37)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 127
CF300328
LOCUS 37 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-K23 g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-K23, mRNA sequence.
ACCESSION CF300328
VERSION CF300328.1 GI:33672089
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 37)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 128

CF301560
LOCUS 37 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-H14 g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-H14, mRNA sequence.
ACCESSION CF301560
VERSION CF301560.1 GI:33673321
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 37)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--06-H14"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 129

CF301864/c
LOCUS 37 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-003.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-003, mRNA sequence.
ACCESSION CF301864
VERSION CF301864.1 GI:33673625
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 37)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm, B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..37
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 130

CF307971/c
LOCUS
DEFINITION
ABF--01-J16.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--01-J16, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 37)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm, B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..37
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="ABF--01-J16"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 131

CF316114
LOCUS
DEFINITION
HD--05-E13.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-E13, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 37)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm, B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..37
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--05-E13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 132

CF321294
LOCUS
DEFINITION
CF321294

DEFINITION HD--12-101.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION HD--12-101, mRNA sequence.

VERSION CF321294

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 37)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..37

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HD-12-101"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.3%; Score 35; DB 1; Length 37;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 133

CF326975/c

LOCUS CF326975.1 GI:33802205

DEFINITION NACL--01-E08.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-E08, mRNA sequence.

ACCESSION CF326975

VERSION CF326975.1 GI:33802205

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 37)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

FEATURES

source

1..37

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

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/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 37;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 134

CF333624/c

LOCUS CF333624.1 GI:33815543

DEFINITION JMT--02-J14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION CF333624

VERSION CF333624.1 GI:33815543

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 37)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..37

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="JMT--02-J14"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"

/note="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 1.3%; Score 35; DB 1; Length 37;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 135
CF336769/c
LOCUS CF336769 37 bp mRNA linear EST 18-AUG-2003
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
SOURCE JMT--06-P04, mRNA sequence.
ACCESSION CF336769.1 GI:33821918
VERSION CF336769
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 37)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtUMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 136
CV724637/c
LOCUS CV724637 37 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--01-F06.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
SOURCE 14Salt--01-F06, mRNA sequence.
ACCESSION CV724637
VERSION CV724637
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 37)

```

```

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 137
CV725878/c
LOCUS CV725878 37 bp mRNA linear EST 04-NOV-2004
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(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
SOURCE 14Salt--03-D12, mRNA sequence.
ACCESSION CV725878
VERSION CV725878
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 37)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli SOLR"

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/clone.lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
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Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 138
 CV726514/c
 LOCUS
 DEFINITION 14Salt--04-D07.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--04-D07, mRNA sequence.

ACCESSION CV726514
 VERSION CV726514
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 37)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;
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Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 139
 CV726571/c
 LOCUS
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14Salt--04-E15, mRNA sequence.

ACCESSION CV726571
 VERSION CV726571.1 GI:55414195
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 37)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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 /note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
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Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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RESULT 140
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 LOCUS
 DEFINITION 14Salt--05-F08.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--05-F08, mRNA sequence.

ACCESSION CV727266
 VERSION CV727266.1 GI:55414890
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 37)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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Query Match 1.3%; Score 35; DB 1; Length 37;
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Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360UM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db |||||||
37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 141
CV727448/c
LOCUS
DEFINITION
14Salt--05-J14.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-J14, mRNA sequence.
ACCESSION
CV727448
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360UM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db |||||||
37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 141
CV727448/c
LOCUS
DEFINITION
14Salt--05-J14.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-J14, mRNA sequence.
ACCESSION
CV727448
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360UM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db |||||||
37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 142
CV727567/c
LOCUS
DEFINITION
14Salt--05-M08.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-M08, mRNA sequence.
ACCESSION
CV727567
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/dev_stage="14 days after germination"
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360UM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db |||||||
37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 143
CV727819/c
LOCUS
DEFINITION
14Salt--06-C16.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--06-C16, mRNA sequence.
ACCESSION
CV727819
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

```

Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B. H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
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 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers
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Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 145
 CV728196/c
 LOCUS
 DEFINITION 14Salt--06-M10.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) CDNA clone
 14Salt--06-M10, mRNA sequence.
 ACCESSION CV728196
 VERSION CV728197.1 GI:55430492
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 37)
 AUTHORS Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
 Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B. H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers
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Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 144
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 LOCUS
 DEFINITION 14Salt--06-M10.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) CDNA clone
 14Salt--06-M10, mRNA sequence.
 ACCESSION CV728196
 VERSION CV728197.1 GI:55430492
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 37)
 AUTHORS Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
 Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B. H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers
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 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 146
 CV730003/c
 LOCUS
 DEFINITION FLO--03-F09.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) CDNA clone FLO--03-F09, mRNA sequence.

library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 145
 CV728197/c
 LOCUS
 DEFINITION 14Salt--06-M11.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) CDNA clone
 14Salt--06-M11, mRNA sequence.
 ACCESSION CV728197
 VERSION CV728197.1 GI:55430493
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 37)
 AUTHORS Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
 Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B. H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers
 1. .37
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--06-M11"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 146
 CV730003/c
 LOCUS
 DEFINITION FLO--03-F09.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) CDNA clone FLO--03-F09, mRNA sequence.

ACCESSION CV730003
 VERSION CV730003.1 GI:55433779
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 37)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..37
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="rRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--03-F09"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5',
 end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
 Matches 35; Conservative 0; Mismatches 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 147
 CV730176/c
 LOCUS
 DEFINITION FLO--03-J09.b1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--03-J09, mRNA
 sequence.

ACCESSION CV730176
 VERSION CV730176.1 GI:55434119
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 37)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..37
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="rRNA"

/cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--03-J09"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5',
 end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
 Matches 35; Conservative 0; Mismatches 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 148
 CV731472/c
 LOCUS
 DEFINITION FLO--05-I10.b1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--05-I10, mRNA
 sequence.

ACCESSION CV731472
 VERSION CV731472.1 GI:55436672
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 37)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..37
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="rRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--05-I10"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5',
 end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 149
 AZ321759
 LOCUS
 DEFINITION 1M0042P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0042P22 F, genomic survey sequence.


```

ACCESSION      AZ321759
VERSION        AZ321759.1  GI:10374820
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0042 row: P column: 22
               Seq primer: CGTTGTAACGACGCGCCAGT
               Class: plasmid ends
               High quality sequence stop: 37.
               Location/Qualifiers
                 1. .37
                   /organism="Mus musculus"
                   /mol_type="genomic DNA"
                   /strain="C57BL/6J"
                   /db_xref="taxon:10090"
                   /clone="UUGC1M0042P22"
                   /sex="Male"
                   /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                   /clone_lib="Mouse 10kb plasmid UUGC1M library"
                   /note="Vector: PWD42nv; Purified genomic DNA from M.
                   musculus C57BL/6J (male) was obtained from the Jackson
                   Laboratory Mouse DNA Resource
                   (http://www.jax.org/resources/documents/dnares/). The DNA
                   was hydrodynamically sheared by repeated passage through a
                   0.005 inch orifice at constant velocity. The sheared DNA
                   was blunt end-repaired with T4 DNA polymerase and T4
                   polynucleotide kinase. Adaptor oligonucleotides were
                   ligated to the blunt ends in high molar excess. The
                   adaptor DNA was purified and size-selected for a 9.5 to
                   10.5 kb range using preparative agarose gel
                   electrophoresis. Vector DNA was prepared from a derivative
                   of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                   inducible derivative of plasmid R1. The vector was ligated
                   with adaptors complementary to the insert adaptors and
                   purified. The sheared, adaptor mouse DNA was annealed to
                   adaptor vector DNA, and transformed into
                   chemically-competent E. coli XL10-Gold (Stratagene) cells
                   and selected for ampicillin resistance."

Query Match      1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 150
AZ463801/c
LOCUS
DEFINITION      1M0272E23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0272E23 R, genomic survey sequence.

```

```

ACCESSION      AZ463801
VERSION        AZ463801.1  GI:10621926
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0272 row: E column: 23
               Seq primer: CACACAGGAACACGCTATGACC
               Class: plasmid ends
               High quality sequence stop: 37.
               Location/Qualifiers
                 1. .37
                   /organism="Mus musculus"
                   /mol_type="genomic DNA"
                   /strain="C57BL/6J"
                   /db_xref="taxon:10090"
                   /clone="UUGC1M0272E23"
                   /sex="Male"
                   /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                   /clone_lib="Mouse 10kb plasmid UUGC1M library"
                   /note="Vector: PWD42nv; Purified genomic DNA from M.
                   musculus C57BL/6J (male) was obtained from the Jackson
                   Laboratory Mouse DNA Resource
                   (http://www.jax.org/resources/documents/dnares/). The DNA
                   was hydrodynamically sheared by repeated passage through a
                   0.005 inch orifice at constant velocity. The sheared DNA
                   was blunt end-repaired with T4 DNA polymerase and T4
                   polynucleotide kinase. Adaptor oligonucleotides were
                   ligated to the blunt ends in high molar excess. The
                   adaptor DNA was purified and size-selected for a 9.5 to
                   10.5 kb range using preparative agarose gel
                   electrophoresis. Vector DNA was prepared from a derivative
                   of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                   inducible derivative of plasmid R1. The vector was ligated
                   with adaptors complementary to the insert adaptors and
                   purified. The sheared, adaptor mouse DNA was annealed to
                   adaptor vector DNA, and transformed into
                   chemically-competent E. coli XL10-Gold (Stratagene) cells
                   and selected for ampicillin resistance."

Query Match      1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
DB 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 151
AZ831214
LOCUS
DEFINITION      2M0110P16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0110P16 R, genomic survey sequence.

```


TITLE
JOURNAL
COMMENT

End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel.: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbsomrda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB081A15
Seq primer: T7
Class: BAC ends.

FEATURES
source

1..37
Location/Qualifiers

/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB081A15"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 154
LOCUS DX072665/c 37 bp DNA linear GSS 10-JAN-2006
DEFINITION KBrB082M17f KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB082M17, genomic survey
sequence.

ACCESSION DX072665
VERSION DX072665.1 GI:84766961
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 37)
AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.

TITLE
JOURNAL
COMMENT

End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel.: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbsomrda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB082M17
Seq primer: T7
Class: BAC ends.

FEATURES
source

1..37
Location/Qualifiers

/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"

/db_xref="taxon:51351"
/clone="KBrB082M17"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 155
LOCUS DR102P24T/c 37 bp DNA linear GSS 21-NOV-2002
DEFINITION Danio rerio genomic clone DKEY-102P24, genomic survey sequence.

ACCESSION AL9771144
VERSION AL9771144.1 GI:25173875
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 37)
AUTHORS Humphray, S.J., Huckle, E. and Hunt, S.E.
TITLE Direct Submission

JOURNAL Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquerry@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the T7 end of BAC 102P24. 102P24
is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.

Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES
source

1..37
Location/Qualifiers

/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-102P24"
/tissue_type="Testis"
/note="vector pindigoBAC-536"

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 156
LOCUS DR102P2T 37 bp DNA linear GSS 21-NOV-2002
DEFINITION Danio rerio genomic clone DKEY-102P2, genomic survey sequence.

ACCESSION AL985556
VERSION AL985556.1 GI:25173839
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 37)
AUTHORS Humphray, S.J., Huckle, E. and Hunt, S.E.
TITLE Direct Submission

JOURNAL Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome

Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquerry@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 102P2. 102P2 is part of the Danokey BAC Library created by R. Plasterk and N.V. Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_orio/.

FEATURES

source

Location/Qualifiers
1..37
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-102P2"
/tissue_type="Testis"
/notes="vector pindigobAC-536"

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 157

CF291176/c

LOCUS
DEFINITION
14ROOT--01-I01.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-I01, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-I01"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 158

CF301164/c

LOCUS

DEFINITION

38 bp mRNA linear EST.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 38)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..38

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--05-O13"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 159

CF301819/c

LOCUS

DEFINITION

38 bp mRNA linear EST.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 38)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF-06-N03"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 160

CF321261/c
LOCUS
DEFINITION HD--12-H08.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--12-H08, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--12-H08"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.3%; Score 35; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 161

CF328351
LOCUS
DEFINITION NACL--03-D10.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--03-D10, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--03-D10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 162

CF329605/c
LOCUS
DEFINITION NACL--04-P21.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-P21, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 38)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
Source
1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--04-P21"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 163
CF329690 38 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--05-B17.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--05-B17, mRNA
sequence.
ACCESSION CF329690.1 GI:33807593
VERSION EST.
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--05-B17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 164
CF329730/c 38 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--05-C15.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--05-C15, mRNA
sequence.
ACCESSION CF329730.1 GI:33807676
VERSION EST.
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--05-C15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 165
BF525501 38 bp mRNA linear EST 11-DEC-2000
LOCUS 602069592P1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212527
DEFINITION 5', mRNA sequence.
ACCESSION BF525501
VERSION BF525501.1 GI:11612862
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 National Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LAM9783 row: 9 column: 24
 High quality sequence stop: 38.

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

1 (bases 1 to 38)

NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

National Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LAM9783 row: 9 column: 24

High quality sequence stop: 38.

FEATURES

source

1..38
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4212527"
 /tissue_type="glioblastoma with EGFR amplification"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Brn64"
 /note="Organ: Brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.57 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 166

BF526154 38 bp mRNA linear EST 11-DEC-2000
 LOCUS 602071057F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213910
 DEFINITION 5', mRNA sequence.

ACCESSION BF526154.1 GI:11613430

VERSION BF526154

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

1 (bases 1 to 38)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

National Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LAM9787 row: a column: 15

High quality sequence stop: 38.

FEATURES

source

1..38

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4213910"
 /tissue_type="glioblastoma with EGFR amplification"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Brn64"

/note="Organ: Brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.57 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

Query Match 1.3%; Score 35; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 167

CV724657/c

LOCUS CV724657 38 bp mRNA linear EST 04-NOV-2004

DEFINITION 14Salt--01-F18.g1 Salt treated rice leaf lambda phage cDNA library

14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

14Salt--01-F18, mRNA sequence.

ACCESSION CV724657

VERSION CV724657.1 GI:55412281

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 38)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

source

1..38

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--01-F18"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA

library (14Salt)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; Leaf was incubated at 4 C(360M/m-2sec-1) for 2hrs.

cDNA was inserted into lamda Uni-ZAP XR vector at 5' end

with EcoRI and 3' end with XhoI site."

Query Match

1.3%; Score 35; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 168

CV725198/c

LOCUS CV725198

38 bp mRNA linear EST 04-NOV-2004

DEFINITION 14Salt--02-C15.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-C15, mRNA sequence.

ACCESSION CV725198

VERSION CV725198.1 GI:55412822

SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 38)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

JOURNAL Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES source

1..38
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-C15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||

Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 169

CV725495/c

LOCUS CV725495 38 bp mRNA linear EST 04-NOV-2004

DEFINITION 14Salt--02-J20.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-J20, mRNA sequence.

ACCESSION CV725495

VERSION CV725495.1 GI:55413119

SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 38)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

JOURNAL Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES source

1..38
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-J20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||

Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 170

CV726250/c

LOCUS CV726250 38 bp mRNA linear EST 04-NOV-2004

DEFINITION 14Salt--03-M16.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-M16, mRNA sequence.

ACCESSION CV726250

VERSION CV726250.1 GI:55413874

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 38)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES source

1..38
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-M16"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

/lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 174

CV727096/c

LOCUS

DEFINITION

CV727096 38 bp mRNA linear EST 04-NOV-2004
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA library

CV727096 14Salt--05-B06, mRNA sequence.
 CV727096.1 GI:55414720

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 38)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
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 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..38
 Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--05-B06"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"

/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 175

CV727478/c

LOCUS

DEFINITION

CV727478 38 bp mRNA linear EST 04-NOV-2004
 14Salt--05-K07, Salt treated rice leaf lambda phage cDNA library

(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--05-K07, mRNA sequence.
 CV727478

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 38)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
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 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..38
 Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--05-K07"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"

/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match

1.3%; Score 35; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 176

CV727598/c

LOCUS

DEFINITION

SOURCE

ORGANISM

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

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COMMENT

CV727598 38 bp mRNA linear EST 04-NOV-2004
 14Salt--05-N02.g1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--05-N02, mRNA sequence.

CV727598

CV727598.1

GI:55415222

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 38)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source

Location/Qualifiers
1. 38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--05-N02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 177
CV727921/c

LOCUS
DEFINITION 14Salt--06-F06.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

CV727921

VERSION

CV727921.1 GI:55415545

KEYWORDS

EST.

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
1. 38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--06-F06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 178

CV728176/c

LOCUS
DEFINITION 14Salt--06-L22.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

CV728176

VERSION

CV728176.1 GI:55430461

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1. 38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--06-L22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

Query Match

Best Local Similarity

100.0%;

Pred. No. 1.9e+02;

Matches 35;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

RESULT 179

CV728223/c

LOCUS
DEFINITION 14Salt--06-N02.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

CV728223

VERSION

CV728223.1 GI:55430523

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 38)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--06-N02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 180

CV728809/c
LOCUS FLO--01-F07.g1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--01-F07, mRNA
sequence.

ACCESSION CV728809
VERSION CV728809.1 GI:55431587
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 38)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-F07"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||

Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 181

CV728835/c
LOCUS FLO--01-F21.g1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--01-F21, mRNA
sequence.

ACCESSION CV728835
VERSION CV728835.1 GI:55431639
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 38)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-F21"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||

Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 182

CV729857/c
LOCUS FLO--03-B18.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--03-B18, mRNA
sequence.

ACCESSION CV729857
VERSION CV729857.1 GI:55433501
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE JOURNAL

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

COMMENT

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES source

Location/Qualifiers

1. 38

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="FLO-03-B18"

/tissue_type="flower"

/lab_host="E.coli SOLR"

/clone_lib="Rice flower lambda phage cDNA library (FLO)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match

Best Local Similarity 1.3%; Score 35; DB 1; Length 38;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

|||||

38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 183

CV731476/c

LOCUS

DEFINITION FLO--05-112.b1 Rice flower lambda phage cDNA library (FLO) Oryza

sativa (japonica cultivar-group) cDNA clone FLO--05-112, mRNA

sequence.

ACCESSION

CV731476.1 GI:55436680

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 38)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1. 38

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="FLO-05-112"

/tissue_type="flower"

/lab_host="E.coli SOLR"

/clone_lib="Rice flower lambda phage cDNA library (FLO)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match

Best Local Similarity 1.3%; Score 35; DB 1; Length 38;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

|||||

38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 184

DR064343

LOCUS

DEFINITION

ip76105.g1 Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA

sequence.

ACCESSION

DR064343

VERSION

DR064343.1

GI:66987911

KEYWORDS

EST.

SOURCE

ORGANISM

Ginkgo biloba (maidenhair tree)

Ginkgo biloba

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

REFERENCE

1 (bases 1 to 38)

Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Ballaj, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo megasporophyll (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.

Location/Qualifiers

1. 38

/organism="Ginkgo biloba"

/mol_type="mRNA"

/db_xref="taxon:3311"

/sex="Female"

/clone_lib="Ginkgo megasporophyll (NYBG)"

/note="Organ: megasporophyll; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA

Synthesis Kit. The library was size-fractionated to enrich for large inserts."

Query Match

Best Local Similarity 1.3%; Score 35; DB 1; Length 38;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

|||||

1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 185

DM337683/c

LOCUS

DEFINITION

EST-AR18G8 Sus scrofa mixed tissue cDNA library Sus scrofa cDNA

clone AR18G8, mRNA sequence.

ACCESSION

DM337683

VERSION

DM337683.1

GI:84566064

KEYWORDS

EST.

SOURCE

ORGANISM

Sus scrofa (pig)

Sus scrofa

Eukaryota; Metazoa; Chordata; Cranita; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

DM337683

EST-AR18G8 Sus scrofa mixed tissue cDNA library Sus scrofa cDNA

clone AR18G8, mRNA sequence.

ACCESSION

DM337683

VERSION

DM337683.1

GI:84566064

KEYWORDS

EST.

SOURCE

ORGANISM

Sus scrofa (pig)

Sus scrofa

Eukaryota; Metazoa; Chordata; Cranita; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

```

Sus.
1. (bases 1 to 38)
Rink,A., Santschi,E.M. and Beattie,C.W.
Normalized cDNA libraries from a porcine model of orthopedic
implant-associated infection
Mamm. Genome 13 (4), 198-205 (2002)
11956763
Contact: Rink, A
Animal Disease and Food Safety Laboratory
Nevada Department of Agriculture
350 Capitol Hill Avenue, Reno, NV 89502, USA
Tel: 775-688-1180 Ext. 232
Fax: 775-688-1198
Email: arink@govmail.state.nv.us
Tissues and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of Staphylococcus
aureus in a tibial transection, reduced and internally fixed with a
dynamic compression plate. NOTE: The sequences contain a 'cDNA
adapter' between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCAGCG'. row: G column: 8.
FEATURES
Location/Qualifiers
1..38
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone="AR1808"
/tissue_type="mixed"
/cell_type="mixed"
/dev_stage="control, 5 month old castrated male"
/lab_host="SOLR"
/clone_lib="Sus scrofa mixed tissue cDNA library"
/notes="Vector: pBSK; Site 1: Eco RI; Site 2: XhoI; Tissues
and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of
Staphylococcus aureus in a tibial transection, reduced and
internally fixed with a dynamic compression plate. NOTE:
The sequences contain a 'cDNA adapter' between the EcoRI
site and the start of the EST. The adapter sequence is
'AATTCGGCAGCG'."
Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 186
A2785034/c
LOCUS 38 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0028106R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0028106 R, genomic survey sequence.
ACCESSION A2785034
VERSION A2785034.1 GI:12921371
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 38)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Sus.
1. (bases 1 to 38)
Rink,A., Santschi,E.M. and Beattie,C.W.
Normalized cDNA libraries from a porcine model of orthopedic
implant-associated infection
Mamm. Genome 13 (4), 198-205 (2002)
11956763
Contact: Rink, A
Animal Disease and Food Safety Laboratory
Nevada Department of Agriculture
350 Capitol Hill Avenue, Reno, NV 89502, USA
Tel: 775-688-1180 Ext. 232
Fax: 775-688-1198
Email: arink@govmail.state.nv.us
Tissues and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of Staphylococcus
aureus in a tibial transection, reduced and internally fixed with a
dynamic compression plate. NOTE: The sequences contain a 'cDNA
adapter' between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCAGCG'. row: G column: 8.
FEATURES
Location/Qualifiers
1..38
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone="AR1808"
/tissue_type="mixed"
/cell_type="mixed"
/dev_stage="control, 5 month old castrated male"
/lab_host="SOLR"
/clone_lib="Sus scrofa mixed tissue cDNA library"
/notes="Vector: pBSK; Site 1: Eco RI; Site 2: XhoI; Tissues
and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of
Staphylococcus aureus in a tibial transection, reduced and
internally fixed with a dynamic compression plate. NOTE:
The sequences contain a 'cDNA adapter' between the EcoRI
site and the start of the EST. The adapter sequence is
'AATTCGGCAGCG'."
Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 187
BG287495
LOCUS 39 bp mRNA linear EST 21-FEB-2001
DEFINITION 602384505F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4513609 5',
mRNA sequence.
ACCESSION BG287495
VERSION BG287495.1 GI:13041394
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 39)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

```

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0028 row: I column: 06
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.

FEATURES

Location/Qualifiers
1..38

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0028106"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

DB 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 187

BG287495
LOCUS 39 bp mRNA linear EST 21-FEB-2001
DEFINITION 602384505F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4513609 5',
mRNA sequence.
ACCESSION BG287495
VERSION BG287495.1 GI:13041394
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

1 (bases 1 to 39)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM10400 row: i column: 02
 High quality sequence stop: 36.
 Location/Qualifiers

FEATURES

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1..39
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4513609"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NTH_MGC_93"
/Note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NTH_MGC Library."

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Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 188
 Bi694035
 LOCUS 603342221F1 NCI_CGAP_Mam2 39 bp mRNA linear EST 18-SEP-2001
 DEFINITION Mus musculus cDNA clone IMAGE:5369956 5', mRNA sequence.

ACCESSION Bi694035
 VERSION Bi694035.1 GI:15656664

KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 39)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
 TITLE Contact: Robert Strausberg, Ph.D.
 JOURNAL Email: cgapbs-remail.nih.gov
 COMMENT Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM11941 row: j column: 05
 High quality sequence stop: 39.
 Location/Qualifiers

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1..39
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5369956"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"

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NOTE="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 189
 CF298508/c

LOCUS CF298508
 DEFINITION 7LEAF--01-O19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-O19, mRNA sequence.

ACCESSION CF298508
 VERSION CF298508.1 GI:33670269

KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 39)
 Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B. H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 Location/Qualifiers

```

1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--01-O19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/Note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 190
 CF302356/c

LOCUS CF302356
 DEFINITION 7LEAF--07-M16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-M16, mRNA sequence.

ACCESSION CF302356
 VERSION CF302356.1 GI:33674117

KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 39)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES source

1. .39
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAP--07-M16"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAP)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 191
 CF315736/c
 LOCUS
 DEFINITION
 HD--04-M06.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--04-M06, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 39)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
 source
 1. .39
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--04-M06"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDACL1-overexpressing transgenic rice plasmid

cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 192
 CF3121323/c
 LOCUS
 DEFINITION
 HD--12-I17.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--12-I17, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 39)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
 source
 1. .39
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--12-I17"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDACL1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 193
 CF330732/c
 LOCUS
 DEFINITION
 NACL--06-J06.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa (japonica cultivar-group) cDNA clone NACL--06-J06, mRNA sequence.
 CF330732.1 GI:33809685
 EST.
 ORGANSIM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 39)
 REFERENCE
 AUTHORS
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE
 Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL
 Unpublished (2003)
 COMMENT
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..39
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--06-J06"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_libs="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
 Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 194
 BF032623
 LOCUS
 DEFINITION
 601453114F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857019 5', mRNA sequence.
 ACCESSION
 BF032623
 VERSION
 BF032623.1 GI:10740335
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANSIM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 39)
 REFERENCE
 NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS
 National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 Unpublished (1999)
 JOURNAL
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Arrayed by: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM9586 row: k column: 04

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3857019"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_66"
 /note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."
 Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 195
 BE891613
 LOCUS
 DEFINITION
 601434505F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919584 5', mRNA sequence.
 ACCESSION
 BE891613
 VERSION
 BE891613.1 GI:10351110
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANSIM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 39)
 REFERENCE
 NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS
 National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 Unpublished (1999)
 JOURNAL
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LLAM9749 row: j column: 01

FEATURES
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 /db_xref="taxon:9606"
 /clone="IMAGE:3919584"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_72"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."
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 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

LOCATION/Qualifiers
1. .39

ORGANISM="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-E22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2709 AA 2743
|||||
Db 39 AA 5

RESULT 198
CV725192/c
LOCUS
DEFINITION
14Salt--02-C12.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--02-C12, mRNA sequence.

ACCESSION
CV725192.1 GI:55412816
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

LOCATION/Qualifiers
1. .39

ORGANISM="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-C12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2709 AA 2743
|||||
Db 39 AA 5

RESULT 197
CV724623/c
LOCUS
DEFINITION
14Salt--01-E22.b1 Salt treated rice leaf lambda phage cDNA library
14Salt--01-E22, mRNA sequence.

ACCESSION
CV724623.1 GI:55412247
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

LOCATION/Qualifiers
1. .39

ORGANISM="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-A17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2709 AA 2743
|||||
Db 39 AA 5

RESULT 196
CV724457/c
LOCUS
DEFINITION
14Salt--01-A17.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--01-A17, mRNA sequence.

ACCESSION
CV724457.1 GI:55412081
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

LOCATION/Qualifiers
1. .39

ORGANISM="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-A17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2709 AA 2743
|||||
Db 39 AA 5

RESULT 197
CV724623/c
LOCUS
DEFINITION
14Salt--01-E22.b1 Salt treated rice leaf lambda phage cDNA library
14Salt--01-E22, mRNA sequence.

ACCESSION
CV724623.1 GI:55412247
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

LOCATION/Qualifiers
1. .39

ORGANISM="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-A17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2709 AA 2743
|||||
Db 39 AA 5

RESULT 197
CV724623/c
LOCUS
DEFINITION
14Salt--01-E22.b1 Salt treated rice leaf lambda phage cDNA library
14Salt--01-E22, mRNA sequence.

ACCESSION
CV724623.1 GI:55412247
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

LOCATION/Qualifiers
1. .39

ORGANISM="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_x

cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

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Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db  39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 199
CV725228/c
LOCUS      39 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--02-D09.g1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
            14Salt--02-D09, mRNA sequence.
ACCESSION  CV725228
VERSION     CV725228.1 GI:55412852
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 39)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
     1..39
     /organism="Oryza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:39947"
     /clone="14Salt--02-D09"
     /tissue_type="leaf"
     /dev_stage="14 days after germination"
     /lab_host="E.coli SOLR"
     /clone_lib="Salt treated rice leaf lambda phage cDNA
     library (14Salt)"
     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
     XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
     cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
     with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db  39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 200
CV725383/c
LOCUS      39 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--02-H03.g1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
            14Salt--02-H03, mRNA sequence.
ACCESSION  CV725383
VERSION     CV725383.1 GI:55413007
KEYWORDS   EST.

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 39)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
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     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:39947"
     /clone="14Salt--02-H03"
     /tissue_type="leaf"
     /dev_stage="14 days after germination"
     /lab_host="E.coli SOLR"
     /clone_lib="Salt treated rice leaf lambda phage cDNA
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     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
     XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
     cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
     with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db  39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 201
CV725570/c
LOCUS      39 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--02-L15.g1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
            14Salt--02-L15, mRNA sequence.
ACCESSION  CV725570
VERSION     CV725570.1 GI:55413194
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 39)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
     1..39
     /organism="Oryza sativa (japonica cultivar-group)"
     /mol_type="mRNA"

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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-L15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 202
CV726046/c
LOCUS
DEFINITION
14Salt--03-H15.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--03-H15, mRNA sequence.
ACCESSION
CV726046
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-H15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 204
CV726327/c
LOCUS
DEFINITION
14Salt--03-O11.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--03-O11, mRNA sequence.
ACCESSION
CV726327
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-H15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

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RESULT 203
CV726057/c
LOCUS
DEFINITION
14Salt--03-H22.b1 Salt treated rice leaf lambda phage cDNA library
14Salt--03-H22, mRNA sequence.
ACCESSION
CV726057
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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1..39
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/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 204
CV726327/c
LOCUS
DEFINITION
14Salt--03-O11.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--03-O11, mRNA sequence.
ACCESSION
CV726327
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

```

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

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1..39
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

```

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 205

CV726361/c

LOCUS

DEFINITION

14Salt--03-P04.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--03-P04, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT

Unpublished (2003)
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

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1..39
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/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end

```

with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 206

CV726728/c

LOCUS

DEFINITION

14Salt--04-I09.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--04-I09, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE

JOURNAL

COMMENT

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

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1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

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Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 207

CV726866/c

LOCUS

DEFINITION

14Salt--04-L17.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--04-L17, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

Oryza sativa (japonica cultivar-group)


```

RESULT 210
CV727002/c
LOCUS
DEFINITION
14Salt--04-P01.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--04-P01, mRNA sequence.
ACCESSION
CV727002
VERSION
CV727002.1 GI:55414626
SOURCE
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 39)
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/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 39
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
FEATURES
source
1. 39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--04-P01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 212
CV727114/c
LOCUS
DEFINITION
CV727114 39 bp mRNA linear EST 04-NOV-2004
14Salt--05-B17.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-B17, mRNA sequence.
ACCESSION
CV727114
VERSION
CV727114.1 GI:55414738
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 39)
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 39
/organism="Oryza sativa (japonica cultivar-group)"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
FEATURES
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1. 39
/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
/db_xref="taxon:39947"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

```

```

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
FEATURES
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1. 39
/organism="Oryza sativa (japonica cultivar-group)"
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/db_xref="taxon:39947"
/clone="14Salt--04-P01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 211
CV727016/c
LOCUS
DEFINITION
14Salt--04-P09.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--04-P09, mRNA sequence.
ACCESSION
CV727016
VERSION
CV727016.1 GI:55414640
SOURCE
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 39)
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
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/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
FEATURES
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1. 39
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/tissue_type="leaf"
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/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

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Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 213
CV727215/c
LOCUS
DEFINITION
14Salt--05-E03.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--05-E03, mRNA sequence.
ACCESSION
CV727215
VERSION
CV727215.1 GI:55414839
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 39)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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JOURNAL
COMMENT
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnmggbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 215
CV727680/c
LOCUS
DEFINITION
14Salt--05-P01.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--05-P01, mRNA sequence.
ACCESSION
CV727680
VERSION
CV727680.1 GI:55415304
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 39)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnmggbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--05-E03"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 214
CV727351/c
LOCUS
DEFINITION
14Salt--05-H08.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--05-H08, mRNA sequence.
ACCESSION
CV727351
VERSION
CV727351.1 GI:55414975
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 39)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnmggbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 39)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Email: bnhnmggbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--05-H08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 215
CV727680/c
LOCUS
DEFINITION
14Salt--05-P01.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--05-P01, mRNA sequence.
ACCESSION
CV727680
VERSION
CV727680.1 GI:55415304
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 39)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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JOURNAL
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Yongin, Kyeonggi, Korea
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Fax: 82 31 321 6355
Email: bnhnmggbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"

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/clone="14Salt--05-P01"
/tissue_type="leaf"
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/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

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Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

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RESULT 216
CV728240/c
LOCUS
DEFINITION
14Salt--06-N13.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--06-N13, mRNA sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

```

```

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

```

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1 (bases 1 to 39)

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AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

```

```

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Fax: 82 31 321 6355
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Location/Qualifiers

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1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

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/cultivar="Nackdong"

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/db_xref="taxon:39947"

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/tissue_type="leaf"

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/dev_stage="14 days after germination"

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/lab_host="E.coli SOLR"

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/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"

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/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

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Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

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RESULT 217

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CV728278/c
LOCUS
DEFINITION

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14Salt--06-O12.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--06-O12, mRNA sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

```

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

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1 (bases 1 to 39)

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AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)

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TITLE
JOURNAL
COMMENT

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```

```

Location/Qualifiers

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1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

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/cultivar="Nackdong"

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/db_xref="taxon:39947"

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/clone="14Salt--06-O12"

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/dev_stage="14 days after germination"

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/lab_host="E.coli SOLR"

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/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"

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/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

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Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

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RESULT 218
CV729217/c
LOCUS
DEFINITION

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```

FLO--01-P02.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-P02, mRNA
sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

```

```

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

```

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1 (bases 1 to 39)

```

```

AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

```

```

TITLE
JOURNAL
COMMENT

```

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1. .39
/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-P02"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 219
CV730113/c
LOCUS
DEFINITION
FLO--03-H21.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--03-H21, mRNA

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1. (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
Location/Qualifiers
1. .39
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-F09"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
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end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 221
CV733026/c
LOCUS
DEFINITION
FLO--07-M05.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-M05, mRNA

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1. (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 220
CV732729/c
LOCUS
DEFINITION
FLO--07-F09.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-F09, mRNA

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1. (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
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end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 221
CV733026/c
LOCUS
DEFINITION
FLO--07-M05.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-M05, mRNA

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1. (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
Location/Qualifiers
1. .39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

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Location/Qualifiers

FEATURES

source
1. 39
/organism="Oryza sativa (japonica cultivar-group)"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 222

CV733160/c
LOCUS
DEFINITION
FLO--07-P05.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-P05, mRNA
sequence.

ACCESSION
CV733160

VERSION
CV733160.1 GI:55439700

KEYWORDS
EST.

SOURCE
Oryza sativa (japonica cultivar-group)

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
1 (bases 1 to 39)

AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
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Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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1. 39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 223

CV733431/c

LOCUS

DEFINITION

FLO--08-F12.g1 Rice flower lambda phage cDNA library (FLO) Oryza

sativa (japonica cultivar-group) cDNA clone FLO--08-F12, mRNA

sequence.

ACCESSION

CV733431

VERSION

CV733431.1 GI:55440243

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE

1 (bases 1 to 39)

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. 39

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="FLO--08-F12"

/tissue_type="flower"

/lab_host="E.coli SOLR"

/clone_lib="Rice flower lambda phage cDNA library (FLO)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'

end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 224

CV733935/c

LOCUS

DEFINITION

FLO--09-B06.g1 Rice flower lambda phage cDNA library (FLO) Oryza

sativa (japonica cultivar-group) cDNA clone FLO--09-B06, mRNA

sequence.

ACCESSION

CV733935

VERSION

CV733935.1 GI:55441239

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE

1 (bases 1 to 39)

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-R06"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AA 2743
|||||
Db 39 AA 5

RESULT 225
CV733973/c

LOCUS
DEFINITION
FLO--09-C05.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--09-C05, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CV733973 39 bp mRNA linear EST 05-NOV-2004
CV733973.1 GI:55441315
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-C05"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AA 2743
|||||
Db 39 AA 5

RESULT 226
AZ639088/c

LOCUS
DEFINITION
1M0499A20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0499A20 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ639088 39 bp DNA linear GSS 14-DEC-2000
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 39)

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0499 row: A column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 39.

Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0499A20"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 227
AL037510 40 bp mRNA linear EST 06-JUL-2004
LOCUS DKFZp564E1872_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
DEFINITION DKFZp564E1872, mRNA sequence.
ACCESSION AL037510
VERSION AL037510.1 GI:49682008
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Blum, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
      source
      1..40
      Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="DKFZp564E1872"
      /tissue_type="brain"
      /dev_stages="fetal"
      /lab_host="Xl-2blue"
      /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 5 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 39

RESULT 228
AL449576/c 40 bp mRNA linear EST 15-NOV-2000
LOCUS AL449576 Homo sapiens Testis (Stavrides GS)
DEFINITION AL449576, mRNA sequence.
ACCESSION AL449576
VERSION AL449576.1 GI:11181211
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS Stavrides,G.S., Huckle,E.J. and Deloukas,P.
TITLE Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P
JOURNAL Unpublished (2000)
COMMENT The Sanger Centre
Contact: Stavrides GS
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name: sccd3232.
      Location/Qualifiers
      1..40
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 5 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 39

RESULT 229
AL037510 40 bp mRNA linear EST 06-FEB-2001
LOCUS BGI66502 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4447702 5',
DEFINITION 602339795F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4447702 5',
mRNA sequence.
ACCESSION BGI66502
VERSION BGI66502.1 GI:12673205
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 40)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0228 row: n column: 23
High quality sequence stop: 40.
FEATURES
      source
      1..40
      Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:4447702"
      /tissue_type="hypernephroma, cell line"
      /lab_host="DH10B (phage-resistant)"
      /clone_lib="NIH_MGC_89"
      /note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI;
      Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
      Average insert size 1.3 kb. Library enriched for
      full-length clones and constructed by Life Technologies.
      Note: this is a NIH_MGC Library."

Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 230
CF311814/c 40 bp mRNA linear EST 15-AUG-2003
LOCUS CF311814 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION ABF--07-D23.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--07-D23, mRNA sequence.

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/map="20"
/tissue_type="Testis"
/clone_lib="Homo sapiens Testis (Stavrides GS)"
/note="cDNA fragment isolated using a cDNA end rescue
technique"

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ACCESSION      CF311814
VERSION        CF311814.1  GI:33683575
KEYWORDS
SOURCE
ORGANISM       Oryza sativa (japonica cultivar-group)
               Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF-07-D23"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 231
CF327027/c
LOCUS
DEFINITION     Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-P21, mRNA
               sequence.
ACCESSION      CF328199
VERSION        CF328199.1  GI:33804646
KEYWORDS
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF-07-D23"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 231
CF327027/c
LOCUS
DEFINITION     Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-F11, mRNA
               sequence.
ACCESSION      CF327027
VERSION        CF327027.1  GI:33802307
KEYWORDS
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

```

FEATURES
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Location/Qualifiers
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--01-F11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 232
CF328199/c
LOCUS
DEFINITION     Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-P21, mRNA
               sequence.
ACCESSION      CF328199
VERSION        CF328199.1  GI:33804646
KEYWORDS
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--02-P21"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

```

```

RESULT 233
CF328306
LOCUS
DEFINITION
  CF328306
  NACL--03-C09.g1 Rice callus plasmid cDNA library (NACL) Oryza
  sativa (japonica cultivar-group) cDNA clone NACL--03-C09, mRNA
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
  CF328306.1 GI:33804858
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 40)
REFERENCE
  AUTHORS
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE
    Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL
    Unpublished (2003)
  COMMENT
    Contact: Nahm B.H.
    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
    of Bioscience and Bioinformatics, Myongji University
    Yongin, Kyeonggi, Korea
    Tel: 82 31 330 6193
    Fax: 82 31 321 6355
    Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
  Location/Qualifiers
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    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /db_xref="taxon:39947"
    /clone="NACL--03-C09"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice callus plasmid cDNA library (NACL)"
    /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Length 40;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 234
CF334545/c
LOCUS
DEFINITION
  CF334545
  JMT--03-002.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
  library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
  JMT--03-002, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
  CF334545.1 GI:33817420
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 40)
REFERENCE
  AUTHORS
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE
    Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL
    Unpublished (2003)
  COMMENT
    Contact: Nahm B.H.
    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
    of Bioscience and Bioinformatics, Myongji University
    Yongin, Kyeonggi, Korea
    Tel: 82 31 330 6193
    Fax: 82 31 321 6355
    Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
  Location/Qualifiers
    1..40
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /db_xref="taxon:39947"
    /clone="NACL--03-C09"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice callus plasmid cDNA library (NACL)"
    /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Length 40;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 235
CV724551/c
LOCUS
DEFINITION
  CV724551
  14Salt--01-D05.b1 Salt treated rice leaf lambda phage cDNA library
  14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
  14Salt--01-D05, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
  CV724551.1 GI:55412175
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 40)
REFERENCE
  AUTHORS
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE
    Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL
    Unpublished (2003)
  COMMENT
    Contact: Nahm B.H.
    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
    of Bioscience and Bioinformatics, Myongji University
    Yongin, Kyeonggi, Korea
    Tel: 82 31 330 6193
    Fax: 82 31 321 6355
    Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
  Location/Qualifiers
    1..40
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /db_xref="taxon:39947"
    /clone="14Salt--01-D05"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli SOLR"
    /clone_lib="Salt treated rice leaf lambda phage cDNA
    library (14Salt)"
    /note="Vector: Bluescript SK(+); Site_1: EcoRI; Site_2:
    XhoI; Leaf was incubated at 4 C(360M/m-2sec-1) for 2hrs.
    cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
    with EcoRI and 3' end with XhoI site."

```

```

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
  1..40
  /organism="Oryza sativa (japonica cultivar-group)"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:39947"
  /clone="JMT--03-002"
  /tissue_type="leaf"
  /dev_stage="14 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="AtJMT-overexpressing transgenic rice plasmid
  cDNA library (JMT)"
  /note="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
  was reverse transcribed and then used for PCR. mRNA was
  prepared from Arabidopsis Jasmonate Carboxyl
  methyltransferase overexpression line."

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Length 40;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 235
CV724551/c
LOCUS
DEFINITION
  CV724551
  14Salt--01-D05.b1 Salt treated rice leaf lambda phage cDNA library
  14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
  14Salt--01-D05, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
  CV724551.1 GI:55412175
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 40)
REFERENCE
  AUTHORS
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE
    Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL
    Unpublished (2003)
  COMMENT
    Contact: Nahm B.H.
    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
    of Bioscience and Bioinformatics, Myongji University
    Yongin, Kyeonggi, Korea
    Tel: 82 31 330 6193
    Fax: 82 31 321 6355
    Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
  Location/Qualifiers
    1..40
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="14Salt--01-D05"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli SOLR"
    /clone_lib="Salt treated rice leaf lambda phage cDNA
    library (14Salt)"
    /note="Vector: Bluescript SK(+); Site_1: EcoRI; Site_2:
    XhoI; Leaf was incubated at 4 C(360M/m-2sec-1) for 2hrs.
    cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
    with EcoRI and 3' end with XhoI site."

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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

```

Query Match 1.3%; Score 35; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 239
 CV727416/c
 LOCUS
 DEFINITION 14Salt--05-121.bi Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--05-121, mRNA sequence.

ACCESSION CV727416 GI:55415040
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 40)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..40
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--05-121"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 240
 CV727587/c

LOCUS
 DEFINITION 14Salt--05-M20.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--05-M20, mRNA sequence.

ACCESSION CV727587 GI:55415211
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 40)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..40
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--05-M20"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 241
 CV727805/c
 LOCUS
 DEFINITION 14Salt--06-C07.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--06-C07, mRNA sequence.

ACCESSION CV727805 GI:55415429
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 40)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1. .40
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--06-C07"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 242
 CV727843/c

LOCUS
 DEFINITION
 14Salt--06-D06.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--06-D06, mRNA sequence.

ACCESSION CV727843.1 GI:55415467

VERSION
 KEYWORDS
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
 1 (bases 1 to 40)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
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 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 243
 CV727858/c

LOCUS
 DEFINITION
 14Salt--06-D16.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--06-D16, mRNA sequence.

ACCESSION CV727858.1 GI:55415482

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
 1 (bases 1 to 40)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1. .40
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--06-D16"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 244
 CV728325/c

LOCUS
 DEFINITION
 14Salt--06-P15.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--06-P15, mRNA sequence.

ACCESSION CV728325.1 GI:55430670

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

Query Match 1.3%; Score 35; DB 1; Length 40;

```

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
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1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--06-P15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 245
LOCUS      CV728655/c
DEFINITION FLO--01-B17.g1 Rice flower lambda phage cDNA library (FLO) Oryza
           sativa (japonica cultivar-group) cDNA clone FLO--01-B17, mRNA
           sequence.
ACCESSION  CV728655
VERSION     CV728655.1 GI:55431284
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 40)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
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1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-B17"
/tissue_type="flower"

clade: Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 40)
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 245
LOCUS      CV728655/c
DEFINITION FLO--01-B17.g1 Rice flower lambda phage cDNA library (FLO) Oryza
           sativa (japonica cultivar-group) cDNA clone FLO--01-B17, mRNA
           sequence.
ACCESSION  CV728655
VERSION     CV728655.1 GI:55431284
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 40)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-B17"
/tissue_type="flower"

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/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 246
LOCUS      CV730371/c
DEFINITION FLO--03-O05.b1 Rice flower lambda phage cDNA library (FLO) Oryza
           sativa (japonica cultivar-group) cDNA clone FLO--03-O05, mRNA
           sequence.
ACCESSION  CV730371
VERSION     CV730371.1 GI:55434492
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 40)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="FLO--03-O05"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 247
LOCUS      CV731031/c
DEFINITION FLO--04-N24.g1 Rice flower lambda phage cDNA library (FLO) Oryza
           sativa (japonica cultivar-group) cDNA clone FLO--04-N24, mRNA
           sequence.
ACCESSION  CV731031
VERSION     CV731031.1 GI:55435791
KEYWORDS   EST.

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SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 248
CV731319/c
LOCUS
DEFINITION
FLO--05-E21.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--05-E21, mRNA
sequence.
ACCESSION
CV731319.1 GI:55436371
VERSION
CV731319
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
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/mol_type="mRNA"
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/tissue_type="flower"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 248
CV731319/c
LOCUS
DEFINITION
FLO--05-E21.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--05-E21, mRNA
sequence.
ACCESSION
CV731319.1 GI:55436371
VERSION
CV731319
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
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/db_xref="taxon:39947"
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/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 249
CV731528/c
LOCUS
DEFINITION
FLO--05-J15.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--05-J15, mRNA
sequence.
ACCESSION
CV731528.1 GI:55436755
VERSION
CV731528
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1..40
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 250
CV732353/c
LOCUS
DEFINITION
FLO--06-M17.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--06-M17, mRNA
sequence.
ACCESSION
CV732353.1 GI:55438119
VERSION
CV732353

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
Query Match
Best Local Similarity
Matches
1.3%; Score 35; DB 1; Length 40;
Pred. No. 1.9e+02;
Conservative 0; Mismatches 0; Indels 0; Gaps 0
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/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6
RESULT 252
CV732629/c
LOCUS
DEFINITION
FLO--07-D02.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-E04, mRNA
sequence.
ACCESSION
VERSION
CV732629.1 GI:55438756
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Bep
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
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/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
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Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6
RESULT 251
CV732629/c
LOCUS
DEFINITION
FLO--07-D02.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-D02, mRNA
sequence.
ACCESSION
VERSION
CV732629.1 GI:55438664
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Bep
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1. .40
/organism="Oryza sativa (japonica cultivar-group)"
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CV733006.1 GI:55439402
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
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/mol_type="mRNA"
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/clone="FLO--07-L19"
/tissue_type="flower"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 254
CV733017/c
LOCUS
DEFINITION
FLO--07-M01.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-M01, mRNA sequence.
CV733017
CV733017.1 GI:55439420
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"

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ACCESSION      CV733638
VERSION        CV733638.1  GI:55440654
KEYWORDS
SOURCE
ORGANISM       Oriza sativa (japonica cultivar-group)
               Oriza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE      1 (bases 1 to 40)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongui University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
               Location/Qualifiers
FEATURES       1..40
               /organism="Oriza sativa (japonica cultivar-group)"
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               /tissue_type="flower"
               /lab_host="E.coli SOLR"
               /clone_libs="Rice flower lambda phage cDNA library (FLO)"
               /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
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Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 257
AZ831983
LOCUS          AZ831983                40 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION    2M0112K02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
               clone UUGC2M0112K02 F, genomic survey sequence.
ACCESSION     AZ831983
VERSION       AZ831983
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 40)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D., Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00

Plate: 0112 row: K column: 02
Seq primer: CGTTGTAACACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 40.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0112K02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 258
DUB35034/c
LOCUS          DUB35034                40 bp      DNA      linear      GSS 22-DEC-2005
DEFINITION    KBR5015N17F KBRs, Brassica rapa Sau3AI BAC library Brassica rapa
               subsp. pekinensis genomic clone KBR5015N17, genomic survey
               sequence.
ACCESSION     DUB35034
VERSION       DUB35034.1  GI:83871630
KEYWORDS      GSS.
SOURCE        Brassica rapa subsp. pekinensis
               Brassica rapa subsp. pekinensis
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 40)
AUTHORS        Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
               Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
               Hahn,J.H. and Park,B.S.
TITLE          End sequence of Brassica rapa Sau3AI (KBRs) BAC clone
JOURNAL        Unpublished (2005)
COMMENT        Contact: Beom-Seok Park
               Brassica Genomics Team
               National Institute of Agricultural Biotechnology
               225 Seodun-Dong, Suwon, 441-707, Korea
               Tel: +82-31-299-1670
               Fax: +82-31-299-1672
               Email: pbeom@da.go.kr
               BAC end sequence of Brassica rapa sep. pekinensis Sau3AI BAC clone
               KBR5015N17
               Seq primer: T7

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    Class: BAC ends
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        /organism="Brassica rapa subsp. pekinensis"
        /mol_type="genomic DNA"
        /cultivar="Chiifu"
        /sub_species="pekinensis"
        /db_xref="taxon:51351"
        /clone="KBR5015N17"
        /lab_host="E. coli DH10B"
        /notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBR5 BAC) is
available at NIMB."
      Query Match
      Best Local Similarity 100.0%; Pred. No. 1.9e+02; Length 40;
      Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 259
AJ792759
LOCUS
DEFINITION
  AJ792759 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
  018.2.12.h22, mRNA sequence.
ACCESSION
  AJ792759
KEYWORDS
  EST.
SOURCE
  Antirrhinum majus (snapdragon)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  asterids; lamids; Lamiales; Plantaginaceae; Antirrhineae;
  Antirrhinum.
REFERENCE
  1 (bases 1 to 41)
  Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
  Saedler,H. and Zachgo,S.
  Characterization of Antirrhinum Petal Development and
  Identification of Target Genes of the Class B MADS Box Gene
  DEFICIENS
  Plant Cell 16 (12), 3197-3215 (2004)
  15539471
  Contact: Schwarz-Sommer Z
  Molekulare Pflanzen-genetik
  MPI fuer Zuechtungs-forschung
  Carl-von-Linne Weg 10, D-50829, Germany.
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    1..41
      /organism="Antirrhinum majus"
      /mol_type="mRNA"
      /db_xref="taxon:4151"
      /clone="018.2.12.h22"
      /tissue_type="whole plant"
      /clone_lib="Antirrhinum majus whole plant"
      Query Match
      Best Local Similarity 100.0%; Pred. No. 2e+02; Length 41;
      Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 260
CF291539/c
LOCUS
DEFINITION
  14ROOT--02-A03.b1 Rice root plasmid cDNA library (14ROOT) Oryza
  sativa (japonica cultivar-group) cDNA clone 14ROOT--02-A03, mRNA

```

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ACCESSION
  CF291539
VERSION
  CF291539.1 GI:33660572
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
ORGANISM
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 41)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 321 6193
  Fax: 82 31 321 6355
  Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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    1..41
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="14ROOT--02-A03"
      /tissue_type="root"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="Rice root plasmid cDNA library (14ROOT)"
      /note="Vector: PCR4-TOPO; Site 1: ECORI; mRNA was capped
      with oligoribonucleotides and then used as templates for
      RT-PCR."
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      Best Local Similarity 100.0%; Pred. No. 2e+02; Length 41;
      Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 261
CF318677/c
LOCUS
DEFINITION
  CF318677 41 bp mRNA linear EST 15-AUG-2003
  HD--08-009.g1 OshDAD1-overexpressing transgenic rice plasmid cDNA
  library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
  HD--08-009, mRNA sequence.
ACCESSION
  CF318677
VERSION
  CF318677.1 GI:33690438
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
ORGANISM
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 41)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 321 6193
  Fax: 82 31 321 6355
  Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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 /clone="HD-08-O09"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDA1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 DB 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 262
 CF320203/c
 LOCUS
 DEFINITION
 HD--10-P19.b1 OSHDA1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--10-P19, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 41)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..41
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD-10-P19"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDA1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 DB 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 263
 CF330464/c

LOCUS
 DEFINITION
 NACL--06-D01.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa (japonica cultivar-group) cDNA clone NACL--06-D01, mRNA
 sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 41)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..41
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--06-D01"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 DB 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 264
 CF334638/c

LOCUS
 DEFINITION
 JMT--04-A03.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--04-A03, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 41)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL
COMMENT

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

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1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="JMT--04-A03"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ATJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
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Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 265
CV725868/c

LOCUS 41 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--03-D07.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-D07, mRNA sequence.

ACCESSION
CV725868

VERSION 1 GI:55413492
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

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1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="14Salt--03-D07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
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Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||

Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 266
CV725993/c

LOCUS 41 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--03-G10.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-G10, mRNA sequence.

ACCESSION
CV725993

VERSION 1 GI:55413617
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

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1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="14Salt--03-G10"
/tissue_type="leaf"
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library (14Salt)"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
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Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||

Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 267
CV726255/c

LOCUS 41 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--03-M18.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-M18, mRNA sequence.

ACCESSION
CV726255

VERSION 1 GI:55413879


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KEYWORDS
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 41)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
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     /organism="Oryza sativa (japonica cultivar-group)"
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     /lab_host="E.coli SOLR"
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     library (14Salt)"
     /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
     XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
     cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
     with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Db   41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 269
CV726393/c
LOCUS      CV726393
DEFINITION 14Salt--04-N03.g1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
            14Salt--04-N03, mRNA sequence.
ACCESSION  CV726393
VERSION     1 GI:55414017
KEYWORDS    EST
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 41)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
            Location/Qualifiers
            1..41
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
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            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli SOLR"
            /clone_lib="Salt treated rice leaf lambda phage cDNA
            library (14Salt)"
            /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
            XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
            cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
            with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Db   41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 268
CV726393/c
LOCUS      CV726393
DEFINITION 14Salt--03-P21.g1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
            14Salt--03-P21, mRNA sequence.
ACCESSION  CV726393
VERSION     1 GI:55414017
KEYWORDS    EST
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 41)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
            Location/Qualifiers
            1..41
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
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            /lab_host="E.coli SOLR"
            /clone_lib="Salt treated rice leaf lambda phage cDNA
            library (14Salt)"
            /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
            XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
            cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
            with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Db   41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 268
CV726393/c
LOCUS      CV726393
DEFINITION 14Salt--04-N03.g1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
            14Salt--04-N03, mRNA sequence.
ACCESSION  CV726393
VERSION     1 GI:55414547
KEYWORDS    EST
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 41)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
            Location/Qualifiers
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            /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
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            cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
            with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Db   41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

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cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 273
CV727841/c
LOCUS
DEFINITION 14Salt--06-D05.g1 Salt treated rice leaf lambda phage cDNA library
14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--06-D05, mRNA sequence.

ACCESSION CV727841 GI:55415465
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 41)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli SOLR"
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/note="Vector: pBluescript SK(+); Site 1: EcoRI, Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 274
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LOCUS
DEFINITION 14Salt--06-I18.g1 Salt treated rice leaf lambda phage cDNA library
14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--06-I18, mRNA sequence.

ACCESSION CV728055 GI:55430231
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 41)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

ORYZA SATIVA (japonica cultivar-group)
ORYZA SATIVA (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 41)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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DB 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 275
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LOCUS
DEFINITION 14Salt--06-N05.g1 Salt treated rice leaf lambda phage cDNA library
14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--06-N05, mRNA sequence.

ACCESSION CV728228 GI:55430529
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 41)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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Query Match 1.3%; Score 35; DB 1; Length 41;
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 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 276
 CV728716/c
 LOCUS
 DEFINITION
 FLO--01-D04.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-D04, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 41)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Query Match 1.3%; Score 35; DB 1; Length 41;
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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 277
 CV728978/c
 LOCUS
 DEFINITION
 FLO--01-K21.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-K21, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 41)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
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 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 278
 CV729041/c
 LOCUS
 DEFINITION
 FLO--01-K21.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-K21, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 41)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
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 Contact: Nahm B.H.
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 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Query Match 1.3%; Score 35; DB 1; Length 41;
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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

LOCUS
 DEFINITION
 FLO--01-J08.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-J08, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
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REFERENCE
 1 (bases 1 to 41)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 279
 CV729041/c
 LOCUS
 DEFINITION
 FLO--01-K21.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-K21, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 278
 CV729041/c
 LOCUS
 DEFINITION
 FLO--01-K21.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-K21, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 41)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 Unpublished (2003)
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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 /clone="FLO--01-D04"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

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FEATURES
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        /mol_type="mRNA"
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        XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
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  Query Match      1.3%; Score 35; DB 1; Length 41;
  Best Local Similarity 100.0%; Pred. No. 2e+02;
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Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 279
CV731427/c
LOCUS
DEFINITION
  FLO--05-H10.b1 Rice flower lambda phage cDNA library (FLO) Oryza
  sativa (japonica cultivar-group) cDNA clone FLO--05-H10, mRNA
  sequence.
ACCESSION
  CV731427
VERSION
  CV731427.1 GI:55436582
KEYWORDS
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SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzae; Oryza.
  1 (bases 1 to 41)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
  Location/Qualifiers
    1..41
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="FLO--05-M20"
      /tissue_type="flower"
      /lab_host="E.coli SOLR"
      /clone_lib="Rice flower lambda phage cDNA library (FLO)"
      /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
      XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
      end with EcoRI and 3' end with XhoI site."

  Query Match      1.3%; Score 35; DB 1; Length 41;
  Best Local Similarity 100.0%; Pred. No. 2e+02;
  Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 281
CV732073/c
LOCUS
DEFINITION
  FLO--06-G04.b1 Rice flower lambda phage cDNA library (FLO) Oryza
  sativa (japonica cultivar-group) cDNA clone FLO--06-G04, mRNA
  sequence.
ACCESSION
  CV732073
VERSION
  CV732073.1 GI:55437579
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzae; Oryza.
  1 (bases 1 to 41)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
  Location/Qualifiers
    1..41
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="FLO--05-H10"
      /tissue_type="flower"
      /lab_host="E.coli SOLR"
      /clone_lib="Rice flower lambda phage cDNA library (FLO)"
      /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
      XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
      end with EcoRI and 3' end with XhoI site."

  Query Match      1.3%; Score 35; DB 1; Length 41;
  Best Local Similarity 100.0%; Pred. No. 2e+02;
  Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 280

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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1..41

/organism="Oryza sativa (japonica cultivar-group)"
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 282
CVT33839/c
LOCUS
DEFINITION CVT33839 41 bp mRNA linear EST 05-NOV-2004
sativa [japonica cultivar-group] cDNA clone FLO--08-O22, mRN
sequence.

ACCESSION CVT33839 GI:55441051
VERSION CVT33839
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 41)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
Contact: Nam B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES source
1..41

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--08-O22"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note=Vector: pbluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0007 row: I column: 01
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0007101"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 285
AZ827008 41 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0103107F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0103107 F, genomic survey sequence.
ACCESSION AZ827008
VERSION AZ827008.1 GI:12996916
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 41)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: I column: 07
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers

FEATURES

source

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1. .41
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0103107"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 286
DU834001/c 41 bp DNA linear GSS 22-DEC-2005
LOCUS KRS013D19F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
DEFINITION subsp. pekinensis genomic clone KBrS013D19, genomic survey sequence.
ACCESSION DU834001
VERSION DU834001.1 GI:83870597
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 41)
AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pbeom@da.go.kr
 BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
 KBrS013D19
 Seq primer: T7
 Class: BAC ends.

FEATURES

source
 Location/Qualifiers
 1. .41
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrS013D19"
 /lab_host="E. coli DH10B"
 /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
 /notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
 ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
 available at NIAB."

Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 287

DU834619 41 bp DNA linear GSS 22-DEC-2005
 LOCUS KBrS014M09F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
 DEFINITION subsp. pekinensis genomic clone KBrS014M09, genomic survey
 sequence.

ACCESSION DU834619.1 GI:83871215
 VERSION DU834619.1
 KEYWORDS GSS.
 SOURCE Brassica rapa subsp. pekinensis
 ORGANISM Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 41)
 AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
 Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
 Hahn,J. H. and Park,B.S.

TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

JOURNAL Unpublished (2005)
 COMMENT Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pbeom@da.go.kr
 BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
 KBrS014M09

Seq primer: T7

Class: BAC ends.

FEATURES

source
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 /sub_species="pekinensis"
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 /lab_host="E. coli DH10B"
 /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
 /notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
 ssp pekinensis var. Chiifu BAC library (KBrS BAC) is

available at NIAB."

Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 288

DU835000/c 41 bp DNA linear GSS 22-DEC-2005
 LOCUS KBrS015L21F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
 DEFINITION subsp. pekinensis genomic clone KBrS015L21, genomic survey
 sequence.

ACCESSION DU835000
 VERSION DU835000.1 GI:83871596
 KEYWORDS GSS.
 SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 41)

AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
 Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
 Hahn,J. H. and Park,B.S.

TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

JOURNAL Unpublished (2005)
 COMMENT Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
 KBrS015L21
 Seq primer: T7
 Class: BAC ends.

FEATURES

source
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 /sub_species="pekinensis"
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 /lab_host="E. coli DH10B"
 /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
 /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
 ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
 available at NIAB."

Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 289

DX049410/c 41 bp DNA linear GSS 10-JAN-2006
 LOCUS KBrB052A12F KBrB, Brassica rapa BamHI BAC library Brassica rapa
 DEFINITION subsp. pekinensis genomic clone KBrB052A12, genomic survey
 sequence.

ACCESSION DX049410
 VERSION DX049410.1 GI:84743707

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

GSS.
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 41)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB052A12
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..41
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB052A12"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/notes="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (GNU)."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 290
AJ691919
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AJ691919 KN261 Bos taurus cDNA clone KN261-025_M11, mRNA sequence.
AJ691919
AJ691919.1 GI:49424527
EST.
Bos taurus (cattle)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 42)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI
R. Site2: SmaI 5', Seq Primer T3 Normalised library constructed from
bovine ovary. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,

FEATURES
source
Location/Qualifiers
1..42
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4515403"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_93"
/notes="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SmaI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

FEATURES
source
Location/Qualifiers
1..42
/organism="Bos taurus"
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/db_xref="taxon:9606"
/clone="IMAGE:4515403"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_93"
/notes="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SmaI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

EH25 9PS, www.arkgenomics.org.
FEATURES
source
Location/Qualifiers
1..42
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-025_M11"
/tissue_type="ovary"
/clone_lib="KN261"
/notes="Vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2:
SmaI; Single pass sequencing. Normalised library
constructed from bovine ovary."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 291
BG292448
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BG292448 602386574P1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4515403 5',
mRNA sequence.
BG292448
BG292448.1 GI:13051253
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 42)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10405 row: c column: 20
High quality sequence stop: 42.
Location/Qualifiers
1..42
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4515403"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_93"
/notes="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SmaI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

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```

RESULT 292
CF318540/c
LOCUS
DEFINITION
HD--08-L07.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--08-L07, mRNA sequence.
CF318540
CF318540.1 GI:33690301
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BAP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--08-L07"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDACL1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr_ Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
FEATURES
source
Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8
RESULT 294
CF319867/c
LOCUS
DEFINITION
HD--10-I15.g1 OshDACL1-overexpressing transgenic rice plasmid
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--10-I15, mRNA sequence.
CF319867
CF319867.1 GI:33691628
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BAP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--10-I15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDACL1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr_ Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
FEATURES
source
Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8
RESULT 293
CF318962/c
LOCUS
DEFINITION
HD--09-E19.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-E19, mRNA sequence.
CF318962
CF318962.1 GI:33690723
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BAP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-E19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDACL1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr_ Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
FEATURES
source
Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8
RESULT 293
CF318962/c
LOCUS
DEFINITION
HD--09-E19.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-E19, mRNA sequence.
CF318962
CF318962.1 GI:33690723
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BAP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-E19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDACL1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr_ Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
FEATURES
source
Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match
Best Local Similarity 1.3%; Score 35; DB 1; Length 42;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 295
CF332408/c
LOCUS
DEFINITION
HD--10-M17.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--10-M17, mRNA sequence.
CF3320056
CF3320056.1 GI:33691817
EST.
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--10-M17"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match
Best Local Similarity 1.3%; Score 35; DB 1; Length 42;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 296
CF332408/c
LOCUS
DEFINITION
NACL--08-O12.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--08-O12, mRNA
sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--08-O12"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 1.3%; Score 35; DB 1; Length 42;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 297
CF343329
LOCUS
DEFINITION
60201593F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4151542
5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 42)
NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM9416 row: j column: 23
High quality sequence stop: 39.
Location/Qualifiers

FEATURES

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source      1. .42
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:4151542"
            /tissue_types="glioblastoma with EGFR amplification"
            /lab_hosts="DH10B (T1 phage-resistant)"
            /clone_lib="NCI_CGAP_Brn64"
            /notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.57 kb. Constructed by Life
            Technologies. Note: this is a NCI_CGAP Library."

Query Match      1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 298
AW334133/c
LOCUS      AW334133      42 bp      mRNA      linear      EST 31-JAN-2000
DEFINITION S30H7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION  AW334133
VERSION     AW334133.1 GI:6830490
KEYWORDS   EST.
SOURCE     Pneumocystis carinii
           Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
           Pneumocystidaceae; Pneumocystis.
REFERENCE  1 (bases 1 to 42)
AUTHORS   Smullan,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
           Edman,J.C., Kovacs,J. and Cushion,M.
TITLE     Expressed sequence tags from Pneumocystis carinii
JOURNAL   Unpublished (2000)
COMMENT   Contact: Staben C
           School of Biological Sciences
           University of Kentucky
           101 Morgan Building, University of Kentucky, Lexington, KY
           40506-0225, USA
           Tel: 606 257 2161
           Fax: 606 257 1717
           Email: staben@pop.uky.edu.

FEATURES             source
     1. .42
     /organism="Pneumocystis carinii"
     /mol_type="mRNA"
     /db_xref="taxon:4754"
     /lab_host="E. coli"
     /clone_lib="AGS-1"
     /notes="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
     P. carinii organisms (3x10e9) from a single rat (99-1-6,
     sacrificed on 3/17/99) at Cincinnati VA facilities.
     Trizol extracted RNA. Oligo dt priming, standard
     conditions described by vendor, Stratagene. Further
     details see www.uky.edu/Project/Pneumocystis/"

Query Match      1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 299
CV062024
LOCUS      CV062024      42 bp      mRNA      linear      EST 24-AUG-2004
DEFINITION BNEL75e2 Barley EST endospore library Hordeum vulgare subsp.

source      1. .42
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:4151542"
            /tissue_types="glioblastoma with EGFR amplification"
            /lab_hosts="DH10B (T1 phage-resistant)"
            /clone_lib="NCI_CGAP_Brn64"
            /notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.57 kb. Constructed by Life
            Technologies. Note: this is a NCI_CGAP Library."

Query Match      1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 300
CV725428/c
LOCUS      CV725428      42 bp      mRNA      linear      EST 04-NOV-2004
DEFINITION 14Salt--02-106.b1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
            14Salt--02-106, mRNA sequence.

ACCESSION  CV725428
VERSION     CV725428.1 GI:55413052
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
           clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 42)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahn,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs

vulgare cDNA clone BNEL75e2 5' similar to Unknown Function, mRNA
sequence.
CV062024
VERSION     CV062024.1 GI:51525163
KEYWORDS   EST.
SOURCE     Hordeum vulgare subsp. vulgare
           Hordeum vulgare subsp. vulgare
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
           clade; Poideae; Triticeae; Hordeum.
REFERENCE  1 (bases 1 to 42)
AUTHORS   Ali,S. Holloway,B. and Taylor,W.C.
TITLE     Normalisation of cereal endospore EST libraries for structural and
           functional genomic analysis
JOURNAL   Plant Mol. Biol. Rep. 18, 123-132 (2000)
COMMENT   Contact: Bill Taylor
           Commonwealth Scientific and Industrial Research Organisation
           Division of Plant Industry.
           CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
           Tel: 61 2 6246 5223
           Fax: 61 2 6246 5000
           Email: Bill.Taylor@csiro.au
           Seq primer: M13 reverse primer
           High quality sequence stop: 42.
           Location/Qualifiers
           1. .42
           /organism="Hordeum vulgare subsp. vulgare"
           /mol_type="mRNA"
           /cultivar="Himalaya"
           /sub_species="vulgare"
           /db_xref="taxon:112509"
           /clone="BNEL75e2"
           /tissue_type="endospore"
           /dev_stage="developing endospore tissue 10, 12, 15 dpa
           (days post anthesis)"
           /lab_host="DH10B (Life Technology)"
           /clone_lib="Barley EST endospore library"
           /note="Vector: ZipLox; Site 1: Sal I; Site 2: Not I; mRNA
           was prepared from endospore tissues of the barley cultivar
           Himalaya. cDNA was synthesised from pooled 10, 12, and 15
           dpa endospore using Not I-oligo(dT)18 primer/adaptor
           (Pharmacia Biotech), and then ligated to the Sal I-Not I
           site of ZipLox vector (Life Technology) after adding a
           Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan
           Ali and Bill Taylor."

Query Match      1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 300
CV725428/c
LOCUS      CV725428      42 bp      mRNA      linear      EST 04-NOV-2004
DEFINITION 14Salt--02-106.b1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
            14Salt--02-106, mRNA sequence.

ACCESSION  CV725428
VERSION     CV725428.1 GI:55413052
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
           clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 42)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahn,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs

```

```

JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES     source
1. .42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-106"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 301
CV726363/c LOCUS
DEFINITION 14Salt--03-P05.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-P05, mRNA sequence.
ACCESSION CV726363
VERSION CV726363.1 GI:55413987
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES     source
1. .42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-P05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 303
CV728634/c LOCUS
DEFINITION FLO--01-B05.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-B05, mRNA
sequence.
ACCESSION CV728634
VERSION CV728634.1 GI:55431251

JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES     source
1. .42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="14Salt--02-106"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 303
CV728634/c LOCUS
DEFINITION FLO--01-B05.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-B05, mRNA
sequence.
ACCESSION CV728634
VERSION CV728634.1 GI:55431251

```

```

XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 302
CV726372/c LOCUS
DEFINITION 14Salt--03-P10.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-P10, mRNA sequence.
ACCESSION CV726372
VERSION CV726372.1 GI:55413996
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES     source
1. .42
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/mol_type="mRNA"
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/clone="14Salt--03-P10"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 303
CV728634/c LOCUS
DEFINITION FLO--01-B05.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-B05, mRNA
sequence.
ACCESSION CV728634
VERSION CV728634.1 GI:55431251

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KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="FLO--01-805"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/notes="Rice flower lambda phage cDNA library (FLO)"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 304
CV728806/c
LOCUS FLO--01-F05.g1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--01-F05, mRNA
sequence.
ACCESSION CV728806.1 GI:55431581
VERSION CV728806
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="FLO--01-F05"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 305
CV729215/c
LOCUS FLO--01-P01.g1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--01-P01, mRNA
sequence.
ACCESSION CV729215.1 GI:55432388
VERSION CV729215
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .42
/organism="Oryza sativa (japonica cultivar-group)"
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/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 306
CV729267/c
LOCUS FLO--02-A05.g1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--02-A05, mRNA
sequence.
ACCESSION CV729267
source
1. .42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"


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VERSION CV729267.1 GI:55432491
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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1..42
/organism="Oryza sativa (japonica cultivar-group)"
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/lab_host="E.coli SOLR"
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/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 307
CV731493/c
LOCUS CV731493 42 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--05-121.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--05-121, mRNA
sequence.
ACCESSION CV731493
VERSION CV731493.1 GI:55436705
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"

CV731493/c
LOCUS CV731493 42 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--05-121.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--05-121, mRNA
sequence.
ACCESSION CV731493
VERSION CV731493.1 GI:55436705
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"

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/db_xref="taxon:39947"
/clone="FLO--05-121"
/tissue_type="flower"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 308
CV731845/c
LOCUS CV731845 42 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--06-A23.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--06-A23, mRNA
sequence.
ACCESSION CV731845
VERSION CV731845.1 GI:55437277
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="FLO--06-A23"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 309
CV732835/c
LOCUS CV732835 42 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--07-H20.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-H20, mRNA
sequence.

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ACCESSION      CV732835
VERSION        CV732835.1  GI:55439068
KEYWORDS
SOURCE
ORGANISM       Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzeae; Oryza.
               1 (bases 1 to 42)
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .42
   /organism="Oryza sativa (japonica cultivar-group)"
   /mol_type="mRNA"
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   /clone_lib="Rice flower lambda phage cDNA library (FLO)"
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   XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
   end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Db   42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 310
CV732860/c
LOCUS          42 bp mRNA linear EST 05-NOV-2004
DEFINITION    sativa (japonica cultivar-group) cDNA clone FLO--07-I10, mRNA
               sequence.
ACCESSION     CV732860
VERSION       CV732860.1  GI:55439116
KEYWORDS
SOURCE
ORGANISM       Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzeae; Oryza.
               1 (bases 1 to 42)
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .42
   /organism="Oryza sativa (japonica cultivar-group)"
   /mol_type="mRNA"

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/cultivar="Nackdong"
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end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db   42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 311
CV733275/c
LOCUS          42 bp mRNA linear EST 05-NOV-2004
DEFINITION    sativa (japonica cultivar-group) cDNA clone FLO--08-B22, mRNA
               sequence.
ACCESSION     CV733275
VERSION       CV733275.1  GI:55439929
KEYWORDS
SOURCE
ORGANISM       Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzeae; Oryza.
               1 (bases 1 to 42)
REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
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   /organism="Oryza sativa (japonica cultivar-group)"
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   /db_xref="taxon:39947"
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   end with EcoRI and 3' end with XhoI site."

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Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db   42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 312
CV73323/c
LOCUS          42 bp mRNA linear EST 05-NOV-2004
DEFINITION    sativa (japonica cultivar-group) cDNA clone FLO--08-D02, mRNA

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sequence.
CV733323
CV733323.1 GI:55440025
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..42
/organism="Oryza sativa (japonica cultivar-group)"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
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end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

Ory
2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 313
CV733544/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-J11, mRNA
sequence.
CV733544
CV733544.1 GI:55440585
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Matches 35; Conservative 0; Mismatches 0;

Ory
2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 313
CV733544/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-J11, mRNA
sequence.
CV733544
CV733544.1 GI:55440585
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/mol_type="mRNA"
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
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end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

Ory
2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 313
CV733544/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-J11, mRNA
sequence.
CV733544
CV733544.1 GI:55440585
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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end with EcoRI and 3' end with XhoI site."

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Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
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Ory
2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 313
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LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-J11, mRNA
sequence.
CV733544
CV733544.1 GI:55440585
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

Ory
2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 313
CV733544/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-J11, mRNA
sequence.
CV733544
CV733544.1 GI:55440585
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
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Ory
2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 313
CV733544/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-J11, mRNA
sequence.
CV733544
CV733544.1 GI:55440585
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321
```

sativa (japonica cultivar-group) cDNA clone FLO--08-L13, mRNA
 sequence.
 CV733690
 CV733690.1 GI:55440757
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 42)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source

1..42
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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 /lab_host="E.coli SOLR"
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 end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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 Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 316 CV733938/c

LOCUS
 DEFINITION
 FLO--09-B08.b1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--09-B08, mRNA
 sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CV733938
 CV733938.1 GI:55441244
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 42)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source

1..42
 Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
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Query Match 1.3%; Score 35; DB 1; Length 42;
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 Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 317 CV734112/c

LOCUS
 DEFINITION
 FLO--09-F07.g1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--09-F07, mRNA
 sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CV734112
 CV734112.1 GI:55441577
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 42)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source

1..42
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/organism="Oryza sativa (japonica cultivar-group)"
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Query Match 1.3%; Score 35; DB 1; Length 42;
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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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 Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 318 CX058845

LOCUS
 CX058845 42 bp mRNA linear EST 31-DEC-2005

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DEFINITION PDUTs2028G11 Porcine testis cDNA library II Sus scrofa cDNA clone
ACCESSION PDUTs2028G11 5', mRNA sequence.
VERSION CX058845
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1 (bases 1 to 42)
AUTHORS Lee,W.C., Lin,E.-C., Huang,M.C., Chiou,S.H., Sun,H.S., Huang,S.Y.,
Chuang,C.K., Chen,M.Y., Liu,M.L., Hsu,M.C., Yang,K.T., Fan,Y.H.,
Lin,J.H., Liu,C.C., Huang,C.H., Chen,Y.C. and Lin,D.T.
Porcine testis EST project
Unpublished (2005)
TITLE Mu-Chiou Huang
JOURNAL Lab of Genetic & breeding
COMMENT Department of Animal Science, National Chung-Hsing University
250 Kuo-Kuang Road, Taichung 402, Taiwan, R.O.C.
Tel: 886 4 22860265
Fax: 886 4 22870613(ext.)239
Email: mchuang@mail.nchu.edu.tw
The EST project for testis from Duroc was granted by Council of
Agriculture, Taiwan. Material with normal function was tested and
heat stress experiments of animals were conducted by Divisions of
Biotechnology and Animal Resources, Animal Technology Institute
Taiwan (ARIT). Library was constructed and EST clones were
sequenced by Graduate Institutes of Veterinary Microbiology and
Department of Animal Science, National Chung-Hsing University.
Bioinformatic work was conducted by a network from ARIT, National
Cheng-Kung University, and Chung-Hua University. The sequences were
stored in a database 'Tropical Pig Bioinformatic Center'. Bases
called and alt trimmed with phred v0.020425.c. Vector identified
and masked by cross match. Sequences were cleaned of vector,
adaptors and repetitions.
Plate: 28 row: G column: 11
Seq primer: T7 promoter primer
High quality sequence stop: 42
POLYA=No.
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                /clone_lib="Porcine testis cDNA library II"
                /note="Organ: testis; Vector: pSPORT1; Site_1: NotI;
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                heat stress experiments of animals were conducted by
                Divisions of Biotechnology and Animal Resources, Animal
                Technology Institute Taiwan (ARIT). First strand cDNA was
                primed with a NotI-oligo(dT) primer and 2nd strand cDNA
                was synthesized by using nick translational replacement of
                the mRNA. Double-strand cDNA was added with SalI adapter,
                then digested with NotI and cloned into the NotI and SalI
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Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 5 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 39
RESULT 319
DUB35485/c

```

```

LOCUS DUB35485
DEFINITION KBrS016M05R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS016M05, genomic survey
sequence.
ACCESSION DUB35485
VERSION DUB35485.1 GI:83872081
SOURCE GSS.
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 42)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
TITLE Brassica rapa subsp. pekinensis
JOURNAL Contact: Beom-Seok Park
COMMENT Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS016M05
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
    source
        1..42
            Location/Qualifiers
                /organism="Brassica rapa subsp. pekinensis"
                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBrS016M05"
                /lab_host="E. coli DH10B"
                /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                /note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
                ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
                available at NIAB."
Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8
RESULT 320
AJ923543
LOCUS Theileria annulata
DEFINITION AJ923543 Theileria annulata piroplasm Theileria annulata cDNA clone
TAC21c10_plka, mRNA sequence.
ACCESSION AJ923543
VERSION AJ923543.1 GI:67493891
KEYWORDS EST.
SOURCE Theileria annulata
ORGANISM Theileria annulata
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
Theileria.
REFERENCE 1 (bases 1 to 43)
AUTHORS Pain,A., Renaud,H., Berriman,M., Murphy,L., Yeats,C.A., Weir,W.,
Kerhornou,A., Aslett,M., Bishop,R., Bouchier,C., Cochet,M.,
Coulson,R.M.R., Cronin,A., de Villiers,E., Fraser,A., Foster,N.,
Gardner,M., Goble,A., Griffiths-Jones,S., Harris,D.E., Katzer,F.,
Larke,N., Lord,A., Maser,P., McKellar,S., Mooney,P., Morton,P.,
Nene,V., O'Neill,S., Price,C., Quail,M.A., Rabinowitsch,E.,
Rawlings,N.D., Rutter,S., Saunders,D., Seeger,K., Shah,T.,
Squares,R., Squares,S., Tivey,A., Walker,A.R., Woodward,J.,

```


Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 43)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11541 row: a column: 09
High quality sequence stop: 43.
Location/Qualifiers

FEATURES

Source

1..43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5215376"
/tissue_type="leukocyte"
/lab_host="DH108"
/clone_lib="NIH_MGC_118"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 324
CF302744/c
LOCUS

DEFINITION
CF302744 43 bp mRNA linear EST 15-AUG-2003
sativa (japonica cultivar-group) cDNA clone 7LEAF--08-123, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF302744 GI:33674505
CF302744
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheggbio.com, bhnaheggbio@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clones="7LEAF--08-123"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 325
CF334344

LOCUS
DEFINITION
CF334344 43 bp mRNA linear EST 18-AUG-2003
Library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--03-J17, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF334344 GI:33817016
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,D.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheggbio.com, bhnaheggbio@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clones="JMT--03-J17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 326
CV724539/c
LOCUS
DEFINITION
14Salt--01-C21.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
CV724539
VERSION
CV724539.1
KEYWORDS
EST.
SOURCE
Hordeum vulgare subsp. vulgare
ORGANISM
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Poaceae; Triticeae; Hordeum.

REFERENCE
1 (bases 1 to 43)
AUTHORS
Ali, S., Holloway, B. and Taylor, W.C.
TITLE
Normalisation of cereal endospERM EST libraries for structural and functional genomic analysis
JOURNAL
Plant Mol. Biol. Rep. 18, 123-132 (2000)
COMMENT
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5223
Fax: 61 2 6246 5000
Email: Bill.Taylor@csiro.au
Seq primer: M13 reverse primer
High quality sequence stop: 43.

FEATURES

source
1. .43
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Himalaya"
/sub_species="vulgare"
/db_xref="taxon:114509"
/clone="BNEL76g12"
/tissue_types="endospERM"
/dev_stage="developing endospERM tissue 10, 12, 15 dpa (days post anthesis)"
/lab_host="DH10B (Life Technology)"
/notes="Vector: ZipLox; Site 1: Sal I; Site 2: Not I; mRNA was prepared from endospERM tissues of the barley cultivar Himalaya. cDNA was synthesised from pooled 10, 12, and 15 dpa endospERM using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of _ziplox vector (Life Technology) after adding a Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 327
CV724539/c
LOCUS
DEFINITION
14Salt--01-C21.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
CV724539
VERSION
CV724539.1
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
1 (bases 1 to 43)
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1. .43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-C21"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 328
CV724959/c
LOCUS
DEFINITION
14Salt--01-M23.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
CV724959
VERSION
CV724959.1
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 329
CV724959/c
LOCUS
DEFINITION
14Salt--01-M23.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
CV724959
VERSION
CV724959.1
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 330
CV724959/c
LOCUS
DEFINITION
14Salt--01-M23.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
CV724959
VERSION
CV724959.1
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

```

Query Match 1.3%; Score 35; DB 1; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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 Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 329
 CV724969/C

LOCUS 14Salt--01-N04.g1 43 bp mRNA linear EST 04-NOV-2004
 DEFINITION 14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--01-N04, mRNA sequence.

ACCESSION CV724969
 VERSION CV724969.1 GI:55412593

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 43)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. 43

FEATURES

source

```

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-N04"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

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Query Match 1.3%; Score 35; DB 1; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 330
 CV725127/C

LOCUS

DEFINITION 14Salt--02-A20.b1 43 bp mRNA linear EST 04-NOV-2004
 14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--02-A20, mRNA sequence.

ACCESSION CV725127

VERSION CV725127.1 GI:55412751

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 43)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. 43

FEATURES

source

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-A20"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

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Query Match 1.3%; Score 35; DB 1; Length 43;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

||||||||||||||||||||||||||||||||||||||||||

Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 331

CV725506/C

LOCUS

DEFINITION 14Salt--02-K02.b1 43 bp mRNA linear EST 04-NOV-2004
 14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--02-K02, mRNA sequence.

ACCESSION CV725506

VERSION CV725506.1 GI:55413130

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 43)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1. .43
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-K02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 332

CV725680/c

LOCUS
DEFINITION
14Salt--02-005.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-005, mRNA sequence.

ACCESSION
CV725680

VERSION
CV725680.1 GI:55413304

KEYWORDS
EST.

SOURCE
Oryza sativa (japonica cultivar-group)

ORGANISM
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 43)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1. .43
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-005"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match

1.3%; Score 35; DB 1; Length 43;

Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 333

CV725720/c

LOCUS

DEFINITION

14Salt--02-P03.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

14Salt--02-P03, mRNA sequence.

ACCESSION

CV725720

VERSION

CV725720.1 GI:55413344

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 43)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1. .43

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--02-P03"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match

1.3%; Score 35; DB 1; Length 43;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 334

CV725822/c

LOCUS

DEFINITION

14Salt--03-C05.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

14Salt--03-C05, mRNA sequence.

ACCESSION

CV725822

VERSION

CV725822.1 GI:55413446

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

```

REFERENCE
AUTHORS   clade: Ehrhartoideae; Oryzae; Oryza.
           1 (bases 1 to 43)
           Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14Salt--03-C05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 335
CV726349/c
LOCUS      43 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--03-022.g1 Salt treated rice leaf lambda phage cDNA library
           (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION  CV726349.1 GI:55413973
VERSION     EST.
KEYWORDS   Oryza sativa (japonica cultivar-group)
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE   1 (bases 1 to 43)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-022"
/tissue_type="leaf"

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/dev stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 336
CV726694/c
LOCUS      43 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--04-H13.b1 Salt treated rice leaf lambda phage cDNA library
           (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION  CV726694.1 GI:55414318
VERSION     EST.
KEYWORDS   Oryza sativa (japonica cultivar-group)
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE   1 (bases 1 to 43)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..43
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/mol_type="mRNA"
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/clone="14Salt--04-H13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 337
CV726751/c
LOCUS      43 bp mRNA linear EST 04-NOV-2004

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DEFINITION 14Salt--04-122.g1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--04-122, mRNA sequence.
CV726751
CV726751.1 GI:55414375
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
     source
     1..43
     /organism="Oryza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
     /cultivar="Nackdong"
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     /tissue_type="leaf"
     /dev_stage="14 days after germination"
     /lab_host="E.coli SOLR"
     /clone_lib="Salt treated rice leaf lambda phage cDNA
     library (14Salt)"
     /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
     XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
     cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
     with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 338
CV727328/c
LOCUS
DEFINITION 14Salt--05-G19.g1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-G19, mRNA sequence.
CV727328
CV727328.1 GI:55414952
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

```

```

Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
     source
     1..43
     /organism="Oryza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
     /cultivar="Nackdong"
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     /clone="14Salt--05-G19"
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     /dev_stage="14 days after germination"
     /lab_host="E.coli SOLR"
     /clone_lib="Salt treated rice leaf lambda phage cDNA
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     /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
     XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
     cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
     with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 339
CV727684/c
LOCUS
DEFINITION 14Salt--05-P03.g1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-P03, mRNA sequence.
CV727684
CV727684.1 GI:55415308
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
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     /mol_type="mRNA"
     /cultivar="Nackdong"
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     /clone="14Salt--05-P03"
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     /dev_stage="14 days after germination"
     /lab_host="E.coli SOLR"
     /clone_lib="Salt treated rice leaf lambda phage cDNA
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     /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
     XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
     cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
     with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

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```

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 340
CV728681/c LOCUS
DEFINITION FLO--01-C09.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-C09, mRNA sequence.
ACCESSION CV728681.1 GI:55431334
VERSION CV728681.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="FLO--01-C09"
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/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 341
CV728686/c LOCUS
DEFINITION FLO--01-C11.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-C11, mRNA sequence.
ACCESSION CV728686.1 GI:55431344
VERSION CV728686.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

```

```

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..43
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/mol_type="mRNA"
/db_xref="taxon:39947"
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/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 342
CV728737/c LOCUS
DEFINITION FLO--01-D16.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-D16, mRNA sequence.
ACCESSION CV728737.1 GI:55431446
VERSION CV728737.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="FLO--01-D16"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;

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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 343
CV728887/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-H03, mRNA
sequence.
CV728887
CV728887.1 GI:55431741
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 43)
REFERENCE
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-H03"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 344
CV729000/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-J22, mRNA
sequence.
CV729000
CV729000.1 GI:55431960
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 43)
REFERENCE
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 345
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LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-N17, mRNA
sequence.
CV729158
CV729158.1 GI:55432276
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 43)
REFERENCE
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

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TITLE
JOURNAL
COMMENT
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
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Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 344
CV729158/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-N17, mRNA
sequence.
CV729158
CV729158.1 GI:55432276
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 43)
REFERENCE
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
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Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 347
CV729970/c
LOCUS FLO--03-E14.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--03-E14, mRNA
sequence.
ACCESSION CV729970
VERSION FLO--03-E14
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
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Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 347
CV730586/c
LOCUS FLO--04-D05.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--04-D05, mRNA
sequence.
ACCESSION CV730586
VERSION FLO--04-D05
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/mol_type="mRNA"
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XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

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```

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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1. 43
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Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 348
CV730813/c
LOCUS FLO--04-I21.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--04-I21, mRNA
sequence.
ACCESSION CV730813
VERSION FLO--04-I21
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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end with EcoRI and 3' end with XhoI site."

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Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 349
CV731060/c
LOCUS
DEFINITION
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    sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
    clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
    1 (bases 1 to 43)
AUTHORS
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    Large-scale Sequencing Analysis of Rice ESTs
    Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 351
CV732091/c
LOCUS
DEFINITION
    FLO--06-G15.b1 Rice flower lambda phage cDNA library (FLO) Oryza
    sativa (japonica cultivar-group) cDNA clone FLO--06-G15, mRNA
    sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
    clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
    1 (bases 1 to 43)
AUTHORS
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    Large-scale Sequencing Analysis of Rice ESTs
    Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
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    end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 350
CV731475/c
LOCUS
DEFINITION
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    sativa (japonica cultivar-group) cDNA clone FLO--05-I11, mRNA
    sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
    clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
    1 (bases 1 to 43)
AUTHORS
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    Large-scale Sequencing Analysis of Rice ESTs
    Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
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    /clone_lib="Rice flower lambda phage cDNA library (FLO)"
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    end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 350
CV732091/c
LOCUS
DEFINITION
    FLO--06-G15.b1 Rice flower lambda phage cDNA library (FLO) Oryza
    sativa (japonica cultivar-group) cDNA clone FLO--06-G15, mRNA
    sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
    clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
    1 (bases 1 to 43)
AUTHORS
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    Large-scale Sequencing Analysis of Rice ESTs
    Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
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    /clone_lib="Rice flower lambda phage cDNA library (FLO)"
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    end with EcoRI and 3' end with XhoI site."

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end with EcoRI and 3' end with XhoI site."

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Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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    43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 352
CV732291/c
LOCUS      43 bp      mRNA      linear      EST 05-NOV-2004
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           sequence.
ACCESSION  CV732291
VERSION     CV732291.1 GI:55437995
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 43)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
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     /mol_type="mRNA"
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Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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    43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 353
CV732533/c
LOCUS      43 bp      mRNA      linear      EST 05-NOV-2004
DEFINITION FLO--07-A19.b1 Rice flower lambda phage cDNA library (FLO) Oryza
           sativa (japonica cultivar-group) cDNA clone FLO--07-A19, mRNA
           sequence.
ACCESSION  CV732533
VERSION     CV732533.1 GI:55438473
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 43)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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     /mol_type="mRNA"
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     /tissue_type="flower"
     /lab_host="E.coli SOLR"
     /clone_lib="Rice flower lambda phage cDNA library (FLO)"
     /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
           XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
           end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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    43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 353
CV732533/c
LOCUS      43 bp      mRNA      linear      EST 05-NOV-2004
DEFINITION FLO--07-A19.b1 Rice flower lambda phage cDNA library (FLO) Oryza
           sativa (japonica cultivar-group) cDNA clone FLO--07-A19, mRNA
           sequence.
ACCESSION  CV732533
VERSION     CV732533.1 GI:55438473
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 43)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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     /lab_host="E.coli SOLR"
     /clone_lib="Rice flower lambda phage cDNA library (FLO)"
     /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
           XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
           end with EcoRI and 3' end with XhoI site."

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clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 43)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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     /clone="FLO--07-A19"
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     /clone_lib="Rice flower lambda phage cDNA library (FLO)"
     /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
           XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
           end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||
    43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 354
CV732664/c
LOCUS      43 bp      mRNA      linear      EST 05-NOV-2004
DEFINITION FLO--07-D21.g1 Rice flower lambda phage cDNA library (FLO) Oryza
           sativa (japonica cultivar-group) cDNA clone FLO--07-D21, mRNA
           sequence.
ACCESSION  CV732664
VERSION     CV732664.1 GI:55438733
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 43)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
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           XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
           end with EcoRI and 3' end with XhoI site."

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XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 355
 CV733072/c
 LOCUS
 DEFINITION
 FLO--07-N05.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-N05, mRNA sequence.
 CV733072.1 GI:55439524
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 43)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
 Location/Qualifiers
 1. .43
 /organism="Oryza sativa (japonica cultivar-group)"
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 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 356
 CV733143/c
 LOCUS
 DEFINITION
 FLO--07-021.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-021, mRNA sequence.
 CV733143.1 GI:55439666
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 357
 CV733227/c
 LOCUS
 DEFINITION
 FLO--08-A18.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-A18, mRNA sequence.
 CV733227.1 GI:55439832
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 43)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
 Location/Qualifiers
 1. .43
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 43)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
 Location/Qualifiers
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 /tissue_type="flower"
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 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
 Query Match 1.3%; Score 35; DB 1; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source

Query Match 1.3%; Score 35; DB 1; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 357
 CV733227/c
 LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

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Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 358

CV733316/C
LOCUS FLO--08-C21.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-C21, mRNA sequence.
DEFINITION CV733316 43 bp mRNA linear EST 05-NOV-2004
ACCESSION CV733316.1 GI:55440010
VERSION CV733316
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 43)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 359

CV734334/C
LOCUS FLO--09-K09.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--09-K09, mRNA sequence.
DEFINITION CV734334 43 bp mRNA linear EST 05-NOV-2004
ACCESSION CV734334.1 GI:55440209
VERSION CV734334
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

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DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

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DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

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Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 43)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 360

CV734334/C
LOCUS iv3lf05.b1 Left Cardiac Ventricle (DOGEST7) Canis familiaris CDNA, mRNA sequence.
DEFINITION CX002408 43 bp mRNA linear EST 03-DEC-2004
ACCESSION CX002408
VERSION CX002408.1 GI:56273824
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 43)
AUTHORS Balijs, V.S., Nascimento, L.U. and McCombie, W.R.
TITLE ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8874
Fax: 516 367 8874
Email: mcombie@cshl.org.

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

FEATURES

source
Location/Qualifiers
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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

Query Match 1.3%; Score 35; DB 1; Length 43;
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Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

Query Match 1.3%; Score 35; DB 1; Length 43;
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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
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DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

ECORI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 28+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 361

AZ355703/c

LOCUS

DEFINITION AZ355703 43 bp DNA linear GSS 02-OCT-2000
IM0095D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0095D02 R, genomic survey sequence.

ACCESSION

AZ355703

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 43)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0095 row: D column: 02

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 43.

FEATURES

source

1..43

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0095D02"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 28+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 362

CR762707

LOCUS

DEFINITION CR762707 40 bp mRNA linear EST 23-SEP-2004
DKFZp469F0617_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DKFZp469F0617 5', mRNA sequence.

ACCESSION

CR762707

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Pongo pygmaeus (orangutan)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominoidea; Pongo.

REFERENCE

1 (bases 1 to 40)

AUTHORS

Ansorge,W., Krieger,S., Regiert,T., Rittmuller,C., Schwager,B.,

Mewes,H.W., Weill,B., Amid,C., Osanger,A., Fobo,G., Han,M. and

Wiemann,S.

TITLE

Pongo pygmaeus mRNA (Ansorge,W., Krieger,S., Regiert,T., et al.)

JOURNAL

Unpublished (2004)

COMMENT

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann,

Molecular Genome Analysis, German Cancer Research Center (DKFZ);

Email s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact

RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469F0617

Further information about the clone and the sequencing project is

available at http://mips.gsf.de/projects/cdna/.

FEATURES

Location/Qualifiers

1..40

/organism="Pongo pygmaeus"

/mol_type="mRNA"

/db_xref="taxon:9600"

/clone="DKFZp469F0617"

/tissue_type="kidney"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="469 (synonym: pkid1)"

/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

Query Match 1.3%; Score 34.8; DB 1; Length 40;

Best Local Similarity 94.7%; Pred. No. 28+02;

Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

|||||

DB 2 ACCACACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 39

RESULT 363

CV066153

LOCUS

DEFINITION

CV066153

WNEI30e11 Wheat EST endosperm library Triticum aestivum cDNA clone

WNEI30e11 5' similar to Unknown Function, mRNA sequence.

ACCESSION

CV066153

VERSION

CV066153.1 GI:51529330

```

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1. .43
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Hartog"
/db_xref="taxon:4565"
/clone="WNEU30611"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 6, 8, 10 dpa (days post anthesis)"
/lab_host="PH108 (Life Technology)"
/clone_lib="Wheat EST endosperm library"
/notes="Vector: ZipLox; Site 1: Sal I; Site 2: Not I; mRNA was prepared from endosperm tissues of the wheat cultivar Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa endosperm using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of ZipLox vector (Life Technology) after adding a Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."

Query Match 1.3%; Score 34.8; DB 1; Length 43;
Best Local Similarity 94.7%; Pred. No. 2.1e+02;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2704 GTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
|||||
Db 1 GTAATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 38

RESULT 364
CV725617/c
LOCUS
DEFINITION
14Salt--02-M17.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-M17, mRNA sequence.
CV725617
VERSION
KEYWORDS
SOURCE
ORGANISM

FEATURES
source
1. .36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-M17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="vector: bluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 34.4; DB 1; Length 36;
Best Local Similarity 97.2%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2708 TAAAAA
Db 36 TCAAAAAA

RESULT 365
DY231388
LOCUS
DEFINITION
DY202142 Bmp Bombyx mori cDNA clone BmpK_K44_2005-10-30_WD-051030
5', mRNA sequence.
ACCESSION
DY231388
VERSION
DY231388.1 GI:86465516
KEYWORDS
SOURCE
ORGANISM
Bombyx mori (domestic silkworm)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
REFERENCE
1 (bases 1 to 41)
AUTHORS
Zhang,Y.Z., Xu,J., Chen,J., Wang,D., Nie,Z.M., Lv,Z.B., Jiang,C.Y.,
Liu,L.L., Song,L., He,P.A., Chen,F. and Wu,X.F.
TITLE
The full-length cDNA library construction of silkworm pupae (Bombyx mori) and large-scale sequencing
JOURNAL
Unpublished (2006)
COMMENT
Contact: Yaohao, Zhang
Biochemistry Laboratory, the college of life science
Zhejiang Sci-Tech University
2th Street, Xiaoha High Education area, Hangzhou City, 310018, P.
R. China
Tel: 86 571 86843194
Fax: 86 571 86843198
Email: yaohao@chinagen.com
Seq primer: M13 Forward
High quality sequence stop: 41
POLYA=Yes.

FEATURES
source
1. .41
/organism="Bombyx mori"
/mol_type="mRNA"
/strain="Qingsong-Haoyue"
/db_xref="taxon:7091"
/clone="BmpK_K44_2005-10-30_WD-051030"
/sex="male and female"
/tissue_type="whole pupae body but for the skin"
/dev_stage="metaphase"
/clone_lib="Bmp"
/notes="vector: pHelix; Site 1: Hind II; The synthesis of double-stranded cDNA from mRNA was based on the method described by Gubler and Hoffman. The obtained cDNA were

```


ligated into the plasmid vector pHelix and subsequently the ligation product was transformed into E.coli competent cells TGI. At last, the recombinant clones were screened by blue-white plaques."

Query Match 1.3%; Score 34.4; DB 1; Length 41;
Best Local Similarity 97.2%; Pred. No. 2.1e+02;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2708 TAAAAA... 34 bp mRNA linear EST 22-OCT-2004
||||| 2743
Db 5 TAAAAA... 40

RESULT 366
CJ038300
LOCUS
DEFINITION
CJ038300 full-length enriched swine cDNA library, adult uterus Sus
scrofa cDNA clone UTR01C110090 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CJ038300.1 GI:54562195
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE
AUTHORS
1 (bases 1 to 34)
Unishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,
Okumura, N., Hamasima, N. and Awata, T.

TITLE
PEDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries

JOURNAL
PUBMED
Nucleic Acids Res. 32 (1), D484-D488 (2004)
14681463

COMMENT
Contact: Hirohide Unishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627

Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library

Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.

FEATURES

source

1..34
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="UTR01C110090"
/tissue_type="uterus"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult uterus"

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAA... 34 bp mRNA linear EST 04-NOV-2004
||||| 2741
Db 1 TAAAAA... 34

RESULT 367
CV724455/c
LOCUS
DEFINITION
CV724455 34 bp mRNA linear EST 04-NOV-2004
14Salt--01-A16.b1 Salt treated rice leaf lambda phage cDNA library

(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--01-A16, mRNA sequence.

ACCESSION
VERSION
KEYWORDS

SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 34)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..34
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--01-A16"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match

Best Local Similarity 1.2%; Score 34; DB 1; Length 34;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742

||||| 2742

Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 368

LOCUS

DEFINITION

CV726231 34 bp mRNA linear EST 04-NOV-2004
14Salt--03-M05.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-M05, mRNA sequence.

ACCESSION
VERSION
KEYWORDS

SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 34)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
Location/Qualifiers
1..34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-M05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 369

CV726784/c
LOCUS
DEFINITION
14Salt--04-J17.bi Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--04-J17, mRNA sequence.
ACCESSION
CV726784
VERSION
CV726784.1 GI:55414408
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 34)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
Location/Qualifiers
1..34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--04-J17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 370

CV727320/c
LOCUS
DEFINITION
14Salt--05-G14.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-G14, mRNA sequence.
ACCESSION
CV727320
VERSION
CV727320.1 GI:55414944
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 34)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
Location/Qualifiers
1..34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--05-G14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 371

CV729064/c
LOCUS
DEFINITION
FLO--01-l10.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-l10, mRNA sequence.
ACCESSION
CV729064
VERSION
CV729064.1 GI:55432090
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 34)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source Location/Qualifiers

1. .34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-L10"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742

Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 372

CV730592/c

LOCUS FLO--04-D09.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--04-D09, mRNA
sequence.

ACCESSION CV730592.1 GI:55434932

VERSION EST.

KEYWORDS Oryza sativa (japonica cultivar-group)

SOURCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 34)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--04-D09"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742

Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 373

CV730644/c

LOCUS FLO--04-E17.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--04-E17, mRNA
sequence.

ACCESSION CV730644.1 GI:55435034

VERSION EST.

KEYWORDS Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 34)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="FLO--04-E17"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match

Best Local Similarity 1.2%; Score 34; DB 1; Length 34;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742

Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 374

CV731182/c

LOCUS FLO--05-B16.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--05-B16, mRNA
sequence.

ACCESSION CV731182.1 GI:55436088

VERSION EST.

KEYWORDS Oryza sativa (japonica cultivar-group)

SOURCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

```

REFERENCE
AUTHORS      1 (bases 1 to 34)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 321 6355
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
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    /organism="Oryza sativa (japonica cultivar-group)"
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    /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
    end with EcoRI and 3' end with XhoI site."

Query Match      1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
DB 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 375
LOCUS      CV734338
DEFINITION FLO--09-K11.g1 Rice flower lambda phage cDNA library (FLO) Oryza
            sativa (japonica cultivar-group) cDNA clone FLO--09-K11, mRNA
            sequence.
ACCESSION  CV734338
VERSION     CV734338.1 GI:55442037
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 34)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 321 6355
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
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    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
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Query Match      1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
DB 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 375
LOCUS      CV734338
DEFINITION FLO--09-K11.g1 Rice flower lambda phage cDNA library (FLO) Oryza
            sativa (japonica cultivar-group) cDNA clone FLO--09-K11, mRNA
            sequence.
ACCESSION  CV734338
VERSION     CV734338.1 GI:55442037
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE  1 (bases 1 to 34)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 321 6355
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
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    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
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    /lab_host="E.coli SOLR"
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    XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
    end with EcoRI and 3' end with XhoI site."

Query Match      1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
DB 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 376
LOCUS      AZ465350
DEFINITION clone UUGC1M0275012 F, genomic survey sequence.
ACCESSION  AZ465350
VERSION     AZ465350.1 GI:10623475
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 34)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            Plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0275 row: 0 column: 12
            Seq primer: CGTTGTAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 34.
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                /clone="UUGC1M0275012"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: pWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid RI. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells

```

and selected for ampicillin resistance."

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
|||||
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 377
AZ501040
LOCUS
DEFINITION
IM0339P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0339P09 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 34)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0339 row: P column: 09
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 34.

FEATURES
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/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
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Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 378
AZ809643
LOCUS
DEFINITION
2M0073C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0073C14 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 34)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: C column: 14
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 34.

FEATURES
source

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
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DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 379
DU835285
LOCUS
DEFINITION
KBrS016F23F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS016F23, genomic survey
sequence.

ACCESSION
DU835285
DU835285.1 GI:83871881

KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
1 (bases 1 to 34)

AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.

TITLE
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

JOURNAL
Unpublished (2005)

COMMENT
Contact: Beom-Seok Park

Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS016F23

Seq primer: T7

Class: BAC ends.

FEATURES
source

Location/Qualifiers

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available at NTAB."

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 380
DX037933
LOCUS
DEFINITION
DX037933
KBrS036016R KBrS, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS036016, genomic survey
sequence.

ACCESSION
DX037933
DX037933.1 GI:84732230

KEYWORDS

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
1 (bases 1 to 34)

AUTHORS

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.

TITLE
End sequence of Brassica rapa BamHI (KBrS) BAC clone

JOURNAL
Unpublished (2005)

COMMENT
Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBrS036016

Seq primer: M13 Reverse

Class: BAC ends.

FEATURES
source

Location/Qualifiers

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/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chiifu BAC library (KBrS BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 1.2%; Score 34; DB 1; Length 34;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 381

CV730365/C

LOCUS

DEFINITION

CV730365

FLO-03-001.b1 Rice flower lambda phage cDNA library (FLO) Oryza

sativa (japonica cultivar-group) cDNA clone FLO-03-001, mRNA

sequence.

CV730365

CV730365.1 GI:55434480

EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 35)

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL
Unpublished (2003)

COMMENT
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .42
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/lab_host="E.coli SOLR"
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 34; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742

Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 385

DX045841/c

LOCUS

DEFINITION KB-R047E15F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB047E15, genomic survey sequence.

ACCESSION DX045841

VERSION DX045841.1 GI:84740138

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 41)

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.

End sequence of Brassica rapa BamHI (KBrB) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBrB047E15

Seq primer: T7

Class: BAC ends.

FEATURES

source

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Location/Qualifiers

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/lab_host="E.coli DH10B"

/clone_lib="KBrB, Brassica rapa BamHI BAC library"

/note="Vector: pCUG1BAC1; Site 1: BamHI; Brassica rapa ssp

pekinensis var. Chilifu BAC library (KBrB BAC) is provided

by Yong-Pyo Lim (CNU)."

Query Match

Best Local Similarity 94.6%; Pred. No. 2.3e+02;

Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 37 CCATAAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAA 1

RESULT 386

CV728107/c

LOCUS

DEFINITION 14Salt--06-K03.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION CV728107

VERSION CV728107.1 GI:55430324

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 42)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. .42
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--06-K03"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA

library (14Salt)"

/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.

cDNA was inserted into lamda Uni-ZAP XR vector at 5' end

with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 33.8; DB 1; Length 42;

Best Local Similarity 94.6%; Pred. No. 2.3e+02;

Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2703 TGTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

Db 37 TGTTCCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 387

CF331029/c

LOCUS

DEFINITION NACL--06-P22.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-P22, mRNA sequence.

ACCESSION CF331029

VERSION CF331029.1 GI:33810274

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 40)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-06-P22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH108"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.2%; Score 33.6; DB 1; Length 40;
Best Local Similarity 90.0%; Pred. No. 2.4e+02;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2702 TTGACTTAAAAA...AAAAAAAAAAAAAAAAAAAAA 2741
||| |
Db 40 TTATTTTCAAAAAA...AAAAAAAAAAAAAAAAAAAAA 1

RESULT 388
AL038483
LOCUS DKFZp566C0246_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DEFINITION DKFZp566C0246, mRNA sequence.

ACCESSION AL038483.1 GI:49682143
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 42)
AUTHORS Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.

TITLE EST (Ottenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

FEATURES Location/Qualifiers

source
1..42
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566C0246"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 1.2%; Score 33.6; DB 1; Length 42;
Best Local Similarity 90.0%; Pred. No. 2.4e+02;

Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2702 TTGACTTAAAAA...AAAAAAAAAAAAAAAAAAAAA 2741
||| |
Db 3 TTCAAAAAA...AAAAAAAAAGAAAAAAAAAAAAA 42

RESULT 389
BE894837
LOCUS 601434018F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919061 5',
DEFINITION mRNA sequence.

ACCESSION BE894837
VERSION BE894837.1 GI:10357627
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 35)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC/DCTD/BTP

cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9748 row: d column: 06
High quality sequence start: 4
High quality sequence stop: 35.

FEATURES Location/Qualifiers

source
1..35
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3919061"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."

Query Match 1.2%; Score 33.4; DB 1; Length 35;

Best Local Similarity 97.1%; Pred. No. 2.2e+02;

Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2706 ACTAAAAA...AAAAAAAAAAAAAAAAAAAAA 2740
||| |
Db 1 ATTTAAAAA...AAAAAAAAAAAAAAAAAAAAA 35

RESULT 390

CO785671/c

LOCUS BL284A_H08 6-Day Axolotl Tail Blastema (6DAXBL) Ambystoma mexicanum
DEFINITION cDNA 57 similar to hypothetical protein, mRNA sequence.

ACCESSION CO785671
VERSION CO785671.1 GI:51001651
KEYWORDS EST.

SOURCE Ambystoma mexicanum (axolotl)
ORGANISM Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.

REFERENCE 1 (bases 1 to 35)

AUTHORS Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
TITLE An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries

JOURNAL Genome Biol. (2004) In press
COMMENT Contact: Elly M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pflotenhauerstrasse 108,01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: BL284A row: 08 column: H
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES
source
1..35
Location/Qualifiers
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Tail Blastema"
/cell_type="regenerating tail blastema"
/clone_lib="6-Day Axolotl Tail Blastema (6DAXBL)"
/Note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.67 kb.
TAG_LIB=6DAXBL"

FEATURES
source
1..35
Location/Qualifiers
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Tail Blastema"
/cell_type="regenerating tail blastema"
/clone_lib="6-Day Axolotl Tail Blastema (6DAXBL)"
/Note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.67 kb.
TAG_LIB=6DAXBL"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 391
LOCUS DN955388
DEFINITION it87b05.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.
ACCESSION DN955388
VERSION DN955388.1 GI:63027526
KEYWORDS EST.
SOURCE Gnetum gnemon
ORGANISM Gnetum gnemon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 35)
/Note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.67 kb.
TAG_LIB=6DAXBL"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 391
LOCUS DN955388
DEFINITION it87b05.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.
ACCESSION DN955388
VERSION DN955388.1 GI:63027526
KEYWORDS EST.
SOURCE Gnetum gnemon
ORGANISM Gnetum gnemon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 35)
/Note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.67 kb.
TAG_LIB=6DAXBL"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 391
LOCUS DN955388
DEFINITION it87b05.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.
ACCESSION DN955388
VERSION DN955388.1 GI:63027526
KEYWORDS EST.
SOURCE Gnetum gnemon
ORGANISM Gnetum gnemon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 35)
/Note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.67 kb.
TAG_LIB=6DAXBL"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 391
LOCUS DN955388
DEFINITION it87b05.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.
ACCESSION DN955388
VERSION DN955388.1 GI:63027526
KEYWORDS EST.
SOURCE Gnetum gnemon
ORGANISM Gnetum gnemon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 35)
/Note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.67 kb.
TAG_LIB=6DAXBL"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 391
LOCUS DN955388
DEFINITION it87b05.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.
ACCESSION DN955388
VERSION DN955388.1 GI:63027526
KEYWORDS EST.
SOURCE Gnetum gnemon
ORGANISM Gnetum gnemon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 35)
/Note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.67 kb.
TAG_LIB=6DAXBL"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 392
LOCUS BE894682
DEFINITION 601435925F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920911 5',
mRNA sequence.
ACCESSION BE894682
VERSION BE894682.1 GI:10357319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 36)
/Note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 392
LOCUS BE894682
DEFINITION 601435925F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920911 5',
mRNA sequence.
ACCESSION BE894682
VERSION BE894682.1 GI:10357319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 36)
/Note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 392
LOCUS BE894682
DEFINITION 601435925F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920911 5',
mRNA sequence.
ACCESSION BE894682
VERSION BE894682.1 GI:10357319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 36)
/Note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 392
LOCUS BE894682
DEFINITION 601435925F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920911 5',
mRNA sequence.
ACCESSION BE894682
VERSION BE894682.1 GI:10357319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 36)
/Note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 392
LOCUS BE894682
DEFINITION 601435925F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920911 5',
mRNA sequence.
ACCESSION BE894682
VERSION BE894682.1 GI:10357319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 36)
/Note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 392
LOCUS BE894682
DEFINITION 601435925F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920911 5',
mRNA sequence.
ACCESSION BE894682
VERSION BE894682.1 GI:10357319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 36)
/Note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 392
LOCUS BE894682
DEFINITION 601435925F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920911 5',
mRNA sequence.
ACCESSION BE894682
VERSION BE894682.1 GI:10357319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 36)
/Note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 392
LOCUS BE894682
DEFINITION 601435925F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920911 5',
mRNA sequence.
ACCESSION BE894682
VERSION BE894682.1 GI:10357319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 36)
/Note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 35 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 392
LOCUS BE894682
DEFINITION 601435925F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920911 5',
mRNA sequence.
ACCESSION BE894682
VERSION BE894682.1 GI:10357319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 36)
/Note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

```

ACCESSION CV724804
VERSION CV724804.1 GI:55412428
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzoideae; Oryza.
REFERENCE 1 (bases 1 to 36)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nam B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Gyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
    1..36
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="cDNA"
        /cultivar="Nackdong"
        /db_xref="taxon:39947"
        /clone="14Salt-01-J08"
        /tissue_type="leaf"
        /dev_stage="14 days after germination"
        /lab_host="E.coli SOLR"
        /clone_lib="Salt treated rice leaf lambda phage cDNA
        library (14Salt)"
        /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
        XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
        cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
        with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 33.4; DB 1; Length 36;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 35 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 394
LOCUS CZ912531
DEFINITION CZ912531 36 bp DNA linear GSS 08-AUG-2005
          survey sequence.
ACCESSION CZ912531
VERSION CZ912531.1 GI:71927929
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 36)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
          Department of Biological Sciences
          Stanford University
          855 California Ave, Palo Alto, CA 94304, USA
          Tel: 650 723 2227
          Fax: 650 725 8221
          Email: walbot@stanford.edu
          Very probable ligation site of ends cut by single endonuclease.
          Reverse complemented post-ligation sequence from source sequence.
          Plate: 4012010 row: G column: 11

Class: transposon-tagged.
Location/Qualifiers
1..36
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4012 - RescueMu Grid BB"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
BB was grown at UC Berkeley in 2001. DNA was extracted
from leaf strips, double digested using BamHI and BglII,
and ligated to form circular plasmids. DH10B cells were
transformed and then screened on LB plates with
ampicillin."

Query Match 1.2%; Score 33.4; DB 1; Length 36;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 395
LOCUS DU830895/c
DEFINITION DU830895/c 36 bp DNA linear GSS 22-DEC-2005
          subsp. pkinsensis genomic clone KBrS007101, genomic survey
          sequence.
ACCESSION DU830895
VERSION DU830895.1 GI:83867491
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pkinsensis
ORGANISM Brassica rapa subsp. pkinsensis
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicotyledons;
          rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 36)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
          Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
          Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
          Brassica Genomics Team
          National Institute of Agricultural Biotechnology
          225 Seodun-Dong, Suwon, 441-707, Korea
          Tel: +82-31-299-1670
          Fax: +82-31-299-1672
          Email: pbeom@da.go.kr
          BAC end sequence of Brassica rapa ssp. pkinsensis Sau3AI BAC clone
          KBrS007101
          Seq primer: T7
          Class: BAC ends.

FEATURES
source
    1..36
        /organism="Brassica rapa subsp. pkinsensis"
        /mol_type="genomic DNA"
        /cultivar="Chiifu"
        /sub_species="pkinsensis"
        /db_xref="taxon:51351"
        /clone="KBrS007101"
        /lab_host="E. coli DH10B"

```

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/clone lib="KBS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chifu BAC library (KBS BAC) is
available at NIAB."

Query Match      1.2%; Score 33.4; DB 1; Length 36;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 396
AL048768
LOCUS      37 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZ556M083.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION AL048768
VERSION DKFZ556M083 mRNA sequence.
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 37)
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
1..37
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ556M083"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: Sall"

Query Match      1.2%; Score 33.4; DB 1; Length 37;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 35

RESULT 397
CV732356/c
LOCUS      37 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--06-M19.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--06-M19, mRNA
sequence.
ACCESSION CV732356
VERSION CV732356.1 GI:55438125
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 37)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs

```

```

JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bbnahm@bio.com, bbnahm@bio.myongji.ac.kr.
FEATURES
source
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--06-M19"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.2%; Score 33.4; DB 1; Length 37;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 35 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 398
AZ824309/c
LOCUS      37 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0098017R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0098017 R, genomic survey sequence.
ACCESSION AZ824309
VERSION AZ824309.1 GI:12994217
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 37)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0098 row: 0 column: 17
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.
FEATURES
source
1..37
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0098017"
/sex="Male"

```

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMW42 (G114732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 33.4; DB 1; Length 37;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 399
DX062077 37 bp DNA linear GSS 10-JAN-2006
LOCUS KBrB068M24F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB068M24, genomic survey
sequence.

ACCESSION DX062077.1 GI:84756373
VERSION DX062077.1
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 37)

REFERENCE Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)

TITLE National Institute of Agricultural Biotechnology
JOURNAL Contact: Beom-Seok Park
COMMENT Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB068M24
Seq primer: T7
Class: BAC ends.

FEATURES
source 1. .37
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB068M24"
/lab_host="E. coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/notes="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp

pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 1.2%; Score 33.4; DB 1; Length 37;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 400
CF302184/c 38 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--07-H22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-H22, mRNA
sequence.

ACCESSION CF302184
VERSION CF302184.1 GI:33673945
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 38)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE Contact: Nahm B.H.
JOURNAL
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source 1. .38
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--07-H22"
/tissue type="leaf"
/dev stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.2%; Score 33.4; DB 1; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
|||||
Db 35 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 401
CF316791 38 bp mRNA linear EST 15-AUG-2003
LOCUS HD--06-D18.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--06-D18, mRNA sequence.
ACCESSION CF316791
VERSION CF316791.1 GI:33688552
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..38
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-06-D18"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match

Best Local Similarity 1.2%; Score 33.4; DB 1; Length 38;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 402

AW333985/ C S28H9 AGS-1 Pneumocystis carinii cDNA 3', mRNA linear EST 31-JAN-2000
LOCUS AW333985
DEFINITION AW333985
ACCESSION AW333985.1 GI:68303342
VERSION EST.
KEYWORDS Pneumocystis carinii
SOURCE Pneumocystis carinii
ORGANISM Pneumocystis carinii

Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae; Pneumocystis.
1 (bases 1 to 38)
Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C., Edman, J.C., Kovacs, J. and Cushion, M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY 40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.

FEATURES

source

1..38
Location/Qualifiers
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"

/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI; P. carinii organisms (3x10e9) from a single rat (99-1-6, sacrificed on 3/17/99) at Cincinnati VA facilities. trizol extracted RNA. Oligo dt priming. Standard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pneumocystis/"

Query Match 1.2%; Score 33.4; DB 1; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

DB 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 403

DR074451

LOCUS

DEFINITION ik94d04.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA linear EST 08-JUN-2005

ACCESSION DR074451

VERSION DR074451.1

KEYWORDS EST.

SOURCE Ginkgo biloba (maidenhair tree)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

REFERENCE 1 (bases 1 to 38)

AUTHORS Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Ginkgo male leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Original 3 prime EST has been reverse completed to be in 5 prime direction

Seq primer: -21M13UnivRev.

FEATURES

source

1..38
Location/Qualifiers
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="male"
/clone_lib="Ginkgo male leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."

Seq primer: -21M13UnivRev.

Location/Qualifiers

1..38

/organism="Ginkgo biloba"

/mol_type="mRNA"

/db_xref="taxon:3311"

/sex="male"

/clone_lib="Ginkgo male leaf (NYBG)"

/note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."

Query Match

Best Local Similarity 1.2%; Score 33.4; DB 1; Length 38;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 404

AZ589726/c

LOCUS

DEFINITION 1M0398I24R Mouse 10kb plasmid UNGC1M library Mus musculus genomic clone UNGC1M0398I24 R, genomic survey sequence.

ACCESSION AZ589726

VERSION AZ589726.1

KEYWORDS GSS.

SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0398 row: I column: 24
Seq primer: CACACGAAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 38.
Location/Qualifiers
1. .38
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0398124"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GII4732114[gB|Afl29072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES
source
Query Match 1.2%; Score 33.4; DB 1; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||

Db 38 AAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4
|||||

RESULT 405
DX060574/c
LOCUS
DEFINITION
DX060574
38 bp DNA linear GSS 10-JAN-2006
KBRB066N13F KBxR, Brassica rapa BAC library Brassica rapa subsp. pекinensis genomic clone KBRB066N13, genomic survey sequence.
ACCESSION
VERSION
DX060574.1 GI:84754870

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source
1. .39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-10-A16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr_ Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 1.2%; Score 33.4; DB 1; Length 39;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 407
CO786273/c
LOCUS BL285D_F07 6-Day Axolotl Tail Blastema (6DaxBL) Ambystoma mexicanum
DEFINITION cDNA 5' similar to hypothetical protein, mRNA sequence.
ACCESSION CO786273
VERSION CO786273.1 GI:51002253
KEYWORDS EST.
SOURCE Ambystoma mexicanum (axolotl)
ORGANISM Ambystoma mexicanum
REFERENCE 1 (bases 1 to 39)
AUTHORS Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
Pehlike,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
TITLE An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
JOURNAL Genome Biol. (2004) In press
COMMENT Contact: Elly M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Protenhauerstrasse 108,01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: BL285D row: 07 column: F
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES
location/Qualifiers
1..39
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Tail Blastema"
/clone_lib="6-Day Axolotl Tail Blastema (6DaxBL)"
/notes="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.67 kb.
TAG_LIB=6DaxBL"

Query Match 1.2%; Score 33.4; DB 1; Length 39;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

source
1. .39
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR10D12"
/clone_lib="RPCI-98"
/notes="end : TET3"

Query Match 1.2%; Score 33.4; DB 1; Length 39;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 409
AL638703/c
LOCUS AL638703 XGC-egg Xenopus tropicalis cDNA clone L1E5G04 5', mRNA
DEFINITION sequence.
ACCESSION AL638703
VERSION AL638703.1 GI:16790682
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

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REFERENCE
AUTHORS      Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
TITLE        Sanger Xenopus tropicalis EST project 2001 (10_2001)
JOURNAL      Unpublished (2001)
COMMENT      Contact: Huckle E
              Sanger Institute
              Hinxton, Cambridgeshire, CB10 1SA, UK
              Email: tropesanger.ac.uk
              Sanger Xenopus tropicalis EST project 2001
              TROPICALIS_SEQUENCE ID: L1E5g04.sp6
              Sequencing primer: SP6
              This sequence is from a Xenopus Gene Collection (XGC) library
              constructed by Aaron M. Zorn.
FEATURES
source
1..40
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="L1E5g04"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-egg"
/notes="Vector: pCSI07; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCSI07 with
EcoRI at the 5' end and NotI at the 3' end"
Query Match      1.2%; Score 33.4; DB 1; Length 40;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 40 AAAAAAAAAAAAAAAAACAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 410
CF336399/C
LOCUS
DEFINITION      Oryza sativa (japonica cultivar-group) cDNA clone
                  library (JMT) AtJMT-overexpressing transgenic rice plasmid cDNA
                  library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
                  JMT-06-H01, mRNA sequence.
ACCESSION      CF336399.1 GI:33821186
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaem@bio.com, bhnaem@bio.myongji.ac.kr.
Location/Qualifiers
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT-06-H01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnaem@bio.com, bhnaem@bio.myongji.ac.kr.
              Location/Qualifiers
              1..40
              /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:39947"
              /clone="JMT-06-H01"
              /tissue_type="leaf"
              /dev_stage="14 days after germination"
              /lab_host="E.coli DH10B"
              /clone_lib="AtJMT-overexpressing transgenic rice plasmid

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```

cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
Query Match      1.2%; Score 33.4; DB 1; Length 40;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
      |||||||
Db 35 ACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 411
DV082973
LOCUS
DEFINITION      327-384-37_O10_KS Nematostella vectensis normalized cDNA library
                  sequence.
ACCESSION      DV082973.1 GI:82864366
VERSION
KEYWORDS
SOURCE
ORGANISM
Nematostella vectensis
Nematostella vectensis
Eukaryota; Metazoa; Chnidaria; Anthozoa; Hexacorallia; Actiniaria;
Edwardsiidae; Nematostella.
1 (bases 1 to 40)
Technau,U., Rudd,S., Maxwell,P., Gordon,P.M.K., Saina,M.,
Grasso,L.C., Hayward,D.C., Sensen,C.W., Saint,R., Holstein,T.W.,
Ball,E.E. and Miller,D.J.
Maintenance of ancestral complexity and non-metazoan genes in two
basal cnidarians
Trends Genet. (2005) In press
Contact: Ulrich Technau
Sars Centre for Marine Molecular Biology
High Technology Building, Thormohlenstgt. 5 5008 Bergen, Norway
Tel: +47-55584340
Email: ulrich.technau@sars.uib.no
Plate: 37 row: 10 column: 0
Seq primer: KS.
Location/Qualifiers
1..40
/organism="Nematostella vectensis"
/mol_type="mRNA"
/db_xref="taxon:45351"
/clone="327-384-37_O10_KS"
/sex="hermaphrodite"
/tissue_type="whole embryos"
/dev_stage="mixed stages from unfertilized eggs to primary
polypos"
/clone_lib="Nematostella vectensis normalized cDNA library
327"
/notes="Vector: pBluescript II SK(+); Site 1: NotI; Site 2:
EcoRI; Normalized oligo dT primed cDNA library using poly
A+ RNA from mixed embryonic stages of Nematostella
vectensis. Cloned directionally into pBluescript II SK(+).
Ligated in NotI, EcoRI"
Query Match      1.2%; Score 33.4; DB 1; Length 40;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 412
DX076358/C
LOCUS
DEFINITION      KBrB087J22F KBrB, Brassica rapa BamHI BAC library Brassica rapa

```

```

subsp. pekinensis genomic clone KBrB087J22, genomic survey
sequence.
DX076358.1 GI:84770654
GSS.
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 40)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB087J22
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..40
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/db_xref="taxon:51351"
/clone="KBrB087J22"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/notes="Vector: PCUG1BAC1; Site_1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Query Match 1.2%; Score 33.4; DB 1; Length 40;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 413
CF300448/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-N15, mRNA
sequence.

ACCESSION CF300448
VERSION CF300448.1 GI:33672209
SOURCE EST.
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 413
CF300448/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-N15, mRNA
sequence.

ACCESSION CF300448
VERSION CF300448.1 GI:33672209
SOURCE EST.
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

```

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-N15"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 414
CF302032/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C22, mRNA
sequence.

ACCESSION CF302032
VERSION CF302032.1 GI:33673793
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 414
CF302032/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C22, mRNA
sequence.

ACCESSION CF302032
VERSION CF302032.1 GI:33673793
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 414
CF302032/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C22, mRNA
sequence.

ACCESSION CF302032
VERSION CF302032.1 GI:33673793
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

```

Db      41  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7
|||||
CF305364      41 bp  mRNA  linear  EST 15-AUG-2003
LOCUS  CLD1--01-I05 b1 Rice cold treated leaf plasmid cDNA library (CLD1)
DEFINITION  Oryza sativa (japonica cultivar-group) cDNA clone CLD1--01-I05,
mRNA sequence.
ACCESSION  CF305364.1 GI:33677125
VERSION  CF305364
KEYWORDS  EST.
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 41)
AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE  Large-scale Sequencing Analysis of Rice ESTs
JOURNAL  Unpublished (2003)
COMMENT  Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
    source
    1..41
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CBCAAC09"
    /tissue_type="cord blood"
    /cell_type="CD34+ hematopoietic stem/progenitor cell"
    /lab_host="BM25.8"
    /clone_lib="CB"
    /notes="Vector: pBluescript; Site 1: EcoRI; The insert is
    cloned randomly with the EcoRI digestion"

Query Match      1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 91.9%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2707  CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||
Db      4  CTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 40
|||||

RESULT 417
CV731029/c
LOCUS  CV731029
DEFINITION  Oryza sativa (japonica cultivar-group) cDNA clone FLO--04-N23, mRNA
sequence.
ACCESSION  CV731029
VERSION  CV731029.1 GI:55435787
KEYWORDS  EST.
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 41)
AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE  Large-scale Sequencing Analysis of Rice ESTs
JOURNAL  Unpublished (2003)
COMMENT  Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
    source
    1..41
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="CLD1--01-I05"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice cold treated leaf plasmid cDNA library
    (CLD1)"
    /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was
    incubated at 4 C (360uM/m-2sec-1) for 2hrs. Oligo-capped
    mRNA was reverse transcribed and then used for PCR."

Query Match      1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db      37  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3
|||||

RESULT 416
AV742106
LOCUS  AV742106
DEFINITION  AV742106 CB Homo sapiens cDNA clone CBCAAC09 5', mRNA sequence.
ACCESSION  AV742106
VERSION  AV742106.1 GI:10859687
KEYWORDS  EST.
SOURCE  Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE  1 (bases 1 to 41)
AUTHORS  Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
Chen,S., Mao,M. and Chen,Z.
TITLE  Homo sapiens CB library cDNA clones
JOURNAL  Unpublished (2000)
COMMENT  Contact: Zhu Chen

Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mbsheims.stn.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
    source
    1..41
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CBCAAC09"
    /tissue_type="cord blood"
    /cell_type="CD34+ hematopoietic stem/progenitor cell"
    /lab_host="BM25.8"
    /clone_lib="CB"
    /notes="Vector: pBluescript; Site 1: EcoRI; The insert is
    cloned randomly with the EcoRI digestion"

Query Match      1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 91.9%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2707  CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||
Db      4  CTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 40
|||||

RESULT 417
CV731029/c
LOCUS  CV731029
DEFINITION  Oryza sativa (japonica cultivar-group) cDNA clone FLO--04-N23, mRNA
sequence.
ACCESSION  CV731029
VERSION  CV731029.1 GI:55435787
KEYWORDS  EST.
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 41)
AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE  Large-scale Sequencing Analysis of Rice ESTs
JOURNAL  Unpublished (2003)
COMMENT  Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
    source
    1..41
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="CLD1--01-I05"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice cold treated leaf plasmid cDNA library
    (CLD1)"
    /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was
    incubated at 4 C (360uM/m-2sec-1) for 2hrs. Oligo-capped
    mRNA was reverse transcribed and then used for PCR."

Query Match      1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db      37  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3
|||||

RESULT 416
AV742106
LOCUS  AV742106
DEFINITION  AV742106 CB Homo sapiens cDNA clone CBCAAC09 5', mRNA sequence.
ACCESSION  AV742106
VERSION  AV742106.1 GI:10859687
KEYWORDS  EST.
SOURCE  Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE  1 (bases 1 to 41)
AUTHORS  Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
Chen,S., Mao,M. and Chen,Z.
TITLE  Homo sapiens CB library cDNA clones
JOURNAL  Unpublished (2000)
COMMENT  Contact: Zhu Chen

```

Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AA 2743
 |||||
 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAAA 7

RESULT 418 DX049794/c

LOCUS DX049794.1 41 bp DNA linear GSS 10-JAN-2006
 DEFINITION KBR052116f KBrB, Brassica rapa BamHI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBR052116, genomic survey
 sequence.

ACCESSION DX049794
 VERSION DX049794.1 GI:84744091

SOURCE

ORGANISM Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
 Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
 Hahn, J.H. and Park, B.S.

TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone

JOURNAL COMMENT

Unpublished (2003)
 Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea
 Tel: +82-31-299-1670
 Fax: +82-31-299-1672

Email: pbeom@da.go.kr
 BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
 KBR052116

Seq primer: T7

Class: BAC ends.

FEATURES

source

1..41
 Location/Qualifiers
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBR052116"
 /lab_host="E.coli DH10B"
 /clone_lib="KBrB, Brassica rapa BamHI BAC library"
 /note="Vector: pCUGBAC1; Site 1: BamHI; Brassica rapa spp
 pekinensis var. Chiifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 1.2%; Score 33.4; DB 1; Length 41;
 Best Local Similarity 97.1%; Pred. No. 2.5e+02;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 419 AL038652

LOCUS AL038652 38 bp mRNA linear EST 06-JUL-2004
 DEFINITION DKFZp56611946_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION AL038652

VERSION AL038652.1 GI:49682177

KEYWORDS

SOURCE EST.

ORGANISM Homo sapiens (human)

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 38)

AUTHORS Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
 Wiemann, S.

TITLE EST (Ottenwaelder, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

1..38
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp56611946"
 /tissue_type="kidney"
 /dev_stage="fetal"
 /lab_host="X1-2blue"
 /clone_lib="566 (synonym: hfkd2)"
 /note="Vector: pAMP1; Site 1: NotI; Site 2: SalI"

Query Match 1.2%; Score 33.2; DB 1; Length 38;
 Best Local Similarity 92.1%; Pred. No. 2.4e+02;
 Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2703 TGTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

|||
 Db 1 TGGACAAAAAAAAAAAAAAAAAGAAAAAAAAA 38

RESULT 420

LOCUS CF328529/c

DEFINITION CF328529 39 bp mRNA linear EST 18-AUG-2003
 NACL--03-H18.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa (japonica cultivar-group) cDNA clone NACL--03-H18, mRNA
 sequence.

ACCESSION CF328529

VERSION CF328529.1 GI:33805303

KEYWORDS

EST.

SOURCE Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 39)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of BioScience and Bioinformatics, Myongji University

Yongin,yeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1..39

FEATURES

source

/organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--03-H18"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.2%; Score 33.2; DB 1; Length 39;
 Best Local Similarity 92.1%; Pred. No. 2.5e+02;

/clone lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.2%; Score 33; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
 |||||
 Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 424
 CF328313 33 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--03-C14.g1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--03-C14, mRNA
 sequence.

ACCESSION CF328313 GI:33804873
 VERSION CF328313
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 33)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongui University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
 Location/Qualifiers
 1..33
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--03-C14"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.2%; Score 33; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33

RESULT 425
 CF336752/c 33 bp mRNA linear EST 18-AUG-2003
 LOCUS JMT--06-019.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--06-019, mRNA sequence.

ACCESSION CF336752
 VERSION CF336752
 KEYWORDS EST.
 CF336752.1 GI:33821884

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 33)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongui University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
 Location/Qualifiers
 1..33
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--06-019"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 1.2%; Score 33; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
 |||||
 Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 426
 CF337105/c 33 bp mRNA linear EST 18-AUG-2003
 LOCUS JMT--07-G18.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--07-G18, mRNA sequence.

ACCESSION CF337105 GI:33822596
 VERSION CF337105
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 33)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongui University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
 Location/Qualifiers
 1..33
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"

/cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--07-G18"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH108"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 1.2%; Score 33; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741

Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 427

CV725203/c

LOCUS

DEFINITION CV725203 33 bp mRNA linear EST 04-NOV-2004
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--02-C18, mRNA sequence.

ACCESSION

CV725203

VERSION

CV725203.1

KEYWORDS

GI:55412827

SOURCE

EST.

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 33)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..33

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--02-C18"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA

library (14Salt)"

/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.

cDNA was inserted into lambda Uni-ZAP XR vector at 5' end

with EcoRI and 3' end with XhoI site."

Query Match

1.2%; Score 33; DB 1; Length 33;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741

Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 428

CV725846/c

LOCUS

DEFINITION

CV725846 33 bp mRNA linear EST 04-NOV-2004

(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

14Salt--03-C19, mRNA sequence.

ACCESSION

CV725846

VERSION

CV725846.1

KEYWORDS

GI:55413470

SOURCE

EST.

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 33)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..33

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--03-C19"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA

library (14Salt)"

/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.

cDNA was inserted into lambda Uni-ZAP XR vector at 5' end

with EcoRI and 3' end with XhoI site."

Query Match

1.2%; Score 33; DB 1; Length 33;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741

Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 429

CV725871/c

LOCUS

DEFINITION

CV725871 33 bp mRNA linear EST 04-NOV-2004

(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

14Salt--03-D09, mRNA sequence.

ACCESSION

CV725871

VERSION

CV725871.1

KEYWORDS

GI:55413495

SOURCE

EST.

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 33)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

```

1..33
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-D09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

```

Query Match 1.2%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
      |||||||
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 430

CV725959/c

LOCUS

DEFINITION

14Salt--03-F12.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

14Salt--03-F12, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 33)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1..33

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--03-F12"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.

cDNA was inserted into lamda Uni-ZAP XR vector at 5' end

with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 33; DB 1; Length 33;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741

|||||

Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 431

CV726801/c

LOCUS

DEFINITION

14Salt--04-K03.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

14Salt--04-K03, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 33)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1..33

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--04-K03"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.

cDNA was inserted into lamda Uni-ZAP XR vector at 5' end

with EcoRI and 3' end with XhoI site."

Query Match

1.2%; Score 33; DB 1; Length 33;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741

|||||

Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 432

CV726984/c

LOCUS

DEFINITION

14Salt--04-O15.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

14Salt--04-O15, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

Oryza sativa (japonica cultivar-group)

CV726984 33 bp mRNA linear EST 04-NOV-2004

(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

14Salt--04-O15, mRNA sequence.

CV726984 33 bp mRNA linear EST 04-NOV-2004

CV726984 33 bp mRNA linear EST 04-NOV-2004

CV726984 33 bp mRNA linear EST 04-NOV-2004

CV726984 33 bp mRNA linear EST 04-NOV-2004

CV726984 33 bp mRNA linear EST 04-NOV-2004

CV726984 33 bp mRNA linear EST 04-NOV-2004

CV726984 33 bp mRNA linear EST 04-NOV-2004

CV726984 33 bp mRNA linear EST 04-NOV-2004

CV726984 33 bp mRNA linear EST 04-NOV-2004

CV726984 33 bp mRNA linear EST 04-NOV-2004

```

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 33)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
     source
1..33
     /organism="Oryza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:39947"
     /clone="14Salt--04-015"
     /tissue_type="leaf"
     /dev_stage="14 days after germination"
     /lab_host="E.coli SOLR"
     /clone_lib="Salt treated rice leaf lambda phage cDNA
     library (14Salt)"
     /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
     XhoI; Leaf was incubated at 4 C(360mM/m-2sec-1) for 2hrs.
     cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
     with EcoRI and 3' end with XhoI site."

Query Match          1.2%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 433
CV732151/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-102, mRNA
sequence.
ACCESSION
CV732151
VERSION
CV732151.1 GI:55437726
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 33)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
     source
1..33
     /organism="Oryza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
     /cultivar="Nackdong"

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     /db_xref="taxon:39947"
     /clone="FLO--06-102"
     /tissue_type="flower"
     /lab_host="E.coli SOLR"
     /clone_lib="Rice flower lambda phage cDNA library (FLO)"
     /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
     XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
     end with EcoRI and 3' end with XhoI site."

Query Match          1.2%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 434
CV732198/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-J03, mRNA
sequence.
ACCESSION
CV732198
VERSION
CV732198.1 GI:55437812
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 33)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1..33
     /organism="Oryza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
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     /clone="FLO--06-J03"
     /tissue_type="flower"
     /lab_host="E.coli SOLR"
     /clone_lib="Rice flower lambda phage cDNA library (FLO)"
     /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
     XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
     end with EcoRI and 3' end with XhoI site."

Query Match          1.2%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 435
CV732853/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-105, mRNA
sequence.

```



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ACCESSION      CX013914
VERSION        CX013914.1
KEYWORDS       GI:56396325
SOURCE         Canis familiaris (dog)
ORGANISM       Canis familiaris
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
               Canis.
REFERENCE      1 (bases 1 to 33)
AUTHORS       Balijs, V.S., Nascimben, L.U. and McCombie, W.R.
TITLE         ESTs from Canis familiaris whole heart (dog)
JOURNAL       Unpublished (2004)
COMMENT       Contact: W. Richard McCombie
               Lita Amberg-Hazen Genome Sequencing Center
               Cold Spring Harbor Laboratory
               PO Box 100, Cold Spring Harbor, NY 11724, USA
               Tel: 516 367 8884
               Fax: 516 367 8874
               Email: mcombie@cshl.org
FEATURES       Location/Qualifiers
               1..33
               /organism="Canis familiaris"
               /mol_type="mRNA"
               /db_xref="taxon:9615"
               /sex="Unknown"
               /dev_stage="3 month old normal canine"
               /lab_host="Xl10 Gold"
               /clone_lib="Whole Heart Library (DOESTS)"
               /notes="Organ: Heart; Vector: pBluescript II SK; Site 1:
               EcoRI; Site 2: XhoI; Library constructed using pluscript
               XR kit from Stratagene. Cloned cDNA was size selected
               between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
               Medical Genetics, School of Veterinary Medicine,
               University of Pennsylvania, 3800 Spruce Street,
               Philadelphia, PA 19104-6051"
               Query Match      1.2%; Score 33; DB 1; Length 33;
               Best Local Similarity 100.0%; Pred. No. 2.3e+02;
               Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
               QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
               Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33
               RESULT 439
               AZ486795/c 33 bp DNA linear GSS 05-OCT-2000
               LOCUS 1M0315P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
               DEFINITION clone UUGC1M0315P22 F, genomic survey sequence.
               ACCESSION AZ486795
               VERSION AZ486795.1
               KEYWORDS GSS.
               SOURCE Mus musculus (house mouse)
               ORGANISM Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Mus.
               REFERENCE 1 (bases 1 to 33)
               AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
               Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
               Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
               Niederhausern, A. and Wright, D., Weiss, R.
               TITLE Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
               JOURNAL Unpublished (2000)
               COMMENT Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: mcombie@cshl.org
               Email: rdunn@genetics.utah.edu
               Insert length: 10000 Std Error: 0.00
               Plate: 0315 row: P column: 22
               Seq primer: CGTTGTAAACGACGCCAGT
               Class: plasmid ends
               High quality sequence stop: 33.
               Location/Qualifiers
               1..33
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC1M0315P22"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adapted DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid RI. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adapted mouse DNA was annealed to
               adapted vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
               Query Match      1.2%; Score 33; DB 1; Length 33;
               Best Local Similarity 100.0%; Pred. No. 2.3e+02;
               Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
               QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
               Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
               RESULT 440
               AZ627839/c 33 bp DNA linear GSS 13-DEC-2000
               LOCUS 1M0474B02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
               DEFINITION clone UUGC1M0474B02 F, genomic survey sequence.
               ACCESSION AZ627839
               VERSION AZ627839.1
               KEYWORDS GSS.
               SOURCE Mus musculus (house mouse)
               ORGANISM Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Mus.
               REFERENCE 1 (bases 1 to 33)
               AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
               Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
               Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
               Niederhausern, A. and Wright, D., Weiss, R.
               TITLE Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
               JOURNAL Unpublished (2000)
               COMMENT Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177

```

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0474 row: B column: 02
 Seq primer: CGTTGTAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 33.
 Location/Qualifiers

FEATURES

source

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1. .33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0474B02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 1.2%; Score 33; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741

Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 441

CZ917348
 LOCUS 4021005C07.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic survey sequence.
 DEFINITION CZ917348 33 bp DNA linear GSS 08-AUG-2005

ACCESSION CZ917348

VERSION CZ917348.1 GI:71936070

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 33)

AUTHORS Walbot,V.

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished (2001)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4021005 row: C column: 07

Class: transposon-tagged.

FEATURES

source

Location/Qualifiers
 1. .33
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_hosts="DH10B"
 /clone_lib="4021 - RescueMu Grid V"
 /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.2%; Score 33; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33

RESULT 442

DU830405/c

LOCUS

DEFINITION DU830405 33 bp DNA linear GSS 22-DEC-2005
 subsp. pekinensis genomic clone KBrS006K01, genomic survey sequence.

ACCESSION DU830405.1 GI:93867001

VERSION GSS.

KEYWORDS

SOURCE ORGANISM

Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 33)

AUTHORS

Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J. H. and Park,B.S.

End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

Unpublished (2005)

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Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa esp. pekinensis Sau3AI BAC clone

KBrS006K01

Seq primer: M13 Reverse

Class: BAC ends.

Location/Qualifiers

1. .33

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrS006K01"

/lab_host="E. coli DH10B"

/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"


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FEATURES
source
    High quality sequence stop: 31.
    Location/Qualifiers
        1..34
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:3855737"
            /tissue_type="adenocarcinoma"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_66"
            /note="Organ: ovary; Vector: pCMV-SPORT6; Site.1: NotI;
            Site.2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.8 kb. Library constructed by Life
            Technologies."
Query Match      1.2%; Score 33; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 446
LOCUS CV734277/c 34 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--09-J02.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--09-J02, mRNA
sequence.
ACCESSION CV734277 GI:55441908
VERSION CV734277.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 34)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
    1..34
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:39847"
        /clone="FLO--09-J02"
        /tissue_type="flower"
        /lab_host="E.coli SOLR"
        /clone_lib="Rice flower lambda phage cDNA library (FLO)"
        /note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2:
        XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
        end with EcoRI and 3' end with XhoI site."
Query Match      1.2%; Score 33; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 447
LOCUS BI761940 36 bp mRNA linear EST 25-SEP-2001
DEFINITION 603048772F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189224 5',
mRNA sequence.
ACCESSION BI761940
VERSION BI761940.1 GI:15753518
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 36)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1472 row: 0 column: 17
High quality sequence stop: 36.
Location/Qualifiers
    1..36
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:5189224"
        /lab_host="DH10B"
        /clone_lib="NIH_MGC_116"
        /note="Organ: pooled colon, kidney, stomach; Vector:
        pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA
        source anonymous pool of 3 colons, age 26 yo male, 49 yo
        female, 71 yo male colon; 46 yo male kidney, and pool of 2
        stomachs, 62 yo male and 70 yo female. Library is
        oligo-dT primed and directionally cloned (EcoRV site is
        destroyed upon cloning). Average insert size 1.4 kb,
        insert size range 1-3 kb. Library is normalized and
        enriched for full-length clones and was constructed by C.
        Gruber (Invitrogen). Research Genetics tracking code
        023. Note: this is a NIH_MGC Library."
Query Match      1.2%; Score 33; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33

RESULT 448
LOCUS AJ792257 38 bp mRNA linear EST 08-DEC-2004
DEFINITION AJ792257 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018.2.11.a08, mRNA sequence.
ACCESSION AJ792257_1 GI:51107585
VERSION AJ792257.1
KEYWORDS EST.
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Antirrhinum majus
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Lamiales; Plantaginaceae; Antirrhineae;
Antirrhinum.
REFERENCE 1 (bases 1 to 38)
AUTHORS Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,

```

Saedler, H. and Zachgo, S.
Characterization of Antirrhinum Petal Development and Identification of Target Genes of the Class B MADS Box Gene DEFICIENS
Plant Cell 16 (12), 3197-3215 (2004)
15539471
Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
source
1. .38
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_2_11_a08"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

Query Match 1.2%; Score 33; DB 1; Length 38;
Best Local Similarity 94.3%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 449
CV064759
LOCUS
DEFINITION
CV064759 38 bp mRNA linear EST 24-AUG-2004
WNE1498 Wheat EST endosperm library Triticum aestivum cDNA clone
WNE1498 5' similar to Unknown Function, mRNA sequence.
CV064759
VERSION
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Ali, S., Holloway, B. and Taylor, W.C.
Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis
Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry.
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5223
Fax: 61 2 6246 5000
Email: Bill.Taylor@csiro.au
Seq primer: M13 reverse primer
High quality sequence stop: 38.
Location/Qualifiers
source
1. .38
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Hartog"
/db_xref="taxon:4565"
/clone="WNE1498"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 6, 8, 10 dpa (days post anthesis)"
/lab_host="DH10B (Life Technology)"
/clone_lib="Wheat EST endosperm library"
/notes="Vector: Ziplox; Site 1: Sal I; Site 2: Not I; mRNA was prepared from endosperm tissues of the wheat cultivar Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa endosperm using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of Ziplox vector (Life Technology) after adding a

Sal I-Xho I adapter (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."

Query Match 1.2%; Score 33; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33

RESULT 450
CF327755/c
LOCUS
DEFINITION
CF327755 39 bp mRNA linear EST 18-AUG-2003
NACL--02-F23.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-F23, mRNA sequence.
CF327755
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
source
1. .39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--02-F23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.2%; Score 33; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
|||||
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 451
CF292043/c
LOCUS
DEFINITION
CF292043 37 bp mRNA linear EST 14-AUG-2003
14ROOT--02-L12.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-L12, mRNA sequence.
CF292043
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 37)

```

survey sequence.
ACCESSION      CZ906552
VERSION        CZ906552.1  GI:71917315
KEYWORDS       GSS.
SOURCE         Zea mays
ORGANISM       Zea mays
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
               clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 34)
AUTHORS        Walbot,V.
TITLE          Maize genomic sequences found using engineered RescueMu transposon
JOURNAL        Unpublished (2001)
COMMENT        Contact: Walbot V
               Department of Biological Sciences
               Stanford University
               855 California Ave, Palo Alto, CA 94304, USA
               Tel: 650 723 2227
               Fax: 650 725 8221
               Email: walbot@stanford.edu
               Very probable ligation site of ends cut by single endonuclease.
               Reverse complemented post-ligation sequence from source sequence.
               Plate: 4011001 row: D column: 06
               Class: transposon-tagged
               Location/Qualifiers
               1..34
               /organism="Zea mays"
               /mol_type="genomic DNA"
               /cultivar="mixed background W23/A188/B73/K55"
               /db_xref="taxon:4577"
               /tissue_type="leaf"
               /dev_stage="adult"
               /lab_host="DH10B"
               /clone_lib="4011 - RescueMu Grid J"
               /notes="Organ: leaf; Vector: RescueMu (engineered from
               pBluescript backbone); Site 1: BamHI; Site 2: BglII;
               RescueMu is a 4.9 kb, modified maize Mu transposon
               designed to allow plasmid rescue from total genomic DNA.
               Mu elements insert preferentially into transcription
               units. For more information on RescueMu, go to the web
               site 'http://www.mutransposon.org/project/RescueMu/'. Grid
               J was grown at UCSD in 2000. DNA was extracted from leaf
               strips, double digested using BamHI and BglII, and ligated
               to form circular plasmids. DH10B cells were transformed
               and then screened on LB plates with ampicillin."

Query Match      1.2%; Score 32.4; DB 1; Length 34;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 455
DX054666/c
LOCUS
DEFINITION
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 34)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.

TITLE          End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL        Unpublished (2005)
COMMENT        Contact: Beom-Seok Park
               Brassica Genomics Team
               National Institute of Agricultural Biotechnology
               225 Seodun-Dong, Suwon, 441-707, Korea
               Tel: +82-31-299-1670
               Fax: +82-31-299-1672
               Email: pbeom@da.go.kr
               BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone
               KBrB058P12
               Class: BAC ends
               Location/Qualifiers
               1..34
               /organism="Brassica rapa subsp. pekinensis"
               /mol_type="genomic DNA"
               /cultivar="Chiifu"
               /sub_species="pekinensis"
               /db_xref="taxon:51351"
               /clone="KBrB058P12"
               /lab_host="E.coli DH10B"
               /clone_lib="KBrB, Brassica rapa BamHI BAC library"
               /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa subsp
               pekinensis var. Chiifu BAC library (KBrB BAC) is provided
               by Yong-Pyo Lim (CNU)."

Query Match      1.2%; Score 32.4; DB 1; Length 34;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 456
DX058168/c
LOCUS
DEFINITION
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 34)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.

TITLE          End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL        Unpublished (2005)
COMMENT        Contact: Beom-Seok Park
               Brassica Genomics Team
               National Institute of Agricultural Biotechnology
               225 Seodun-Dong, Suwon, 441-707, Korea
               Tel: +82-31-299-1670
               Fax: +82-31-299-1672
               Email: pbeom@da.go.kr
               BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone
               KBrB063K14
               Class: BAC ends
               Location/Qualifiers
               1..34
               /organism="Brassica rapa subsp. pekinensis"
               /mol_type="genomic DNA"
               /cultivar="Chiifu"
               /sub_species="pekinensis"

Query Match      1.2%; Score 32.4; DB 1; Length 34;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 455
DX054666/c
LOCUS
DEFINITION
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 34)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.

TITLE          End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL        Unpublished (2005)
COMMENT        Contact: Beom-Seok Park
               Brassica Genomics Team
               National Institute of Agricultural Biotechnology
               225 Seodun-Dong, Suwon, 441-707, Korea
               Tel: +82-31-299-1670
               Fax: +82-31-299-1672
               Email: pbeom@da.go.kr
               BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone
               KBrB058P12F KBrB, Brassica rapa BamHI BAC library Brassica rapa
               subsp. pekinensis genomic clone KBrB058P12, genomic survey
               sequence.
               DX054666
               VERSION        DX054666.1  GI:84748963
               KEYWORDS       GSS.
               SOURCE         Brassica rapa subsp. pekinensis
               ORGANISM       Brassica rapa subsp. pekinensis
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
               1 (bases 1 to 34)
               Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
               Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
               Hahn, J.H. and Park, B.S.

```

```

/db_xref="taxon:51351"
/clone="KB-B063K14"
/lab_host="E.coli DH10B"
/clone_lib="KBRB, Brassica rapa BamHI BAC library"
/notes="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pkinsensis var. Chifu BAC library (KBRB BAC) is provided
by Yong-Pyo Lim (GNU)."

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Query Match      1.2%; Score 32.4; DB 1; Length 34;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
      |||||||
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

```

```

RESULT 457
DR41A4T
LOCUS      34 bp      DNA      linear      GSS 22-NOV-2002
DEFINITION Danio rerio genomic clone DKEY-41A4, genomic survey sequence.
ACCESSION  AL980969
VERSION     AL980969.1 GI:25182658
KEYWORDS   GSS.
SOURCE     Danio rerio (zebrafish)
ORGANISM   Danio rerio

```

```

REFERENCE
AUTHORS    Humphray, S.J., Huckle, E. and Hunt, S.E.
TITLE      Direct Submission
JOURNAL    Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquerry@sanger.ac.uk Unpublished
COMMENT    This sequence was generated from the T7 end of BAC 41A4. 41A4 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

```

```

FEATURES
source
Location/Qualifiers
1..34
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-41A4"
/tissue_type="Testis"
/notes="vector pindigobac-536"

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```

Query Match      1.2%; Score 32.4; DB 1; Length 34;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
      |||||||
Db 1 AAAAAAAAAAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

```

```

RESULT 458
AM047864/c
LOCUS      36 bp      mRNA      linear      EST 20-SEP-2005
DEFINITION AM047864 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC18b04.q1k, mRNA sequence.
ACCESSION  AM047864
VERSION     AM047864.1 GI:75967439
KEYWORDS   EST.
SOURCE     Schistosoma mansoni
ORGANISM   Schistosoma mansoni

```

```

REFERENCE
AUTHORS    Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.,
Nikolaïdou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
TITLE      Microarray analysis identifies genes preferentially expressed in

```

```

the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
1..36
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC18b04.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="Country: Puerto Rico"

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FEATURES

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source
Location/Qualifiers
1..36
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC18b04.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="Country: Puerto Rico"

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Query Match      1.2%; Score 32.4; DB 1; Length 36;
Best Local Similarity 94.3%; Pred. No. 2.6e+02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

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RESULT 459
CN545543/c
LOCUS      38 bp      mRNA      linear      EST 30-APR-2004
DEFINITION EST 17487 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL003C10 3', mRNA sequence.
ACCESSION  CN545543
VERSION     CN545543.1 GI:46910168
KEYWORDS   EST.
SOURCE     Vitis vinifera
ORGANISM   Vitis vinifera

```

```

REFERENCE
AUTHORS    Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
TITLE      Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL    Unpublished (2002)
COMMENT    Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Université de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

```

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FEATURES
source
Location/Qualifiers
1..38
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL003C10"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiI; Site_2: SfiIB; Oriented library"

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Query Match      1.2%; Score 32.4; DB 1; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.7e+02;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
      |||||||

```



```

/notes="country: Puerto Rico"

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
    |||||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 466
AM044934
LOCUS
DEFINITION
AM044934 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC13d02.q1k, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Schistosoma mansoni
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 32)
AUTHORS
Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL
Unpublished (2005)
COMMENT
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxtion, CB10 1SA, UNITED KINGDOM.
FEATURES
source
1..32
/mol_type="mRNA"
/db_xref="taxon:6183"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="country: Puerto Rico"

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
    |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 467
AM045405
LOCUS
DEFINITION
AM045405 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC13c05.q1k, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Schistosoma mansoni
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 32)
AUTHORS
Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL
Unpublished (2005)
COMMENT
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxtion, CB10 1SA, UNITED KINGDOM.

```

```

Hinxtion, CB10 1SA, UNITED KINGDOM.
FEATURES
source
1..32
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="country: Puerto Rico"

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
    |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 468
CF291773/c
LOCUS
DEFINITION
CF291773 32 bp mRNA linear EST 14-AUG-2003
14ROOT--02-F12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-F12, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 32)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Naim,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..32
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-F12"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
    |||||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 469
CF299386/c
LOCUS
DEFINITION
CF299386 32 bp mRNA linear EST 15-AUG-2003

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DEFINITION 7LEAF--03-G07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-G07, mRNA sequence.

ACCESSION CF299386

VERSION CF299386.1 GI:33671147

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 32)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1..32

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--03-G07"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 470

CF309233

LOCUS ABF--03-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

DEFINITION ABF--03-F14, mRNA sequence.

ACCESSION CF309233

VERSION CF309233.1 GI:33680994

KEYWORDS EST.

ORGANISM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 32)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES

source

Location/Qualifiers

1..32

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="ABF--03-F14"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 471

CF309345/c

LOCUS ABP--03-I03.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

DEFINITION ABP--03-I03, mRNA sequence.

ACCESSION CF309345

VERSION CF309345.1 GI:33681106

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 32)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 470

CF309233

LOCUS ABF--03-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

DEFINITION ABF--03-F14, mRNA sequence.

ACCESSION CF309233

VERSION CF309233.1 GI:33680994

KEYWORDS EST.

ORGANISM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 32)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 472
CF313717/c
LOCUS
DEFINITION HD--01-P05.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION CF313717
VERSION CF313717.1 GI:33685478
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota: Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 32)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..32
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--01-P05"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH108"
/clone_lib="OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 473
CF321046/c
LOCUS
DEFINITION HD--12-C15.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION CF321046
VERSION CF321046.1 GI:33692807
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota: Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..32
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--12-C15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH108"
/clone_lib="OshDACL1-overexpressing transgenic rice plasmid cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 474
CF328471/c
LOCUS
DEFINITION CF328471 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--03-G09, mRNA sequence.

ACCESSION CF328471
VERSION CF328471.1 GI:33805189
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 32)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..32
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--03-G09"

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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db  32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 475
CF331270/c
LOCUS      32 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--07-F08.b1 Rice callus plasmid cDNA library (NACL) Oryza
           sativa (japonica cultivar-group) cDNA clone NACL--07-F08, mRNA
           sequence.
ACCESSION  CF331270
VERSION     CF331270.1 GI:33810751
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 32)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES             source
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   1..32
   /organism="Oryza sativa (japonica cultivar-group)"
   /mol_type="mRNA"
   /db_xref="taxon:39947"
   /clone="NACL--07-F08"
   /tissue_type="callus"
   /dev_stage="proliferated callus on 2N6 media for 30 days"
   /lab_host="E.coli DH10B"
   /clone_lib="Rice callus plasmid cDNA library (NACL)"
   /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
   with oligoribonucleotides and then used as templates for
   RT-PCR."

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db  32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 476
AW327277
LOCUS      32 bp      mRNA      linear      EST 28-JAN-2000
DEFINITION dq01d07.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846628 5', mRNA
           sequence.
ACCESSION  AW327277

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AW327277.1 GI:6797772
EST.      Homo sapiens (human)
SOURCE    Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
REFERENCE  1 (bases 1 to 32)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/
           National Institutes of Health, Mammalian Gene Collection (MGC)
           Unpublished (1999)
JOURNAL   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
COMMENT   Tissue Procurement: ATCC
           cDNA Library Preparation: Edge Biosystems
           CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www-bio-llnl.gov/bbrp/image/image.html
           Plate: LCM00028 row: G column: 13
           Seq primer: -21M13 forward primer (ABI).
           Location/Qualifiers
             1..32
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             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:2846628"
             /tissue_type="T cell leukemia"
             /cell_line="MGC2"
             /clone_lib="NIH MGC 2"
             /note="Organ: Blood; Vector: pOTB7a; Library prepared by
             Edge Biosystems."

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db  1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 477
CV724815/c
LOCUS      32 bp      mRNA      linear      EST 04-NOV-2004
DEFINITION 14Salt--01-J14.g1 Salt treated rice leaf lambda phage cDNA library
           (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
           14Salt--01-J14, mRNA sequence.
ACCESSION  CV724815
VERSION     CV724815.1 GI:55412439
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 32)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES             source
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   1..32
   /organism="Oryza sativa (japonica cultivar-group)"

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/cultivar="Nackdong"
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 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
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 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 |||
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

CV725190 32 bp mRNA linear EST 04-NOV-2004
 14Salt--02-C11.g1 Salt treated rice leaf lambda phage cDNA library
 14Salt--02-C11, mRNA sequence.

ACCESSION CV725190.1 GI:55412814
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 32)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

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 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 |||
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 479
 CV725571/c
 LOCUS
 DEFINITION

CV725571 32 bp mRNA linear EST 04-NOV-2004
 14Salt--02-L16.b1 Salt treated rice leaf lambda phage cDNA library
 14Salt--02-L16, mRNA sequence.

ACCESSION CV725571.1 GI:55413195
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 32)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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Query Match 1.2%; Score 32; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 |||
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 480
 CV726012/c
 LOCUS
 DEFINITION

CV726012 32 bp mRNA linear EST 04-NOV-2004
 14Salt--03-G20.b1 Salt treated rice leaf lambda phage cDNA library
 14Salt--03-G20, mRNA sequence.

ACCESSION CV726012.1 GI:55413636
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 32)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 481
CV726385/c
LOCUS
DEFINITION
14Salt--03-P17.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-P17, mRNA sequence.
ACCESSION
CV726385
VERSION
CV726385.1 GI:55414009
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 32)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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/tissue_type="leaf"
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/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 482
CV727659/c
LOCUS
DEFINITION
14Salt--05-O14.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-O14, mRNA sequence.
ACCESSION
CV727659
VERSION
CV727659.1 GI:55415283
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 32)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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/tissue_type="leaf"
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 483
CV728625/c
LOCUS
DEFINITION
FLO--01-A24.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-A24, mRNA sequence.
ACCESSION
CV728625
VERSION
CV728625.1 GI:55431234
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..32
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
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/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
DB 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 484

CV729255/c

LOCUS CV729255 32 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--01-P21.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-P21, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 32)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..32
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 485

CV732146/c

LOCUS CV732146 32 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--06-H23.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-H23, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 32)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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Query Match

Best Local Similarity

Matches

32;

Conservative

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Mismatches

0;

Indels

0;

Gaps

0;

QY

2709

A

A

A

A

A

A

A

A

A

SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
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Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 487
AZ459536/c
LOCUS AZ459536 32 bp DNA linear GSS 04-OCT-2000
DEFINITION LM0264M16F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0264M16 F, genomic survey sequence.
ACCESSION AZ459536
VERSION AZ459536.1 GI:10617577
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0264 row: M column: 16
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends

FEATURES
source

High quality sequence stop: 32.
Location/Qualifiers
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 /clone="UUGCLM0264M16"
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 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi14732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 |||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 488
AZ470832
LOCUS AZ470832 32 bp DNA linear GSS 04-OCT-2000
DEFINITION LM0285F14F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0285F14 F, genomic survey sequence.
ACCESSION AZ470832
VERSION AZ470832.1 GI:10628957
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0285 row: F column: 14
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends

High quality sequence stop: 32.
Location/Qualifiers
1. .32

FEATURES

Source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0285F14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 489

AZ611890/c 32 bp DNA linear GSS 13-DBC-2000
LOCUS
DEFINITION
1M0438E02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0438E02 R, genomic survey sequence.

ACCESSION
AZ611890
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 32)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0438 row: E column: 02

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

FEATURES

Source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0438E02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 490

AZ778018 32 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION
2M0012020R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0012020 R, genomic survey sequence.

ACCESSION
AZ778018
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 32)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0012 row: O column: 20

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 32.

FEATURES
sourceLocation/Qualifiers
1..32

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0012020"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 491

DU835386

LOCUS KBRS016J03F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016J03, genomic survey sequence.
32 bp DNA linear GSS 22-DEC-2005

ACCESSION

DU835386

VERSION

DU835386.1 GI:83871982

KEYWORDS

GSS.

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 32)

Yang, I.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

Hahn, J. H. and Park, B.S.

End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel.: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.90.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone

KBrS016J03

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..32

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrS016J03"

/lab_host="E. coli DH10B"

/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"

/notes="vector: pCUGIBAC1; Site 1; Sau3AI; Brassica rapa

ssp pekinensis var. Chiifu BAC library (KBrS BAC) is

available at NIAB."

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 492

DR85L21T

LOCUS

DR85L21T

DEFINITION

Danio rerio genomic clone DKEY-85L21, genomic survey sequence.

ACCESSION

AL986044

VERSION

AL986044.1 GI:25187956

KEYWORDS

GSS.

SOURCE

ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 32)

Humphray, S.J., Huckle, E. and Hunt, S.E.

Direct Submission

Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome

Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:

humphray@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 85L21. 85L21 is

part of the Daniokey BAC Library created by R. Plasterk and N.V.

Keygene.

Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES

source

1..32

/organism="Danio rerio"

/mol_type="genomic DNA"

/db_xref="taxon:7955"

/clone="DKEY-85L21"

/tissue_type="Testis"

/note="vector pIndigoBAC-536"

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 493

AL587609/c

LOCUS

AL587609

DEFINITION

AL587609 BP Chicken Brain Library Gallus gallus cDNA clone

ROS059G05, mRNA sequence.

ACCESSION

AL587609

VERSION

AL587609.1 GI:13192643

KEYWORDS

EST.

SOURCE

ORGANISM

Gallus gallus (chicken)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

electroporation. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 32; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 3 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 496
LOCUS BF338797 35 bp mRNA linear EST 22-NOV-2000
DEFINITION 602036229F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184167
5', mRNA sequence.

ACCESSION BF338797
VERSION BF338797
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 35)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM9501 row: j column: 08
High quality sequence stop: 30.

FEATURES
source

1..35
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4184167"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: oligo dt. Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 497
LOCUS DR073823 35 bp mRNA linear EST 08-JUN-2005
DEFINITION ik86e02.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA

sequence.
ACCESSION DR073823
VERSION DR073823.1 GI:67051746
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 35)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8894
Fax: 516 367 8874
Email: mcombie@cshl.org
Original 3 prime EST has been reverse completed to be in 5 prime
direction
Seq primer: -21M13UnivRev.
Location/Qualifiers

1..35
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."

FEATURES
source

1..35
Location/Qualifiers
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 498
LOCUS AM046479 39 bp mRNA linear EST 20-SEP-2005
DEFINITION AM046479 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmlC21f11.q1k, mRNA sequence.

ACCESSION AM046479
VERSION AM046479.1 GI:75970558
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigida; Schistosomatoidea; Schistosomatidae; Schistosoma.

REFERENCE 1 (bases 1 to 39)
AUTHORS Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaïdou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of *Schistosoma mansoni*
Unpublished (2005)
Contact: Ivens AC

JOURNAL Pathogen Microarrays Group
COMMENT Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers

FEATURES
source

1..39
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC21f11.q1k"

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/dev stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="country: Puerto Rico"

Query Match      1.2%; Score 32; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 499
CV723737/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone root--04-J23, mRNA
sequence.
ACCESSION
CV723737.1 GI:55411361
VERSION
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="root--04-J23"
/tissue_type="root"
/dev stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Rice root lambda phage cDNA library (root)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.2%; Score 32; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 500
BQ590703/c
LOCUS
DEFINITION
S013312-024-018-B02-T7 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-018-B02 3-PRIME, mRNA sequence.
ACCESSION
BQ590703
VERSION
EST.
KEYWORDS
Beta vulgaris
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="root--04-J23"
/tissue_type="root"
/dev stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Rice root lambda phage cDNA library (root)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

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```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 35)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radloff,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 35 Std Error: 0.00
Plate: 18 row: B column: 02
Seq primer: T7; GTAATACGACTCACTATAGGCG.
FEATURES
source
1..35
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189418"
/clone="024-018-B02"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet. Library provided by KWS
Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.2%; Score 31.8; DB 1; Length 35;
Best Local Similarity 94.3%; Pred. No. 2.8e+02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 35 AAAAAAAAAAAAAAAAAAAGGAAAAAAAAAAAAAAAAAAAA 1

RESULT 501
CV724720/c
LOCUS
DEFINITION
14Salt--01-H08.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--01-H08, mRNA sequence.
ACCESSION
CV724720
VERSION
EST.
KEYWORDS
GI:55412344
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

```


of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

```

1..35
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-H08"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

```

Query Match 1.2%; Score 31.8; DB 1; Length 35;
Best Local Similarity 94.3%; Pred. No. 2.8e+02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2704 GTACTTAAAAA 2738
DB 35 GCAGCTGAAAAA 1

RESULT 502

AZ945733/C

LOCUS

DEFINITION 2M0207B13F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0207B13 F, genomic survey sequence.

ACCESSION AZ945733

VERSION AZ945733.1

KEYWORDS GSS.

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 36)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 595 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000

Std Error: 0.00

Plate: 0207

row: B

column: 13

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 36.

Location/Qualifiers

1..36

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0207B13"

/sex="Female"

FEATURES

source

```

1..36
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA."

```

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: pWD42nv. Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 31.8; DB 1; Length 36;
Best Local Similarity 94.3%; Pred. No. 2.9e+02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 2743
DB 36 AAAAAA 2

RESULT 503

CZ919025

LOCUS

DEFINITION 4021011F02.2EL_Y1 4021 - RescueMu Grid V Zea mays genomic, genomic survey sequence.

ACCESSION CZ919025

VERSION CZ919025.1

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 36)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

AUTHORS Walbot,V.

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished (2001)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 8221

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4021011 row: F

column: 02

Class: transposon-tagged.

Location/Qualifiers

1..36

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev stage="adult"

/lab_host="DH10B"

/clone_lib="4021 - RescueMu Grid V"

/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA."

FEATURES

source

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of *T. brucei* sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES

source

1..39
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="116f09"

Query Match 1.2%; Score 31.8; DB 1; Length 39;

Best Local Similarity 94.3%; Pred. No. 3e+02; Mismatches 2; Indels 0; Gaps 0;

Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2706 ACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 35 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 507

CZ908819

LOCUS

4018005H03.2EL x1 4018 - RescueMu Grid X Zea mays genomic, genomic survey sequence.

ACCESSION

CZ908819

VERSION

CZ908819.1

KEYWORDS

GSS.

SOURCE

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 33)

Walbot.V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4018005 row: H column: 03

Class: transposon-tagged.

Location/Qualifiers

1..33

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="4018 - RescueMu Grid X"

/note="Organ: leaf; Vector: RescueMu (engineered from plasmid backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web

site '<http://www.mutransposon.org/project/RescueMu/>'. Grid X was grown at UCSD in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.1%; Score 31.4; DB 1; Length 33;

Best Local Similarity 97.0%; Pred. No. 2.9e+02; Mismatches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33

RESULT 508

CF298131/c

LOCUS

7LEAF--01-G07.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-G07, mRNA sequence.

ACCESSION

CF298131

VERSION

CF298131.1

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 36)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..36

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-G07"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 31.4; DB 1; Length 36;

Best Local Similarity 97.0%; Pred. No. 3e+02; Mismatches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
Db 33 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 509

CF278363/c

LOCUS

14ETL--04-D24.g1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-D24, mRNA sequence.

ACCESSION

CF278363

VERSION

CF278363.1

GI:33655749


```

RESULT 512
CF308197/c 39 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--01-018.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--01-018, mRNA sequence.
ACCESSION CF308197
VERSION CF308197.1 GI:33679958
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--01-018"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match 1.1%; Score 31.2; DB 1; Length 39;
Best Local Similarity 91.7%; Pred. No. 3.2e+02;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2708 TAAAAAATCCAAAAA 2743
|||||
Db 37 TAAAAAATCCAAAAA 2

RESULT 513
AJ659810 31 bp mRNA linear EST 28-JUN-2004
LOCUS AJ659810 KN277 Sus scrofa cDNA clone C0005217_I13, mRNA sequence.
DEFINITION AJ659810
ACCESSION AJ659810
VERSION AJ659810.1 GI:49343941
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 31)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI

FEATURES
Location/Qualifiers
1..31
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-042 M08"
/tissue_type="ovary"
/clone_lib="KN261"
/notes="Vector: pBlueScriptII (SK+); Site 1: EcoRI; Site 2:
SmaI; Single pass sequencing. Normalised library
constructed from bovine ovary."

Query Match 1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAA 2739
|||||
Db 1 AAAAAAAAAA 31

RESULT 514
AJ693992 31 bp mRNA linear EST 29-JUN-2004
LOCUS AJ693992 KN261 Bos taurus cDNA clone KN261-042_M08, mRNA sequence.
DEFINITION AJ693992
ACCESSION AJ693992
VERSION AJ693992.1 GI:49427411
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
1 (bases 1 to 31)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI

FEATURES
Location/Qualifiers
1..31
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-042 M08"
/tissue_type="ovary"
/clone_lib="KN261"
/notes="Vector: pBlueScriptII (SK+); Site 1: EcoRI; Site 2:
SmaI; Single pass sequencing. Normalised library
constructed from bovine ovary."

```

Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII (SK+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13f Normalised library constructed
from pooled early embryos, from 8- cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,
www.arkgenomics.org.

FEATURES
Location/Qualifiers
1..31

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005217_I13"
/tissue_type="embryo"
/clone_lib="KN277"
/notes="Vector: pBlueScriptII (SK+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
to blastocysts."

Query Match 1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAA 2739
|||||
Db 1 AAAAAAAAAA 31

RESULT 514
AJ693992 31 bp mRNA linear EST 29-JUN-2004
LOCUS AJ693992 KN261 Bos taurus cDNA clone KN261-042_M08, mRNA sequence.
DEFINITION AJ693992
ACCESSION AJ693992
VERSION AJ693992.1 GI:49427411
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 31)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI

Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII (SK+) R. Site1: EcoRI
R. Site2: SmaI 5' Seq Primer T3 Normalised library constructed from
bovine ovary. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.

FEATURES
Location/Qualifiers
1..31

/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-042 M08"
/tissue_type="ovary"
/clone_lib="KN261"
/notes="Vector: pBlueScriptII (SK+); Site 1: EcoRI; Site 2:
SmaI; Single pass sequencing. Normalised library
constructed from bovine ovary."

```

Query Match      1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 515
AM044121
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
1. .31
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="Smlclif01.glk"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="country: Puerto Rico"

Query Match      1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 516
BX569502/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

```

```

The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2OW
All clones with suffix qtc are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
1. .31
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse9a03_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
      |||||||
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 517
CF278807
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
1. .31
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--04-N15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

Query Match 1.1%; Score 31; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02; Indels 0; Gaps 0;
 Matches 31; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
 |||||
 DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 518
 CF300345/c
 LOCUS
 DEFINITION 31 bp mRNA linear EST 15-AUG-2003
 7LEAF--04-L08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--04-L08, mRNA
 sequence.

ACCESSION
 VERSION CF300345.1 GI:33672106
 KEYWORDS EST.

SOURCE
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 31)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

TITLE
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongsin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES
 source
 1..31
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--04-L08"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.1%; Score 31; DB 1; Length 31;
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 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
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 DB 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 519
 AZ333315/c
 LOCUS
 DEFINITION 31 bp DNA linear GSS 29-SEP-2000
 1M0062A21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0062A21 F, genomic survey sequence.

ACCESSION
 VERSION AZ333315.1 GI:10397811
 KEYWORDS GSS

SOURCE
 ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS

1 (bases 1 to 31)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0062 row: A column: 21
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 31.
 Location/Qualifiers

FEATURES
 source

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 /sex="Male"
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.1%; Score 31; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
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 DB 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 520
 AZ375973

LOCUS
 DEFINITION 31 bp DNA linear GSS 02-OCT-2000
 1M0129D08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0129D08 R, genomic survey sequence.

ACCESSION
 VERSION AZ375973
 KEYWORDS GSS

SOURCE
 ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 31)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: D column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.

FEATURES
source

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 521
AZ510092

LOCUS
DEFINITION
AZ510092
1M0354P14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0354P14 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ510092.1 GI:10691408
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 31)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0354 row: P column: 14
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 31.

FEATURES
source

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 522
AZ623538/c

LOCUS
DEFINITION
AZ623538
1M0461G21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0461G21 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ623538.1 GI:11745728
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 31)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0461 row: G column: 21
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 31.
 Location/Qualifiers
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 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES
 source

REFERENCE 1 (bases 1 to 31)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0469 row: C column: 09
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 31.
 Location/Qualifiers
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES
 source

Query Match 1.1%; Score 31; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 523
 AZ627692
 LOCUS IM0469C09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0469C09 R, genomic survey sequence.
 ACCESSION AZ627692
 VERSION AZ627692.1 GI:11749882
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

Query Match 1.1%; Score 31; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
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 DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 524
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 DEFINITION clone UUGC2M0014002 F, genomic survey sequence.
 ACCESSION AZ778697
 VERSION AZ778697.1 GI:12908605
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D. Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0014 row: 0 column: 02
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              Class: plasmid ends
              High quality sequence stop: 31.
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              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptored DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptored mouse DNA was annealed to
              adaptored vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
              Query Match      1.1%; Score 31; DB 1; Length 31;
              Best Local Similarity 100.0%; Pred. No. 2.9e+02;
              Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
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RESULT 525
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2M0093F21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0093F21 R, genomic survey sequence.
ACCESSION AZ821215
VERSION   AZ821215.1 GI:12991123
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

```

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D. Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0093 row: F column: 21
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 31.
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              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptored DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptored mouse DNA was annealed to
              adaptored vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
              Query Match      1.1%; Score 31; DB 1; Length 31;
              Best Local Similarity 100.0%; Pred. No. 2.9e+02;
              Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
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RESULT 526
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LOCUS
DEFINITION 31 bp DNA linear GSS 20-FEB-2001
2M0102C19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0102C19 F, genomic survey sequence.
ACCESSION AZ826618
VERSION   AZ826618.1 GI:12996442
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

```

REFERENCE 1 (bases 1 to 31)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
        Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
        Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
        Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
        plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
        University of Utah
        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
        84112, USA
        Tel: 801 585 5605
        Fax: 801 585 7177
        Email: ddunn@genetics.utah.edu
        Insert Length: 10000 Std Error: 0.00
        Plate: 0102 row: C column: 19
        Seq primer: CGTTGTAACGACGCCAGT
        Class: plasmid ends
        High quality sequence stop: 31.
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0102C19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."
Query Match          1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
    |||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 527
LOCUS CZ917108
DEFINITION 4021004C05.1EL_Y1 4021 - RescueMu Grid V Zea mays genomic, genomic
        survey sequence.
ACCESSION CZ917108
VERSION CZ917108
KEYWORDS CZ917108.1 GI:71935671
SOURCE Zea mays
        ORGANISM Zea mays
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
        clade; Panicoideae; Andropogoneae; Zea.

```

```

REFERENCE 1 (bases 1 to 31)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
        Unpublished (2001)
JOURNAL Contact: Walbot V
        Department of Biological Sciences
        Stanford University
        855 California Ave, Palo Alto, CA 94304, USA
        Tel: 650 723 2227
        Fax: 650 725 8221
        Email: walbot@stanford.edu
        Very probable ligation site of ends cut by single endonuclease.
        Reverse complemented post-ligation sequence from source sequence.
        Plate: 4021004 row: C column: 05
        Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1..31
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="mixed background W23/A188/B73/K55"
                     /db_xref="taxon:4577"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="4021 - RescueMu Grid V"
                     /note="Organ: leaf; Vector: RescueMu (engineered from
        pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
        RescueMu is a 4.9 kb, modified maize Mu transposon
        designed to allow plasmid rescue from total genomic DNA.
        Mu elements insert preferentially into transcription
        units. For more information on RescueMu, go to the web
        site 'http://www.mutranposon.org/project/RescueMu/'. Grid
        V was grown at University of Arizona in 2003. DNA was
        extracted from leaf strips, double digested using BamHI
        and BglII, and ligated to form circular plasmids. DH10B
        cells were transformed and then screened on LB plates with
        ampicillin."
Query Match          1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
    |||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 528
LOCUS DUB35031/c
DEFINITION KB-S015N15F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
        subsp. pekinensis genomic clone KBrS015N15, genomic survey
        sequence.
ACCESSION DUB35031
VERSION DUB35031.1 GI:83871627
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
        ORGANISM Brassica rapa subsp. pekinensis
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
        rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 31)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
        Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
        Hahn,J. H. and Park,B.S.
        End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
        Unpublished (2005)
        Contact: Beom-Seok Park
        Brassica Genomics Team
        National Institute of Agricultural Biotechnology
        225 Seodun-Dong, Suwon, 441-707, Korea
        Tel: +82-31-299-1670
        Fax: +82-31-299-1672

```

Email: pbeom@da.go.kr
 BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
 KBrS015N15
 Seq primer: T7
 Class: BAC ends.

FEATURES

source
 1..31
 Location/Qualifiers
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrS015N15"
 /lab_host="E. coli DH10B"
 /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
 /note="vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
 ssp pekinensis var. Chifu BAC library (KBrS BAC) is
 available at NIB."

Query Match 1.1%; Score 31; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 529

DX063750
 LOCUS
 DEFINITION
 KBrB071A09F KBrB, Brassica rapa BamHI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBrB071A09, genomic survey
 sequence.

ACCESSION
 DX063750.1 GI:84758046

KEYWORDS

SOURCE

ORGANISM
 Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1. (bases 1 to 31)
 Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
 Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
 Hahn,J.H. and Park,B.S.

End sequence of Brassica rapa BamHI (KBrB) BAC clone

Unpublished (2005)

JOURNAL

COMMENT

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBrB071A09

Seq primer: T7

Class: BAC ends.

FEATURES

source
 1..31
 Location/Qualifiers
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrB071A09"
 /lab_host="E. coli DH10B"
 /clone_lib="KBrB, Brassica rapa BamHI BAC library"
 /note="vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
 pekinensis var. Chifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 1.1%; Score 31; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 530

AV674152/c
 LOCUS
 DEFINITION
 AV674152 Nori Satoh unpublished cDNA library Ciona intestinalis
 cDNA clone citb14122 5', mRNA sequence.

ACCESSION
 AV674152

VERSION

KEYWORDS

SOURCE

ORGANISM

Ciona intestinalis
 Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 Phlebobranchia; Clonidae; Ciona.

REFERENCE
 1. (bases 1 to 34)

AUTHORS
 Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.

TITLE
 Expressed genes in Ciona intestinalis

JOURNAL
 Unpublished (2000)

COMMENT
 Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@scidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

FEATURES

source

1..34
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="citb14122"
 /tissue_type="whole animal"
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 /clone_lib="Nori Satoh unpublished cDNA library"

Query Match 1.1%; Score 31; DB 1; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

Db 33 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 531

AW334249/c
 LOCUS
 DEFINITION
 S32B4 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.

ACCESSION
 AW334249

VERSION
 AW334249.1 GI:6830606

KEYWORDS

SOURCE

ORGANISM

Pneumocystis carinii
 Pneumocystis carinii
 Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
 Pneumocystidaceae; Pneumocystis.

REFERENCE
 1. (bases 1 to 34)

AUTHORS
 Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,

Edman,J.C., Kovacs,J. and Cushion,M.

Expressed sequence tags from Pneumocystis carinii

Unpublished (2000)

Contact: Staben C

School of Biological Sciences

University of Kentucky

101 Morgan Building, University of Kentucky, Lexington, KY

40506-0225, USA

Tel: 606 257 2161

```

Fax: 606 257 1717
Email: staben@pop.uky.edu.
Location/Qualifiers
1. .34
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/notes="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match
Best Local Similarity 100.0%; Score 31; DB 1; Length 34;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES
source
1. .34
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/notes="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

CV066718 36 bp mRNA linear EST 24-AUG-2004
WNEU7d3 wheat EST endospERM library Triticum aestivum CDNA clone
WNEU7d3 5' similar to Unknown Function, mRNA sequence.
CV066718
ACCESSION CV066718.1 GI:51529895
VERSION CV066718
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Poodeae; Triticeae; Triticum.
1 (bases 1 to 36)
Ali.S, Holloway,B. and Taylor,W.C.
Normalisation of cereal endospERM EST libraries for structural and
functional genomic analysis
Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry.
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5223
Fax: 61 2 6246 5000
Email: Bill.Taylor@csiro.au
Seq primer: M13 reverse primer
High quality sequence stop: 36.
Location/Qualifiers
1. .36
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Hartog"
/db_xref="taxon:4565"
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/tissue_type="endospERM"
/dev_stages="developing endospERM tissue 6, 8, 10 dpa (days
post anthesis)"
/lab_host="DH10B (Life Technology)"
/clone_lib="wheat EST endospERM library"
/notes="Vector: ZipLox; Site 1: Sal I; Site 2: Not I; mRNA
was prepared from endospERM tissues of the wheat cultivar
Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa
endospERM using Not I-oligo(dT)18 primer/adaptor
(Pharmacia Biotech), and then ligated to the Sal I-Not I
site of ZipLox vector (Life Technology) after adding a
Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan
Ali and Bill Taylor."

CV066718 34 bp mRNA linear EST 06-DEC-2002
WNEU7d3 wheat EST endospERM library Triticum aestivum CDNA clone
WNEU7d3 5' similar to Unknown Function, mRNA sequence.
CV066718
ACCESSION CV066718.1 GI:26117014
VERSION CV066718
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 34)
Herwig,R.; Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
Contact: Weishaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 34 Std Etox: 0.00
Plate: 10 row: B column: 02
Seq primer: T7; GTAATACGACTCTACTATAGGCG.
Location/Qualifiers
1. .34
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:185440"
/db_xref="taxon:161934"
/clone="024-010-B02"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPZ-ADIS-024-leaf"
/notes="Vector: pCMVSPOR16; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7. Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPP/GABI-Primary database:http://gabi.rzpd.de"

Query Match
Best Local Similarity 94.1%; Score 30.8; DB 1; Length 34;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

FEATURES
source
1. .34
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:185440"
/db_xref="taxon:161934"
/clone="024-010-B02"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPZ-ADIS-024-leaf"
/notes="Vector: pCMVSPOR16; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7. Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPP/GABI-Primary database:http://gabi.rzpd.de"

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Query Match
Best Local Similarity 100.0%; Score 31; DB 1; Length 36;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES
source
1. .34
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/notes="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

CV066718 36 bp mRNA linear EST 24-AUG-2004
WNEU7d3 wheat EST endospERM library Triticum aestivum CDNA clone
WNEU7d3 5' similar to Unknown Function, mRNA sequence.
CV066718
ACCESSION CV066718.1 GI:51529895
VERSION CV066718
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Poodeae; Triticeae; Triticum.
1 (bases 1 to 36)
Ali.S, Holloway,B. and Taylor,W.C.
Normalisation of cereal endospERM EST libraries for structural and
functional genomic analysis
Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry.
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5223
Fax: 61 2 6246 5000
Email: Bill.Taylor@csiro.au
Seq primer: M13 reverse primer
High quality sequence stop: 36.
Location/Qualifiers
1. .36
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Hartog"
/db_xref="taxon:4565"
/clone="WNEU7d3"
/tissue_type="endospERM"
/dev_stages="developing endospERM tissue 6, 8, 10 dpa (days
post anthesis)"
/lab_host="DH10B (Life Technology)"
/clone_lib="wheat EST endospERM library"
/notes="Vector: ZipLox; Site 1: Sal I; Site 2: Not I; mRNA
was prepared from endospERM tissues of the wheat cultivar
Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa
endospERM using Not I-oligo(dT)18 primer/adaptor
(Pharmacia Biotech), and then ligated to the Sal I-Not I
site of ZipLox vector (Life Technology) after adding a
Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan
Ali and Bill Taylor."

CV066718 34 bp mRNA linear EST 06-DEC-2002
WNEU7d3 wheat EST endospERM library Triticum aestivum CDNA clone
WNEU7d3 5' similar to Unknown Function, mRNA sequence.
CV066718
ACCESSION CV066718.1 GI:26117014
VERSION CV066718
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 34)
Herwig,R.; Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
Contact: Weishaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 34 Std Etox: 0.00
Plate: 10 row: B column: 02
Seq primer: T7; GTAATACGACTCTACTATAGGCG.
Location/Qualifiers
1. .34
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:185440"
/db_xref="taxon:161934"
/clone="024-010-B02"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPZ-ADIS-024-leaf"
/notes="Vector: pCMVSPOR16; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7. Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPP/GABI-Primary database:http://gabi.rzpd.de"

Query Match
Best Local Similarity 94.1%; Score 30.8; DB 1; Length 34;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

FEATURES
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1. .34
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:185440"
/db_xref="taxon:161934"
/clone="024-010-B02"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPZ-ADIS-024-leaf"
/notes="Vector: pCMVSPOR16; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7. Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPP/GABI-Primary database:http://gabi.rzpd.de"

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RESULT 534
DU832879/c

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LOCUS       DU832879                34 bp    DNA        linear    GSS 22-DEC-2005
DEFINITION   KBrS011B02F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
              subsp. pekinensis genomic clone KBrS011B02, genomic survey
              sequence.
ACCESSION    DU832879
VERSION      DU832879.1   GI:83869475
KEYWORDS     GSS.
SOURCE       Brassica rapa subsp. pekinensis
              Brassica rapa subsp. pekinensis
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE    1 (bases 1 to 34)
AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
              Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
              Hahn,J.H. and Park,B.S.
TITLE        End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
              Brassica Genomics Team
              National Institute of Agricultural Biotechnology
              225 Seodun-Dong, Suwon, 441-707, Korea
              Tel: +82-31-299-1670
              Fax: +82-31-299-1672
              Email: pbeom@da.go.kr
              BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
              KBrS011B02
              Seq primer: T7
              Class: BAC ends.
              Location/Qualifiers
                  1..34
                  /organism="Brassica rapa subsp. pekinensis"
                  /mol_type="genomic DNA"
                  /cultivar="Chiifu"
                  /sub_species="pekinensis"
                  /db_xref="taxon:51351"
                  /clone="KBrS011B02"
                  /lab_host="E. coli DH10B"
                  /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                  /notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                  ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
                  available at NIAH."

Query Match      1.1%; Score 30.8; DB 1; Length 34;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB   34 AAAAAAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 535
DX048708    34 bp    DNA        linear    GSS 10-JAN-2006
LOCUS       KBrS011B15F KBrS, Brassica rapa BamHI BAC library Brassica rapa
              subsp. pekinensis genomic clone KBrS011B15, genomic survey
              sequence.
ACCESSION    DX048708
VERSION      DX048708.1   GI:84743005
KEYWORDS     GSS.
SOURCE       Brassica rapa subsp. pekinensis
              Brassica rapa subsp. pekinensis
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE    1 (bases 1 to 34)
AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
              Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
              Hahn,J.H. and Park,B.S.
TITLE        End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park

```

```

Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrS051B15
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
    1..34
    /organism="Brassica rapa subsp. pekinensis"
    /mol_type="genomic DNA"
    /cultivar="Chiifu"
    /sub_species="pekinensis"
    /db_xref="taxon:51351"
    /clone="KBrS051B15"
    /lab_host="E. coli DH10B"
    /clone_lib="KBrB, Brassica rapa BamHI BAC library"
    /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
    pekinensis var. Chiifu BAC library (KBrB BAC) is provided
    by Yong-Pyo Lim (CNU)."

Query Match      1.1%; Score 30.8; DB 1; Length 34;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB   1 AAAAAAAAAAAAAAAAAAACAAGAAAAAAAAAAAAAAAAA 34

RESULT 536
CV848473/c   37 bp    mRNA        linear    EST 17-NOV-2004
LOCUS       ID0AEE5CH01RM1 ID0AEE Acyrthosiphon pisum cDNA clone ID0AEE5CH01
              5', mRNA sequence.
ACCESSION    CV848473
VERSION      CV848473.1   GI:55814156
KEYWORDS     EST.
SOURCE       Acyrthosiphon pisum (pea aphid)
              Acyrthosiphon pisum
              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
              Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
              Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE    1 (bases 1 to 37)
AUTHORS      Sabater-Munoz,B., Legai,F., Bonhomme,J., Dang,P., Dossat,C.,
              Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
              Nakabachi,A., Prunier-Leterme,N., Rahbe,Y., Shigenobu,S.,
              Simon,J.C., Stern,D., Wincker,P. and Tagu,D.
TITLE        Annotated ESTs of the pea aphid
JOURNAL      Unpublished (2004)
COMMENT      Contact: D. Tagu
              INRA Rennes
              UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
              Tel: +33.2.23.48.51.65
              Fax: +33.2.23.48.51.50
              PCR Primers
              FORWARD: CAGGAACAGCTATGACC
              Plate: 5C row: H column: 1.
              Location/Qualifiers
                  1..37
                  /organism="Acyrthosiphon pisum"
                  /mol_type="mRNA"
                  /cultivar="yr2"
                  /db_xref="taxon:7029"
                  /clone="ID0AEE5CH01"
                  /tissue_type="antennae"
                  /dev_stage="L3"
                  /lab_host="XL1-Blue"
                  /clone_lib="ID0AEE"
                  /note="Vector: pBS-SKminus; Site_1: EcoRI; Site_2: XhoI;

FEATURES
source

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Sample name: IDOAE; Plant growth place: INRA Rennes, UMR BiO3P, 35327, 35653 Le Rheu Cedex France; Soil conditions: Soil; Sowing date: 15/04/2004; Harvesting date: 15/04/2004; Description: Aphids inoculated on a one-week old *Vicia faba* under non-sterile conditions. A. pisum YR2 is holocyclic, i.e. able to change its reproductive mode under short photoperiods (sexual) versus long photoperiods (clonal). experimental condition: long photoperiod (16-hr light/8-hr dark at 18 °C)

AZ579652/C
 LOCUS
 DEFINITION IM0367C12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0367C12 R, genomic survey sequence.
 ACCESSION AZ579652
 VERSION
 KEYWORDS GSS
 SOURCE AZ579652.1 GI:11694081
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0367 row: C column: 12
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 32.

FEATURES

source
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0367C12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114[9b]AF129072.1), a copy-number inducible derivative of plasmid Ri. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 30.4; DB 1; Length 32;
 Best Local Similarity 96.9%; Pred. No. 3.3e+02;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

|||||
 DB 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA 1

RESULT 543

DU834670
 LOCUS
 DEFINITION KBrS014013F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS014013, genomic survey sequence.
 ACCESSION DU834670
 VERSION DU834670.1 GI:83871266
 KEYWORDS GSS
 SOURCE Brassica rapa subsp. pekinensis
 ORGANISM Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
 TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
 JOURNAL
 COMMENT Unpublished (2005)
 Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea
 Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pheom@da.go.kr
 BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBrS014013
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1..32
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrS014013"
 /lab_host="E. coli DH10B"
 /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
 /note="vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."

Query Match 1.1%; Score 30.4; DB 1; Length 32;
 Best Local Similarity 96.9%; Pred. No. 3.3e+02;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 |||||
 DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 544
 DX033610
 LOCUS
 DEFINITION KBrB031B19R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB031B19, genomic survey sequence.
 ACCESSION DX033610
 VERSION DX033610.1 GI:84727907
 KEYWORDS GSS
 SOURCE Brassica rapa subsp. pekinensis
 ORGANISM Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
 TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
 JOURNAL
 COMMENT Unpublished (2005)

COMMENT

Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea
 Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pbeom@da.90.kr
 BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
 KBrB031B19
 Seq primer: M13 Reverse
 Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..32

/organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrB031B19"
 /lab_host="E.coli DH10B"
 /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
 pekinensis var. Chiifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 1.1%; Score 30.4; DB 1; Length 32;
 Best Local Similarity 96.9%; Pred. No. 3.3e+02;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 545

DR1F7S/c

LOCUS

DEFINITION Danio rerio genomic clone DKEY-1F7, genomic survey sequence.

AL735323

VERSION AL735323.1 GI:21343938

KEYWORDS GSS.

SOURCE Danio rerio (zebrafish)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 32)

AUTHORS Humphray, S.J., Huckle, E. and Hunt, S.E.

TITLE Direct Submission

JOURNAL Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
 humquery@sanger.ac.uk Unpublished

COMMENT This sequence was generated from the SP6 end of BAC 1F7. 1F7 is
 part of the Daniokey BAC Library created by R. Plasterk and N.V.
 Keygene.

Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES

source

Location/Qualifiers

1..32

/organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="DKEY-1F7"
 /tissue_type="Testis"
 /note="vector pindigoBAC-536"

Query Match 1.1%; Score 30.4; DB 1; Length 32;
 Best Local Similarity 96.9%; Pred. No. 3.3e+02;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

Db 32 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 546

CF334899/c

LOCUS

DEFINITION

JMT--04-F19, g1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--04-F19, mRNA sequence.

CF334899

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 33)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..33

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="JMT--04-F19"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 1.1%; Score 30.4; DB 1; Length 33;

Best Local Similarity 96.9%; Pred. No. 3.3e+02;

Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 33 AAAAAAAAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 547

AZ307192

LOCUS

DEFINITION

clone UUGC1M0008B07 R, genomic survey sequence.

AZ307192

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 34)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

CF334899 33 bp mRNA linear EST 18-AUG-2003
 JMT--04-F19, g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--04-F19, mRNA sequence.

CF334899

CF334899.1 GI:33818141

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 33)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..33

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="JMT--04-F19"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 1.1%; Score 30.4; DB 1; Length 33;

Best Local Similarity 96.9%; Pred. No. 3.3e+02;

Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 33 AAAAAAAAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

AZ307192 34 bp DNA linear GSS 29-SEP-2000
 1M0008B07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0008B07 R, genomic survey sequence.

AZ307192

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 34)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

```

JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunne@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0008 row: B column: 07
             Seq primer: CACACAGGAACAGCTATGACC
             Class: plasmid ends
             High quality sequence stop: 34.

FEATURES     source
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             /mol_type="genomic DNA"
             /strain="C57BL/6J"
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             /clone="UUGCLM008B07"
             /sex="Male"
             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
             /clone_lib="Mouse 10kb plasmid UUGCLM library"
             /note="Vector: PWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male) was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptor DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel
             electrophoresis. Vector DNA was prepared from a derivative
             of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
             inducible derivative of plasmid R1. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptor mouse DNA was annealed to
             adaptor vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."

             Query Match      1.1%; Score 30.4; DB 1; Length 34;
             Best Local Similarity 96.9%; Pred. No. 3.4e+02;
             Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
    ||||||| ||||||| ||||||| ||||||| |||||||
Db 3 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 548
LOCUS   CN545906
DEFINITION EST 17850 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION CN545906
VERSION   CN545906.1 GI:46910531
KEYWORDS EST.
SOURCE   Vitis vinifera
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 36)
AUTHORS  Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
          Couture,C., Dedadechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
          Hamdi,S., Romieu,C. and Terrier,N.
          Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
          or seeds) at Various Developmental Stages
          Unpublished (2002)
JOURNAL
COMMENT  Contact: Hamdi S.
          UMR 619 - Equipe Biologie de la Vigne
          Universite de Bordeaux I, Institut National de la Recherche
          Agronomique
          71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
          France
          Tel: 00-33-(0)5-57-12-25-50
          Fax: 00-33-(0)5-57-12-25-48
          Email: s.hamdi@bordeaux.inra.fr
          Seq primer: T7.

FEATURES     source
             1..36
             /organism="Vitis vinifera"
             /mol_type="mRNA"
             /cultivar="Cabernet Sauvignon"
             /db_xref="taxon:29760"
             /clone="B3CS00RL006C01"
             /dev_stage="ripening stage"
             /clone_lib="Ripe Grape Skin Triplex2 Library"
             /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
             SfiIA; Site_2: SfiIB; Oriented library"

             Query Match      1.1%; Score 30.4; DB 1; Length 36;
             Best Local Similarity 96.9%; Pred. No. 3.5e+02;
             Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
    ||||||| ||||||| ||||||| ||||||| |||||||
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 549
LOCUS   CN546158
DEFINITION EST 18110 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION CN546158
VERSION   CN546158.1 GI:46910783
KEYWORDS EST.
SOURCE   Vitis vinifera
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 36)
AUTHORS  Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
          Couture,C., Dedadechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
          Hamdi,S., Romieu,C. and Terrier,N.
          Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
          or seeds) at Various Developmental Stages
          Unpublished (2002)
JOURNAL
COMMENT  Contact: Hamdi S.
          UMR 619 - Equipe Biologie de la Vigne
          Universite de Bordeaux I, Institut National de la Recherche
          Agronomique
          71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
          France
          Tel: 00-33-(0)5-57-12-25-50
          Fax: 00-33-(0)5-57-12-25-48
          Email: s.hamdi@bordeaux.inra.fr
          Seq primer: T7.

FEATURES     source
             1..36
             /organism="Vitis vinifera"
             /mol_type="mRNA"
             /cultivar="Cabernet Sauvignon"
             /db_xref="taxon:29760"
             /clone="B3CS00RL009A10"
             /dev_stage="ripening stage"
             /clone_lib="Ripe Grape Skin Triplex2 Library"
             /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
             SfiIA; Site_2: SfiIB; Oriented library"

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Query Match      1.1%; Score 30.4; DB 1; Length 36;
Best Local Similarity 96.9%; Pred. No. 3.5e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
      |||||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 550
CN546709/c
LOCUS
DEFINITION      36 bp mRNA linear EST 30-APR-2004
CN546709
vinifera cDNA clone B3CS37TB007H08 3', mRNA sequence.
ACCESSION      CN546709.1 GI:46911334
VERSION
KEYWORDS
SOURCE
ORGANISM      Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
AUTHORS      Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE      Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL      Unpublished (2002)
COMMENT      Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1. .36
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS37TB007H08"
/dev_stage="veraison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.1%; Score 30.4; DB 1; Length 36;
Best Local Similarity 96.9%; Pred. No. 3.5e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
      |||||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 551
DU834429/c
LOCUS
DEFINITION      36 bp DNA linear GSS 22-DEC-2005
DU834429
KBrS014E10R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS014E10, genomic survey
sequence.
ACCESSION      DU834429
VERSION
KEYWORDS      GSS.
SOURCE
ORGANISM      Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

```

```

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 36)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS014E10
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .36
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS014E10"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

Query Match      1.1%; Score 30.4; DB 1; Length 36;
Best Local Similarity 96.9%; Pred. No. 3.5e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
      |||||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 552
CN545897/c
LOCUS
DEFINITION      37 bp mRNA linear EST 30-APR-2004
CN545897
clone B3CS00RL006B04 3', mRNA sequence.
ACCESSION      CN545897.1 GI:46910522
VERSION
KEYWORDS      EST.
SOURCE
ORGANISM      Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 37)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1. .37
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006B04"
/dev_stage="veraison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.1%; Score 30.4; DB 1; Length 36;
Best Local Similarity 96.9%; Pred. No. 3.5e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
      |||||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 553
DU834429/c
LOCUS
DEFINITION      36 bp DNA linear GSS 22-DEC-2005
DU834429
KBrS014E10R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS014E10, genomic survey
sequence.
ACCESSION      DU834429
VERSION
KEYWORDS      GSS.
SOURCE
ORGANISM      Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

```


JOURNAL
COMMENT

Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES

source

Location/Qualifiers

1. .38
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58R008C04"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 30.4; DB 1; Length 38;
Best Local Similarity 96.9%; Pred. No. 3.6e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 556

CN546633/C

LOCUS

DEFINITION EST 18404 Turning Grape Berry Lambda Triplex2 Library Vitis
vinifera cDNA clone B3CS37B007B04 3', mRNA sequence.

ACCESSION

CN546633

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr

FEATURES

source

Location/Qualifiers

1. .38
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS37B007B04"
/dev_stage="vexaison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 30.4; DB 1; Length 38;
Best Local Similarity 96.9%; Pred. No. 3.6e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 37 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 557

CN546633/C

LOCUS

DEFINITION 4013015C08.1EL_xl 4013 - RescueMu Grid O Zea mays genomic,
survey sequence.

ACCESSION

CN546633

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013015 row: C column: 08
Class: transposon-tagged.
Location/Qualifiers
1. .36
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"

/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
O was grown at Stanford in 2001. DNA was extracted from
leaf strips, double digested using BamHI and BglII, and
ligated to form circular plasmids. DH10B cells were
transformed and then screened on LB plates with
ampicillin."

FEATURES

source

Query Match 1.1%; Score 30.2; DB 1; Length 36;
Best Local Similarity 91.4%; Pred. No. 3.6e+02;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAACACAAAAAAAAAAAAAAAAAAAAATA 35

RESULT 558

AL038650

LOCUS

30 bp mRNA linear EST 06-JUL-2004

```

DEFINITION DKFZp566i1846_r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION DKFZp566i1846_mRNA sequence.
VERSION AL038650
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Ottenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
    source
        1..30
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKFZp566i1846"
            /tissue_type="kidney"
            /dev_stage="fetal"
            /lab_host="Xl-2blue"
            /clone_lib="566 (synonym: hfkd2)"
            /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 559
LOCUS AM044444 30 bp mRNA linear EST 20-SEP-2005
DEFINITION Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmIC13a04.q1k, mRNA sequence.
ACCESSION AM044444
VERSION AM044444
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 30)
AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
    source
        1..30
            /organism="Schistosoma mansoni"
            /mol_type="mRNA"
            /db_xref="taxon:6183"
            /clone="SmIC13a04.q1k"
            /dev_stage="lung schistosomulum"
            /clone_lib="Schistosoma mansoni lung schistosomulum"
            /note="country: Puerto Rico"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 561
LOCUS CF280699/c 30 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--07-H15.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-H15,
mRNA sequence.
ACCESSION CF280699
VERSION CF280699.1 GI:33658085

```

```

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 560
LOCUS BG666435 30 bp mRNA linear EST 30-APR-2001
DEFINITION DRACRC02 Rat DRG Library Rattus norvegicus cDNA clone DRACRC02 5',
mRNA sequence.
ACCESSION BG666435
VERSION BG666435.1 GI:13888357
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 30)
AUTHORS Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,
Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
TITLE Identification of gene expression profile of dorsal root ganglion
in the rat peripheral axotomy model of neuropathic pain
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
PUBMED 12060780
COMMENT Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
PCR Primers
FORWARD: T7
BACKWARD: T3
Seq primer: T3
POLYA=NO.

FEATURES
    source
        1..30
            /organism="Rattus norvegicus"
            /mol_type="mRNA"
            /strain="Sprague-Dawley"
            /db_xref="taxon:10116"
            /clone="DRACRC02"
            /sex="male"
            /tissue_type="dorsal root ganglion"
            /dev_stage="adult"
            /clone_lib="Rat DRG Library"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 561
LOCUS CF280699/c 30 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--07-H15.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-H15,
mRNA sequence.
ACCESSION CF280699
VERSION CF280699.1 GI:33658085

```

KEYWORDS	EST.
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group)
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE	1 (bases 1 to 30)
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomic and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Gyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@bio.myongji.ac.kr.

```

source
FEATURES
Location/Qualifiers
1. .30
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL-07-H15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match	1.1%;	Score 30;	DB 1;	Length 30;
Best Local Similarity	100.0%;	Pred. No. 3.3e+02;		
Matches 30;	Conservative	0;	Mismatches 0;	Indels 0;
			Gaps	0;

Qy	2709	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2738
D_b	30	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1

RESULT 562
CF292086
LOCUS CF292086 30 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-M10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (Japonica cultivar-group) cDNA clone 14ROOT--02-M10, mRNA
sequence.

VERSION	KEYWORDS	SOURCE	ORGANISM
CF292086.1	GI:33651119	Est.	
			<i>Oryza sativa</i> (japonica cultivar-group)
			<i>Oryza sativa</i> (japonica cultivar-group)
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
			clade: Ehrhartoideae; Oryzae; <i>Oryza</i> .

REFERENCE	1. (bases 1 to 30)
AUTHORS	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, Y.-K. and Nahm, B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@bio.myongji.ac.kr

```

FEATURES
source
1. .30
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

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/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT-02-M10"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="rice root plasmid cDNA library (14ROOT)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;

[illegible]

RESULT 563
CF299555/c
LOCUS
DEFINITION
30 bp mRNA linear EST 15-AUG-2003
7LEAF--03-K01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K01, mRNA
sequence.
CF299555
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
ORGYza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

clade; ennrartoideae; Oryzeae; Oryza.
1 (bases 1 to 30)
Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B. H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B. H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

FEATURES
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Location/Qualifiers
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="7LEAF-03-K01"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10b"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site: 1: ECGRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
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 Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 564	linear	EST 15-AUG-2003
CF312417/c		
LOCUS	30 bp	
CF312417	mRNA	

DEFINITION ABF--08-C19.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION ABF--08-C19, mRNA sequence.

VERSION CF312417

KEYWORDS CF312417.1 GI:33684178

SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 30)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..30

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="ABF--08-C19"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

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Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 565

CF322226/c

LOCUS

DEFINITION HD--13-M02.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION HD--13-M02, mRNA sequence.

VERSION CF322226

KEYWORDS CF322226.1 GI:33693987

SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 30)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..30

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

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/clone="HB--13-M02"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

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Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 566

CF327835

LOCUS

DEFINITION CF327835 30 bp mRNA linear EST 18-AUG-2003

DEFINITION NACL--02-H17.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-H17, mRNA sequence.

ACCESSION CF327835

VERSION CF327835.1 GI:33803920

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 30)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

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/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

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/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 30; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 567
CF336555/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) 30 bp mRNA linear EST 18-AUG-2003
library (JMT) Oryza sativa transgenic rice plasmid cDNA
JMT--06-K13, mRNA sequence.
CF336555
CF336555.1 GI:33821487
EST.
ACCESSION
VERSION
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Unpublished (2003)
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/tissue_type="leaf"
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/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 568
CN545913/c
LOCUS
DEFINITION
EST 17857 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL006C10 3', mRNA sequence.
CN545913
CN545913.1 GI:46910538
EST.
ACCESSION
VERSION
SOURCE
ORGANISM
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 569
CN546459/c
LOCUS
DEFINITION
EST 18603 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS57RB007C01 3', mRNA sequence.
CN546459
CN546459.1 GI:46911084
EST.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.

REFERENCE
AUTHORS
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
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or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.

JOURNAL
COMMENT
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
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SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 569
CN546459/c
LOCUS
DEFINITION
EST 18603 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS57RB007C01 3', mRNA sequence.
CN546459
CN546459.1 GI:46911084
EST.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.

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Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
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/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"

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AUTHORS
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
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Unpublished (2002)
Contact: Hamdi S.

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France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
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Location/Qualifiers
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/mol_type="mRNA"
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/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 569
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LOCUS
DEFINITION
EST 18603 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS57RB007C01 3', mRNA sequence.
CN546459
CN546459.1 GI:46911084
EST.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
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or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.

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Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..30
Location/Qualifiers
1..30
/organism="Vitis vinifera"
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/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"

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/clone="B3CS57RB007C01"
/dev stage="ripe stage"
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/Note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db  30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 570
CN546474/c
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DEFINITION
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CDNA clone B3CS57RB007D06 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
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Unpublished (2002)
Contact: Hamdi S.
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Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
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/organism="Vitis vinifera"
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/cultivar="Cabernet Sauvignon"
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/dev stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/Note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db  30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 571
CN546789/c
LOCUS
DEFINITION
EST 18560 Turning Grape Berry Lambda Triplex2 Library Vitis
vinifera cDNA clone B3CS38TB008G04 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gpio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..30
/organism="Oryza sativa (japonica cultivar-group)"

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```

KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
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Unpublished (2002)
Contact: Hamdi S.
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Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1..30
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS38TB008G04"
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/Note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db  30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 572
CN546764/c
LOCUS
DEFINITION
FLO--01-E06.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-E06, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gpio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..30
/organism="Oryza sativa (japonica cultivar-group)"

```

```

/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-E06"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 573
CX014987/c
LOCUS
DEFINITION
io78a02.b1 whole Heart Library (DOGEST5) Canis familiaris cDNA,
mRNA sequence.
ACCESSION
CX014987
VERSION
EST.
KEYWORDS
Canis familiaris (dog)
ORGANISM
Canis familiaris
REFERENCE
1 (bases 1 to 30)
AUTHORS
Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE
ESTs from Canis familiaris whole heart (dog)
JOURNAL
Unpublished (2004)
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcmbie@cshl.org.
Location/Qualifiers
1..30
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Whole Heart Library (DOGEST5)"
/notes="Organ: Heart; Vector: pBluescript II SK; Site_1:
EcoRI; Site_2: XhoI; Library constructed using pluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 574
DR073060/c
LOCUS
DEFINITION
io78a02.b1 whole Heart Library (DOGEST5) Canis familiaris cDNA,
mRNA sequence.
ACCESSION
DR073060
VERSION
EST.
KEYWORDS
Canis familiaris (dog)
ORGANISM
Canis familiaris
REFERENCE
1 (bases 1 to 30)
AUTHORS
Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE
ESTs from Canis familiaris whole heart (dog)
JOURNAL
Unpublished (2004)
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcmbie@cshl.org.
Location/Qualifiers
1..30
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Whole Heart Library (DOGEST5)"
/notes="Organ: Heart; Vector: pBluescript II SK; Site_1:
EcoRI; Site_2: XhoI; Library constructed using pluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 575
AZ357603/c
LOCUS
DEFINITION
IM0099HL7F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0099HL7 F, genomic survey sequence.
ACCESSION
AZ357603
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
1 (bases 1 to 30)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

```

```

ik85b01.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION
DR073060
VERSION
EST.
KEYWORDS
Ginkgo biloba (maidenhair tree)
SOURCE
Ginkgo biloba
ORGANISM
Ginkgo biloba
REFERENCE
1 (bases 1 to 30)
AUTHORS
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE
Expressed tag sequences from Ginkgo female leaf (NYBG)
JOURNAL
Unpublished (2005)
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcmbie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..30
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/notes="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 575
AZ357603/c
LOCUS
DEFINITION
IM0099HL7F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0099HL7 F, genomic survey sequence.
ACCESSION
AZ357603
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
1 (bases 1 to 30)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

```


Insert Length: 10000 Std Error: 0.00
 Plate: 0099 row: H column: 17
 Seq primer: CTTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers

FEATURES

source

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1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0099H17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 1.1%; Score 30; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
      |||||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
```

RESULT 576
 A2455741
 LOCUS
 DEFINITION
 clone UUGC1M0258D16 F, genomic survey sequence.

ACCESSION
 A2455741
 VERSION
 A2455741.1 GI:10613866
 GSS.
 SOURCE
 Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 30)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0258 row: D column: 16
 Seq primer: CTTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers

FEATURES

source

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1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0258D16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 1.1%; Score 30; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30
```

RESULT 577
 A2481739
 LOCUS
 DEFINITION
 clone UUGC1M0306N12 F, genomic survey sequence.

ACCESSION
 A2481739
 VERSION
 A2481739.1 GI:10642804
 GSS.
 SOURCE
 Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 30)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0306 row: N column: 12
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers

FEATURES

1..30
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0306N12"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 30; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
 |||||
 Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 578

AZ582114/C
 LOCUS 30 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0374J17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0374J17 F, genomic survey sequence.

ACCESSION AZ582114
 VERSION AZ582114.1 GI:11700674
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 30)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0374 row: J column: 17
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers

FEATURES

1..30
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0374J17"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 30; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
 |||||
 Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 579

CZ917652
 LOCUS 30 bp DNA linear GSS 08-AUG-2005
 DEFINITION 4021006E03.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic survey sequence.

ACCESSION CZ917652
 VERSION CZ917652.1 GI:71936647
 KEYWORDS GSS.

SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 30)

AUTHORS Walbot,V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)

JOURNAL Contact: Walbot V

COMMENT Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence.

Plate: 4021006 row: E column: 03

Class: transposon-tagged.

Location/Qualifiers

FEATURES

source

```

1. .30
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

```

```

Query Match      1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
```

```
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30
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RESULT 580

```
CZ919796
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```
LOCUS
```

```
DEFINITION 4021014H02.2ELy1 4021 - RescueMu Grid V Zea mays genomic, GSS 08-AUG-2005 survey sequence.
```

```
ACCESSION CZ919796
```

```
VERSION CZ919796.1 GI:71940664
```

```
KEYWORDS GSS.
```

```
SOURCE Zea mays
```

```
ORGANISM Zea mays
```

```
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
```

```
1 (bases 1 to 30)
```

```
Walbot.V.
```

```
Maize genomic sequences found using engineered RescueMu transposon
```

```
Unpublished (2001)
```

```
Contact: Walbot V
```

```
Department of Biological Sciences
```

```
Stanford University
```

```
855 California Ave, Palo Alto, CA 94304, USA
```

```
Tel: 650 723 2227
```

```
Fax: 650 725 8221
```

```
Email: walbot@stanford.edu
```

```
Possible ligation site of ends cut by 2 different endonucleases.
```

```
Reverse complemented post-ligation sequence from source sequence.
```

```
Plate: 4021014 row: H column: 02
```

```
Class: transposon-tagged.
```

FEATURES

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source
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```
1. .30
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/organism="Zea mays"
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/mol_type="genomic DNA"
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/cultivar="mixed background W23/A188/B73/K55"
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/db_xref="taxon:4577"
```

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/tissue_type="leaf"
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/dev_stage="adult"
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/lab_host="DH10B"
```

```
/clone_lib="4021 - RescueMu Grid V"
```

```
/notes="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
```

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

```
Query Match      1.1%; Score 30; DB 1; Length 30;
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```
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
```

```
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30
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RESULT 581

```
CW020481/c
```

```
LOCUS
```

```
DEFINITION CW020481 TIGEM gene trap library Mus musculus cDNA clone A015.C10, mRNA sequence.
```

```
ACCESSION CW020481
```

```
VERSION CW020481.1 GI:52789741
```

```
KEYWORDS GSS.
```

```
SOURCE Mus musculus (house mouse)
```

```
ORGANISM Mus musculus
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
```

```
1 (bases 1 to 30)
```

```
Cobellis G., Nicolaus G., Iovino M., Romito A., Marra E.,
```

```
Barbarisi M., Sardiello M., Di Giorgio F.P., Iovino N., Zollo M.,
```

```
Ballabio A. and Cortese R.
```

```
Tagging genes with cassette-exchange sites
```

```
Nucleic Acids Res. 33 (4), e44 (2005)
```

```
15741177
```

```
Contact: TIGEM
```

```
107
```

```
TIGEM
```

```
Via P. Castellino, 111, 80131 NAPOLI, ITALY
```

```
Tel: +390816132205
```

```
Fax: +390815790919
```

```
Email: cobellis@tigem.it
```

Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM

```
Class: Gene Trap.
```

FEATURES

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source
```

```
1. .30
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/organism="Mus musculus"
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/mol_type="mRNA"
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/strain="129 Ola"
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/db_xref="taxon:10090"
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/clone="A015.C10"
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/sex="male"
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/cell_type="Embryonic stem cell"
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/cell_line="E14"
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/clone_lib="TIGEM gene trap library"
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/note="Vector: pFLIPI"
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Query Match      1.1%; Score 30; DB 1; Length 30;
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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
```

```
DB 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
```

RESULT 582

```

DU835531
LOCUS      DU835531                30 bp    DNA          linear      GSS 22-DEC-2005
DEFINITION KRS016N21F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBrS016N21, genomic survey
            sequence.
ACCESSION  DU835531
VERSION    DU835531.1  GI:83872127
KEYWORDS   GSS.
SOURCE     Brassica rapa subsp. pekinensis
ORGANISM   Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 30)
AUTHORS   Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J. H. and Park,B.S.
TITLE     End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL   Unpublished (2005)
COMMENT   Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-295-1670
            Fax: +82-31-295-1672
            Email: pbeom@rda.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
            KBrS016N21
            Seq primer: T7
            Class: BAC ends.

FEATURES             source
            Location/Qualifiers
                1..30
                /organism="Brassica rapa subsp. pekinensis"
                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBrS016N21"
                /lab_host="E. coli DH10B"
                /notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
                available at NIBAF."

Query Match      1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
      |||
      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 583
AG191161/C
LOCUS      AG191161                30 bp    DNA          linear      GSS 06-MAR-2004
DEFINITION Pan troglodytes DNA, clone: RP43-066P20.T7, genomic survey
            sequence.
ACCESSION  AG191161
VERSION    AG191161.1  GI:45223337
KEYWORDS   GSS.
SOURCE     Pan troglodytes (chimpanzee)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Pan.
REFERENCE  1
AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
TITLE     BAC end sequences of Library RP-43
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 30)
AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,

```

```

Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector      : pBACe3.6
R.Site 1   : EcoRI
R.Site 2   : EcoRI.
            Location/Qualifiers
                1..30
                /organism="Pan troglodytes"
                /mol_type="genomic DNA"
                /db_xref="taxon:9598"
                /clone="RP43-066P20.T7"
                /sex="male"
                /cell_type="lymphocytes"
                /clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match      1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
      |||
      30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 584
BG292912
LOCUS      BG292912                31 bp    mRNA          linear      EST 21-FEB-2001
DEFINITION mRNA sequence.
ACCESSION  BG292912
VERSION    BG292912.1  GI:13052227
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 31)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10368 row: b column: 13
            High quality sequence stop: 31.

FEATURES             source
            Location/Qualifiers
                1..31
                /organism="Mus musculus"
                /mol_type="mRNA"
                /db_xref="taxon:10090"
                /clone="IMAGE:4501164"
                /tissue_type="retina"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_94"
                /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;

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Site 2: SalI: Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life technologies.
Note: this is a NIH_MGC Library."

Query Match 1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 585
CN545579/c
LOCUS EST 17523 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
DEFINITION clone B3CS00RL003F11 3', mRNA sequence.
ACCESSION CN545579
VERSION CN545579.1 GI:46910204
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

TITLE 1 (bases 1 to 31)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.

JOURNAL Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
COMMENT or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: F7.

FEATURES
source
1..31
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL003F11"
/dev_stages="ripening stage"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 586
CN545867/c
LOCUS EST 17811 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
DEFINITION clone B3CS00RL002G09 3', mRNA sequence.
ACCESSION CN545867
VERSION CN545867.1 GI:46910492
KEYWORDS EST.

SOURCE
ORGANISM

Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

REFERENCE
AUTHORS

1 (bases 1 to 31)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.

TITLE

UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France

JOURNAL
COMMENT

Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: F7.

FEATURES
source

1..31
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL002G09"
/dev_stages="ripening stage"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 587
CN545921/c

LOCUS EST 17865 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
DEFINITION clone B3CS00RL006D06 3', mRNA sequence.
ACCESSION CN545921
VERSION CN545921.1 GI:46910546
KEYWORDS EST.

SOURCE Vitis vinifera
ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

REFERENCE
AUTHORS

1 (bases 1 to 31)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.

TITLE

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71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France

JOURNAL
COMMENT

Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
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Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

```

FEATURES
source
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    1..31
      /organism="Vitis vinifera"
      /mol_type="mRNA"
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      /clone="B3CS00RL006D06"
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      SfiIA; Site_2: SfiIB; Oriented library"

Query Match
  1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 588
CN546024/c
LOCUS
DEFINITION
  CN546024
  EST 17974 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Vitis vinifera
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; Vitaceae; Vitis.
  1 (bases 1 to 31)
  Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
  Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
  Hamdi,S., Romieu,C. and Terrier,N.
  Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
  or seeds) at Various Developmental Stages
  Unpublished (2002)
  Contact: Hamdi S.
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  Agronomique
  71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
  France
  Tel: 00-33-(0)5-57-12-25-50
  Fax: 00-33-(0)5-57-12-25-48
  Email: s.hamdi@bordeaux.inra.fr
  Seq primer: T7.
  Location/Qualifiers
    1..31
      /organism="Vitis vinifera"
      /mol_type="mRNA"
      /cultivar="Cabernet Sauvignon"
      /db_xref="taxon:29760"
      /clone="B3CS00RL006G05"
      /dev_stage="ripening stage"
      /clone_lib="Ripe Grape Skin Triplex2 Library"
      /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
      SfiIA; Site_2: SfiIB; Oriented library"

Query Match
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Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 590
CN597046/c
LOCUS
DEFINITION
  CN597046
  EST 17974 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Vitis vinifera
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; Vitaceae; Vitis.
  1 (bases 1 to 31)
  Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
  Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
  Hamdi,S., Romieu,C. and Terrier,N.
  Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
  or seeds) at Various Developmental Stages
  Unpublished (2002)
  Contact: Hamdi S.
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  France
  Tel: 00-33-(0)5-57-12-25-50
  Fax: 00-33-(0)5-57-12-25-48
  Email: s.hamdi@bordeaux.inra.fr
  Seq primer: T7.
  Location/Qualifiers
    1..31
      /organism="Vitis vinifera"
      /mol_type="mRNA"
      /cultivar="Cabernet Sauvignon"
      /db_xref="taxon:29760"
      /clone="B3CS00RL007F01"
      /dev_stage="ripening stage"
      /clone_lib="Ripe Grape Skin Triplex2 Library"
      /note="Organ: Fruit skin; Vector: Lambda triplex2; Site_1:
      SfiIA; Site_2: SfiIB; Oriented library"

Query Match
  1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 589
CN546130/c
LOCUS
DEFINITION
  CN546130
  EST 18082 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Vitis vinifera
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; Vitaceae; Vitis.
  1 (bases 1 to 31)
  Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
  Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
  Hamdi,S., Romieu,C. and Terrier,N.
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  or seeds) at Various Developmental Stages
  Unpublished (2002)
  Contact: Hamdi S.
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  France
  Tel: 00-33-(0)5-57-12-25-50
  Fax: 00-33-(0)5-57-12-25-48
  Email: s.hamdi@bordeaux.inra.fr
  Seq primer: T7.
  Location/Qualifiers
    1..31
      /organism="Vitis vinifera"
      /mol_type="mRNA"
      /cultivar="Cabernet Sauvignon"
      /db_xref="taxon:29760"
      /clone="B3CS00RL008G05"
      /dev_stage="ripening stage"
      /clone_lib="Ripe Grape Skin Triplex2 Library"
      /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
      SfiIA; Site_2: SfiIB; Oriented library"

Query Match
  1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 590
CN597046/c
LOCUS
DEFINITION
  CN597046
  EST 18082 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Vitis vinifera
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 31)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Federsen,T.,
  Reilly,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center

```

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0410 row: K column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.

FEATURES

source

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1. 31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0410K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

```
Query Match 1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30
```

```
RESULT 591
CZ917966
LOCUS 31 bp DNA linear GSS 08-AUG-2005
DEFINITION 4021007E11.2EL y1 4021 - RescueMu Grid V Zea mays genomic, genomic survey sequence.
ACCESSION CZ917966
VERSION CZ917966.1 GI:71937128
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 31)
REFERENCE Walbot,V.
AUTHORS Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
```

```
FEATURES
source
1. 31
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; pRescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
```

```
Query Match 1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31
```

```
RESULT 592
AZ400441
LOCUS 32 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0166C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0166C14 R, genomic survey sequence.
ACCESSION AZ400441
VERSION AZ400441.1 GI:10515515
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 32)
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Igiam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0166 row: C column: 14
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.
FEATURES
source
1. 32
```

Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021007 row: E column: 11
Class: transposon-tagged.
Location/Qualifiers


```

REFERENCE
AUTHORS Ali,S, Holloway,B. and Taylor,W.C.
TITLE Normalisation of cereal endosperm EST libraries for structural and
JOURNAL functional genomic analysis
COMMENT Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry.
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5223
Fax: 61 2 6246 5000
Email: Bill.Taylor@csiro.au
Seq primer: M13 reverse primer
High quality sequence stop: 35.
Location/Qualifiers
1. .33
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Hartog"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 6, 8, 10 dpa (days post_anthesis)"
/lab_host="DH108 (Life Technology)"
/clone_lib="Wheat EST endosperm library"
/notes="Vector: ZipLox; Site 1: Sal I; Site 2: Not I; mRNA was prepared from endosperm tissues of the wheat cultivar Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa endosperm using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of ZipLox vector (Life Technology) after adding a Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."

Query Match 1.1%; Score 30; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

CN545607 33 bp mRNA linear EST 30-APR-2004
EST 17551 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL004A03 3', mRNA sequence.
CN545607
CN545607.1 GI:46910232
EST.
KEYWORDS Vitis vinifera
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 33)
Abbal,P., Agasse,A., Agorces,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimpet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48

clade: Pooidae; Triticaceae; Triticum.
1 (bases 1 to 35)
Ali,S, Holloway,B. and Taylor,W.C.
Normalisation of cereal endosperm EST libraries for structural and
functional genomic analysis
Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry.
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5223
Fax: 61 2 6246 5000
Email: Bill.Taylor@csiro.au
Seq primer: M13 reverse primer
High quality sequence stop: 35.
Location/Qualifiers
1. .33
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Hartog"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 6, 8, 10 dpa (days post_anthesis)"
/lab_host="DH108 (Life Technology)"
/clone_lib="Wheat EST endosperm library"
/notes="Vector: ZipLox; Site 1: Sal I; Site 2: Not I; mRNA was prepared from endosperm tissues of the wheat cultivar Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa endosperm using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of ZipLox vector (Life Technology) after adding a Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."

Query Match 1.1%; Score 30; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

CN545607 33 bp mRNA linear EST 30-APR-2004
EST 17551 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL004A03 3', mRNA sequence.
CN545607
CN545607.1 GI:46910232
EST.
KEYWORDS Vitis vinifera
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 33)
Abbal,P., Agasse,A., Agorces,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimpet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48

```

```

Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1. .33
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL004A03"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site 1: SfiIA; Site 2: SfiIB; Oriented library"

Query Match 1.1%; Score 29.8; DB 1; Length 33;
Best Local Similarity 93.9%; Pred. No. 3.6e+02;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2707 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 33 CTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 597
DX050853 33 bp DNA linear GSS 10-JAN-2006
LOCUS KRB0503024R KRB, Brassica rapa BamHI BAC library Brassica rapa
DEFINITION subsp. pekinensis genomic clone KRB0503024, genomic survey
sequence.
ACCESSION DX050853
VERSION DX050853.1 GI:84745150
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 33)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KRB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KRB0503024
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .33
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KRB0503024"
/lab_host="E.coli DH108"
/clone_lib="KRB, Brassica rapa BamHI BAC library"
/notes="vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KRB BAC) is provided
by Yong-Pyo Lim (CNU)."
```

```

Query Match 1.1%; Score 29.8; DB 1; Length 33;
Best Local Similarity 93.9%; Pred. No. 3.6e+02;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741

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[illegible]

```

Clontech (*6854-1) "

Query Match          1.1%; Score 29.6; DB 1; Length 37;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 32; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2708 TAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAA 2743
        | | | | | | | | | | | | | | | | | | | | | | | |
Db      36  TGAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAATGAACA 1

RESULT 601
BQ591372/c
LOCUS           31 bp mRNA linear EST 06-DEC-2002
DEFINITION     E012712-024-017-I15-T7 MP12-ADIS-024-storage root Beta vulgaris
                cDNA clone 024-017-I15 3-PRIME, mRNA sequence.
ACCESSION     BQ591372 GI:26120955
VERSION       EST.
KEYWORDS
SOURCE        Beta vulgaris
ORGANISM      Beta vulgaris
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              Caryophyllales; Amaranthaceae; Beta.
REFERENCE     1 (bases 1 to 31)
AUTHORS      Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.
TITLE         Construction of a 'unigenes' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL       Plant J. 32 (5), 845-857 (2002)
PUBMED       12472698
COMMENT      Contact: Weishaar B
              ADIS DNA core facility at MPIZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 31 Std Error: 0.00
Plate: 17 row: I column: 15
Seq primer: T7; GTAATTACGACTCACTATAGGGC.
FEATURES             Location/Qualifiers
    source            1..31
                        /organism="Beta vulgaris"
                        /mol_type="RNA"
                        /cultivar="KWS320 (double haploid, monogerm breeding
                        line)"
                        /db_xref="GABI:188741"
                        /gb_xref="taxon:161934"
                        /clone="024-017-I15"
                        /tissue_type="storage root"
                        /lab_host="EMDH108"
                        /clone_lib="MP12-ADIS-024-storage root"
                        /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
                        cDNA library from sugar beet, library provided by KWS
                        Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
                        b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
                        orientation:
                        SP6-Sali-CACCGGTCCG-GspI-CNA-polyA-CC-NotI-T7; Note:
                        Sequencing granted in the context of the GABI-Beet
                        project, local PI: Dr. Katharina Schneider, coordinator:
                        Prof. Christian Jung; Sequence submission managed by
                        R2PD/GABI-Primary database; http://gabi.rzp.dg.de"

Query Match          1.1%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2709 AAAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAAA 2739
        | | | | | | | | | | | | | | | | | | | | | | | |
Db      31  AAAAAA.....AGAAAAA.....AAAAAAAAAAAAAAA 1

Query Match          1.1%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CD577356
IGor3_E10_Q2_081 ESTs from wild-caught Anopheles funestus
POPulations Anopheles funestus cDNA 5', mRNA sequence.
CD577356
GI:48718371
EST.
Anopheles funestus
Anopheles funestus
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 31)
Besansky,N.J., Serazin,A.C. and Dana,A.
Towards the transcriptome of Anopheles funestus: a molecular
snapshot
Unpublished (2003)
Contact: Andrew Serazin
Collins/Besansky Lab
Center for Tropical Disease Research and Training, University of
Notre Dame
317 Galvin Life Science, Notre Dame, IN 46556, USA
Tel: 5746319321
Email: nbesansk@nd.edu
These sequences may be of either nuclear or mitochondrial origin.
FEATURES             Location/Qualifiers
    source            1..31
                        /organism="Anopheles funestus"
                        /mol_type="mRNA"
                        /strain="West African"
                        /db_xref="taxon:62324"
                        /sex="male and female"
                        /dev_stage="embryo, larvae, pupae, and adult"
                        /clone_lib="ESTs from wild-caught Anopheles funestus
                        populations"
                        /note="Vector: LambdaTriplex2"

Query Match          1.1%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2706 ACTAAAAA.....AAAAAAAAAAAAAAAAAAAAAA 2736
        | | | | | | | | | | | | | | | | | | | | | | | |
Db      1   AGTAAAAA.....AAAAAAAAAAAAAAAAAAAAAA 31

Query Match          1.1%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CN545785
EST 17729 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
Clone B3CS00RL005H07 3', mRNA sequence.
CN545785
GI:46910410
EST.
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 31)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Courtue,C., Bedaldechamp,F., Delrot,S., Gliseant,D., Grimpiet,J.,
Hamdi,S., Romeu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
```

Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES

source
 Location/Qualifiers
 1..31
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS00RL005H07"
 /dev_stage="ripening stage"
 /clone_lib="Ripe Grape Skin Triplex2 Library"
 /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29.4; DB 1; Length 31;

Best Local Similarity 96.8%; Pred. No. 3.7e+02;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 604

CN546374/c

LOCUS

DEFINITION

EST 18327 Green Grape Berry Lambda Triplex2 Library Vitis vinifera

CN546374 cDNA clone B3CS1XGB016C11 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Vitis vinifera

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

1 (bases 1 to 31)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourdeaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

FEATURES

source
 Location/Qualifiers
 1..31
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS1XGB016C11"
 /dev_stage="green stage"
 /clone_lib="Green Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda
 Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29.4; DB 1; Length 31;

Best Local Similarity 96.8%; Pred. No. 3.7e+02;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

|||||

Db

RESULT 605

AZ486763/c

LOCUS

DEFINITION

1M0315A11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 31)

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: rduffy@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0315 row: A column: 11

Seq primer: CGTTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 31.

Location/Qualifiers

1..31

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0315A11"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 [gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match

Best Local Similarity

Matches 30; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

|||||

```

Db      31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 606
LOCUS   A2785111/c
DEFINITION
2M0028B14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0028B14 R, genomic survey sequence.
ACCESSION
VERSION A2785111
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 31)
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0028 row: B column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.

FEATURES
source
1..31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0028B14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/vector="PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 608
LOCUS   DX033882
DEFINITION
KBRB031101R KBRs, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBRB031101, genomic survey
sequence.
ACCESSION
VERSION DX033882
KEYWORDS GSS.
SOURCE   Brassica rapa subsp. pekinensis
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 31)
REFERENCE
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE   End sequence of Brassica rapa Sau3AI (KBRs) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBR-S016D03
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
1..31
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBR-S016D03"
/lab_host="E. coli DH10B"
/clone_lib="KBRs, Brassica rapa Sau3AI BAC library"
/note="vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBRs BAC) is
available at NIAB."

Query Match 1.1%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 608
LOCUS   DX033882
DEFINITION
KBRB031101R KBRs, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBRB031101, genomic survey
sequence.
ACCESSION
VERSION DX033882
KEYWORDS GSS.
SOURCE   Brassica rapa subsp. pekinensis
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 31)
REFERENCE
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE   End sequence of Brassica rapa Sau3AI (KBRs) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBR-S016D03
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
1..31
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBR-S016D03"
/lab_host="E. coli DH10B"
/clone_lib="KBRs, Brassica rapa Sau3AI BAC library"
/note="vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBRs BAC) is
available at NIAB."

Query Match 1.1%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

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Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBRB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBRB031101
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES

source
1. .31
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBRB031101"
/lab_host="E.coli DH10B"
/clone_lib="KBRB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa ssp
pekinensis var. Chiifu BAC library (KBRB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 1.1%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 609

AL038680 32 bp mRNA linear EST 06-JUL-2004
LOCUS DKF2566J0246.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
DKF2566J0246, mRNA sequence.

ACCESSION AL038680
VERSION AL038680.1 GI:49682182
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 32)
Ottewaelder, B., Oberwarter, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.

EST (Ottewaelder, et al.)

Unpublished (1999)

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source
1. .32
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2566J0246"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 1.1%; Score 29.4; DB 1; Length 32;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 2 TAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 610

CN545857/c 34 bp mRNA linear EST 30-APR-2004
LOCUS EST 17801 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL002F10.3', mRNA sequence.

ACCESSION CN545857

VERSION CN545857.1 GI:46910482

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 34)

Aubal, P., Agasse, A., Agasse, A., Agasse, A., Agasse, A., Agasse, A.,
Couture, C., Dedaidecham, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

JOURNAL UMR 619 - Equipe Biologie de la Vigne

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France

Tel: 00-33- (0)5-57-12-25-50

Fax: 00-33- (0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: 77.

Location/Qualifiers

1. .34

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS00RL002F10"

/dev_stage="ripening stage"

/clone_lib="Ripe Grape Skin Triplex2 Library"

/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:

SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29.4; DB 1; Length 34;

Best Local Similarity 96.8%; Pred. No. 3.9e+02;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737

|||||

Db 32 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 611

CN546360/c 34 bp mRNA linear EST 30-APR-2004
LOCUS EST 18313 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS1XGB016B08.3', mRNA sequence.

ACCESSION CN546360

VERSION CN546360.1 GI:46910985

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 34)

Aubal, P., Agasse, A., Agasse, A., Agasse, A., Agasse, A., Agasse, A.,

Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimpellet,J., Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES source

1..34
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS1XGB016B08"
/dev_stage="green stage"
/clone_lib="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29.4; DB 1; Length 34;
Best Local Similarity 96.8%; Pred. No. 3.9e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 612

CN546656/c
LOCUS
DEFINITION EST 18427 Turning Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS37TB007D03 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

1 (bases 1 to 34)
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimpellet,J., Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne
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Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES source

1..34
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS37TB007D03"

/dev_stage="veraison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 613

CN545982/c
LOCUS
DEFINITION EST 17931 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00RL007B06 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

1 (bases 1 to 35)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F., Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimpellet,J., Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..35

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS00RL007B06"

/dev_stage="ripening stage"

/clone_lib="Ripe Grape Skin Triplex2 Library"

/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Qy

Db

RESULT 614

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

1 (bases 1 to 35)

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS37TB007D03"

/dev_stage="ripening stage"

/clone_lib="Ripe Grape Skin Triplex2 Library"

/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Qy

Db

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SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera
REFERENCE   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; Vitaceae; Vitis.
TITLE       1 (bases 1 to 35)
JOURNAL     Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimpellet,J.,
COMMENT     Hamdi,S., Romieu,C. and Terrier,N.
            Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
            Unpublished (2002)
            Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.
FEATURES    source
            1..35
            /organism="Vitis vinifera"
            /mol_type="mRNA"
            /cultivar="Cabernet Sauvignon"
            /db_xref="taxon:29760"
            /clone="B3CS38TB008B09"
            /dev_stage="veraison stage"
            /clone_lib="Turning Grape Berry Lambda Triplex2 Library"
            /note="Organ: Fruit without seeds; Vector: Lambda
            Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
Query Match      1.1%; Score 29.4; DB 1; Length 35;
Best Local Similarity 96.8%; Pred. No. 3 9e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACA 5

RESULT 615
AL036993
LOCUS      DKFZp564F0564.r1.564 (synonym: hfbr2) Homo sapiens cDNA clone
DEFINITION DKFZp564F0564_r1.564 (synonym: hfbr2) Homo sapiens cDNA clone
ACCESSION  AL036993
VERSION     AL036993.1 GI:49681922
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 36)
AUTHORS     Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
            Wiemann,S.
TITLE       EST (Duesterhoeft, et al.)
JOURNAL     Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES    source
            1..36
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKFZp564F0564"
            /tissue_type="brain"
            /dev_stage="fetal"
            /lab_host="X1-2blue"

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/clone_lib="564 (synonym: hfbr2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
Query Match      1.1%; Score 29.4; DB 1; Length 36;
Best Local Similarity 96.8%; Pred. No. 4e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2707 CTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 6 CTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 36

RESULT 616
CN545377/c
LOCUS      EST 17321 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
DEFINITION clone B3CS00GL007D11 3', mRNA sequence.
ACCESSION  CN545377
VERSION     CN545377.1 GI:46910002
KEYWORDS    EST.
SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; Vitaceae; Vitis.
REFERENCE   1 (bases 1 to 36)
AUTHORS     Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimpellet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
            Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
            Unpublished (2002)
            Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.
FEATURES    Location/Qualifiers
            1..36
            /organism="Vitis vinifera"
            /mol_type="mRNA"
            /cultivar="Cabernet Sauvignon"
            /db_xref="taxon:29760"
            /clone="B3CS00GL007D11"
            /dev_stage="green stage"
            /clone_lib="Green Grape Skin Triplex2 Library"
            /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
            SfiIA; Site_2: SfiIB; Oriented library"
Query Match      1.1%; Score 29.4; DB 1; Length 36;
Best Local Similarity 96.8%; Pred. No. 4e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACA 6

RESULT 617
CN546215/c
LOCUS      EST 18167 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
DEFINITION clone B3CS00RL009F07 3', mRNA sequence.
ACCESSION  CN546215
VERSION     CN546215.1 GI:46910840
KEYWORDS    EST.
SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

REFERENCE

AUTHORS

1 (bases 1 to 36)
Abbal,P., Agase,A., Agorces,A., Atanasova,R., Barrieu,F., Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Ronieu,C. and Terrier,N.
Handi,S., Ronieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

JOURNAL

COMMENT

Unpublished (2002)

Contact: Hamdi S.

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Agronomique

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France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

FEATURES

source

Location/Qualifiers
1..36

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS00RL009F07"

/dev_stage="ripening stage"

/clone_lib="Ripe Grape Skin Triplex2 Library"

/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match

Best Local Similarity 1.1%; Score 29.4; DB 1; Length 36;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

Db

36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACA 6

RESULT 618

CN546685/c

LOCUS

EST 18456 Turning Grape Berry Lambda Triplex2 Library Vitis

vinifera cDNA clone B3CS37TB007F08 3', mRNA sequence.

Accession

Version

Keywords

Source

Organism

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

1 (bases 1 to 36)

Abbal,P., Agase,A., Agorces,A., Atanasova,R., Barrieu,F.,

Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,

Hamdi,S., Ronieu,C. and Terrier,N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche

Agronomique

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Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

FEATURES

source

Location/Qualifiers
1..36

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS37TB007F08"

/dev_stage="veraison stage"

/clone_lib="Turning Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda

Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match

Best Local Similarity 1.1%; Score 29.4; DB 1; Length 36;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

Db

36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACA 6

RESULT 619

CN546685/c

LOCUS

EST 18456 Turning Grape Berry Lambda Triplex2 Library Vitis

vinifera cDNA non acclimated Bluecrop library Vaccinium corymbosum

Accession

Version

Keywords

Source

Organism

Vaccinium corymbosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; Ericales; Ericaceae; Vaccinioideae; Vaccinieae;

Vaccinium.

1 (bases 1 to 36)

Dhanaraj,A.L., Alkharouf,N.W., Beard,H.S., Choukha,I.B.,

Matthews,B.F. and Rowland,L.J.

Monitoring gene expression changes during cold acclimation of

blueberry (Vaccinium corymbosum L.) using a cDNA microarray

Unpublished (2004)

Contact: Rowland, L.J.

Fruit Lab

US Department of Agriculture (USDA), ARS, PSI

Bldg 010A, 10300 Baltimore avenue, BARC West, Beltsville, MD

20705-2350, USA

Tel: 301-504-6654

Fax: 301-504-5653

Email: rowlandj@ba.ars.usda.gov.

Location/Qualifiers

1..36

/organism="Vaccinium corymbosum"

/mol_type="mRNA"

/cultivar="Bluecrop"

/db_xref="taxon:69286"

/tissue_type="Flower buds including bud scales"

/dev_stage="Mature plants"

/clone_lib="cDNA non acclimated Bluecrop library"

/note="Vector: Bluescript SK-; cDNA clones from Vaccinium

corymbosum cv. Bluecrop. RNA for preparation of library

was extracted from flower buds collected in the fall from

non acclimated plants"

Query Match

Best Local Similarity 1.1%; Score 29.4; DB 1; Length 36;

Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy

2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db

33 TCAANNAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 620

AL038356

LOCUS

EST 06-JUL-2004

Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -21ml3
High quality sequence stop: 1.
Location/Qualifiers
1. .35
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GB:493063"
/db_xref="taxon:9606"
/clone="IMAGE:71398"
/tissue_type="fetal spleen"
/dev_stage="fetal"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene fetal spleen (#937205)"
/notes="Organ: spleen; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pooled splens. Average insert size: 1.0 kb;
Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTGGGACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'."

Query Match 1.1%; Score 29.2; DB 1; Length 35;
Best Local Similarity 88.6%; Pred. No. 4e+02;
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 35 TCAAAAAAAAAAAAAAAAAAAAAAAAAAAATNATAAAAAA 1

RESULT 622
AZ351309
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ351309 35 bp DNA linear GSS 29-SEP-2000
1M0089K13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0089K13 F, genomic survey sequence.
AZ351309
GSS.
AZ351309.1 GI:10430546
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 35)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: K column: 13
Seq primer: CGTTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 35.
Location/Qualifiers
1. .35
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0089K13"

FEATURES
source

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUG1M library"
 /note="Vector: PW42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29.2; DB 1; Length 35;
 Best Local Similarity 91.2%; Pred. No. 4e+02;
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
 |||||
 Db 2 AAAAAAAAAAAAAAAAAATTTAAAAAAAAAAAAAAAAAAAA 35

RESULT 623
 C2914519
 LOCUS
 DEFINITION C2914519 35 bp DNA linear GSS 08-AUG-2005
 4013007D07.2EL x1 4013 - RescueMu Grid O Zea mays genomic, genomic survey sequence.
 ACCESSION C2914519
 VERSION C2914519.1 GI:71931175
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 35)
 Walbot.V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 4013007 row: D column: 07
 Class: transposon-tagged.
 Location/Qualifiers

FEATURES
 source
 1..35
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /issue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="4013 - RescueMu Grid O"
 /note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.1%; Score 29.2; DB 1; Length 35;
 Best Local Similarity 91.2%; Pred. No. 4e+02;
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
 |||||
 Db 2 AAAAAAAAAAAAAAAAAAGTAAAAAAAAAAAAAAAAAAA 35

RESULT 624
 AM044739
 LOCUS
 DEFINITION AM044739 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmIC32g07.glk, mRNA sequence.
 ACCESSION AM044739
 VERSION AM044739.1 GI:75967229
 KEYWORDS EST.
 SOURCE Schistosoma mansoni
 ORGANISM Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

REFERENCE
 AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S., Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
 TITLE Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
 JOURNAL Unpublished (2005)
 COMMENT Contact: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.
 Location/Qualifiers

FEATURES
 source
 1..29
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmIC32g07.glk"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /note="Country: Puerto Rico"

Query Match 1.1%; Score 29; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 625
 AM048584
 LOCUS
 DEFINITION AM048584 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmIC12e02.glk, mRNA sequence.
 ACCESSION AM048584
 VERSION AM048584.1 GI:75968755
 KEYWORDS EST.
 SOURCE Schistosoma mansoni
 ORGANISM Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

REFERENCE
 1 (bases 1 to 29)

AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S., Nikolaïdou-Katariadou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
 TITLE Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of *Schistosoma mansoni*
 JOURNAL Unpublished (2005)
 COMMENT Contact: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
 source 1. .29
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmlC12e02.gik"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /notes="country: Puerto Rico"

Query Match 1.1%; Score 29; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 626
 CF279536/c 29 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ETL--05-N22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-N22, mRNA sequence.

ACCESSION CF279536.1 GI:33656922
 VERSION
 KEYWORDS
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 29)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE Oryza sativa (japonica cultivar-group)
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source 1. .29
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14ETL--05-N22"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 29; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 628
 CF312601 29 bp mRNA linear EST 15-AUG-2003
 LOCUS ABF--08-G22.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 DEFINITION ABF--08-G22, mRNA sequence.

ACCESSION CF312601
 VERSION
 KEYWORDS
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 29)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 |||||
 Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 627
 CF299920 29 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--04-C02.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--04-C02, mRNA sequence.

ACCESSION CF299920
 VERSION CF299920.1 GI:33671681
 KEYWORDS
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 29)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE Oryza sativa (japonica cultivar-group)
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source 1. .29
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--04-C02"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 29; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 628
 CF312601 29 bp mRNA linear EST 15-AUG-2003
 LOCUS ABF--08-G22.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 DEFINITION ABF--08-G22, mRNA sequence.

ACCESSION CF312601
 VERSION CF312601.1 GI:33684362
 KEYWORDS
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 29)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 310 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
1..29
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--08-G22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 629

CN545237/c EST 17181 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
LOCUS clone B3CS00GL004G11 3', mRNA sequence.

ACCESSION CN545237.1 GI:46909862
VERSION
KEYWORDS
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE 1 (bases 1 to 29)
AUTHORS Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES

Location/Qualifiers
1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00GL004G11"

/dev_stage="green stage"
/clone_lib="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 630

CN546188/c EST 18140 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
LOCUS clone B3CS00RL009D04 3', mRNA sequence.

ACCESSION CN546188.1 GI:46910813
VERSION
KEYWORDS
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE 1 (bases 1 to 29)
AUTHORS Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES

Location/Qualifiers
1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL009D04"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 631

CN546382/c EST 18335 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
LOCUS cDNA clone B3CS1XGB016D07 3', mRNA sequence.

ACCESSION CN546382
VERSION
KEYWORDS
SOURCE Vitis vinifera
REFERENCE 1 (bases 1 to 29)
AUTHORS Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 29)
AUTHORS Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS1XGB016D07"
/dev_stage="green stage"
/clone_lib="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 632
CN546438/c
LOCUS EST 18592 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION CDNA clone B3CS57RB007A03 3', mRNA sequence.
ACCESSION CN546438
VERSION
KEYWORDS
SOURCE
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 29)
AUTHORS Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
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/clone="B3CS57RB007A03"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 633
CN546557/c
LOCUS EST 18701 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION CDNA clone B3CS58RB008C10 3', mRNA sequence.
ACCESSION CN546557
VERSION
KEYWORDS
SOURCE
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 29)
AUTHORS Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
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/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 634

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CV999708/c
LOCUS          CV999708                29 bp    mRNA    linear    EST 03-DEC-2004
DEFINITION    ivs2f08.b1 Right Cardiac Ventricle (DOGESt6) Canis familiaris cDNA,
               mRNA sequence.
ACCESSION     CV999708
VERSION       CV999708.1   GI:56271125
KEYWORDS      EST.
SOURCE        Canis familiaris (dog)
ORGANISM      Canis familiaris
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
               Canis.
REFERENCE     1 (bases 1 to 29)
AUTHORS      Balija,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE        ESTs from Canis familiaris right cardiac ventricle (dog)
JOURNAL      Unpublished (2004)
COMMENT      Contact: W. Richard McCombie
               Lita Annenberg Hazen Genome Sequencing Center
               Cold Spring Harbor Laboratory
               PO Box 100, Cold Spring Harbor, NY 11724, USA
               Tel: 516 367 8884
               Fax: 516 367 8874
               Email: mcombie@cshl.org.

FEATURES             source
     source           1..29
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /sex="Unknown"
                     /tissue_type="Cardiac muscle"
                     /dev_stage="3 month old normal canine"
                     /lab_host="XL10 Gold"
                     /clone_lib="Right Cardiac Ventricle (DOGESt6)"
                     /note="Organ: Heart; Vector: pBluescript II SK; Site 1:
                     EcoRI; Site 2: XhoI; Library constructed using pBluescript
                     XR kit from Stratagene. Cloned cDNA was size selected
                     between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,
                     Pathology and Medical Genetics, School of Veterinary
                     Medicine, University of Pennsylvania, 3800 Spruce Street,
                     Philadelphia, PA 19104-6051"

Query Match      1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
      |||||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 635
LOCUS          DR073120/c                29 bp    DNA    linear    GSS 02-OCT-2000
DEFINITION    ik86f04.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
               sequence.
ACCESSION     DR073120
VERSION       DR073120.1   GI:67050971
KEYWORDS      EST.
SOURCE        Ginkgo biloba (maidenhair tree)
ORGANISM      Ginkgo biloba
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
REFERENCE     1 (bases 1 to 29)
AUTHORS      Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
               O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
               Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE        Expressed tag sequences from Ginkgo female leaf (NYBG)
JOURNAL      Unpublished (2003)
COMMENT      Contact: W. Richard McCombie
               Lita Annenberg Hazen Genome Sequencing Center
               Cold Spring Harbor Laboratory
               PO Box 100, Cold Spring Harbor, NY 11724, USA
               Tel: 516 367 8884

CV999708
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
     source           1..29
                     /organism="Ginkgo biloba"
                     /mol_type="mRNA"
                     /db_xref="taxon:3311"
                     /sex="female"
                     /clone_lib="Ginkgo female leaf (NYBG)"
                     /note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
                     Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
                     The library was size-fractionated to enrich for large
                     inserts."

Query Match      1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
      |||||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 636
LOCUS          AZ389566                29 bp    DNA    linear    GSS 02-OCT-2000
DEFINITION    1M0150D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
               clone UUGC1M0150D21 F, genomic survey sequence.
ACCESSION     AZ389566
VERSION       AZ389566.1   GI:10503274
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 29)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0150 row: D column: 21
               Seq primer: CGTTGTAACACGACGCCAGT
               Class: plasmid ends
               High quality sequence stop: 29.
               Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
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                     /clone="UUGC1M0150D21"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.fax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a

```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 637
AZ414283/C
LOCUS
DEFINITION
1M0188G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0188G12 R, genomic survey sequence.

ACCESSION
AZ414283
VERSION
GSS.
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0188 row: G column: 12

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

FEATURES

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/organism="Mus musculus"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 638

AZ451930/C

LOCUS

DEFINITION

1M0251E05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0251E05 R, genomic survey sequence.

ACCESSION

AZ451930

VERSION

GSS.

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 29)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0251 row: E column: 05

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

FEATURES

source

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/strain="C57BL/6J"

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/clone="UUGC1M0251E05"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
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 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 643
 AZ806470 29 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0068102R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0068102 R, genomic survey sequence.

ACCESSION AZ806470
 VERSION AZ806470.1 GI:12969849

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0068 row: I column: 02

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0068102"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
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 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 644
 AZ812242

LOCUS 2M0078J18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0078J15 R, genomic survey sequence.

ACCESSION AZ812242

VERSION AZ812242.1 GI:12981296

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0078 row: J column: 15

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

1..29
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0078J15"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1/4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 645

AZ868731

LOCUS

DEFINITION 29 bp DNA linear GSS 21-FEB-2001
clone UUGC2M0180L02 R, genomic survey sequence.

ACCESSION

AZ868731

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 29)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0180 row: L column: 02

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

1..29

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0180L02"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PW42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1/4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 646

CZ919318

LOCUS

DEFINITION 29 bp DNA linear GSS 08-AUG-2005
4021012F10.2EL.Y1 4021 - RescueMu Grid V Zea mays genomic, genomic survey sequence.

ACCESSION

CZ919318

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 29)

REFERENCE

AUTHORS

Walbot,V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4021012 row: F column: 10

Class: transposon-tagged.

Location/Qualifiers

1..29

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="4021 - RescueMu Grid V"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'http://www.mutransposon.org/project/RescueMu/'. Grid

V was grown at University of Arizona in 2003. DNA was

extracted from leaf strips, double digested using BamHI

and BglII, and ligated to form circular plasmids. DH10B

cells were transformed and then screened on LB plates with


```

ampicillin."

Query Match      1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 647
DU833998/c
LOCUS      29 bp      DNA      linear      GSS 22-DEC-2005
DEFINITION KBrS013D17f KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBrS013D17, genomic survey
            sequence.
ACCESSION  DU833998
VERSION     DU833998.1 GI:83870594
KEYWORDS   GSS.
SOURCE     Brassica rapa subsp. pekinensis
ORGANISM   Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 29)
AUTHORS   Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
            Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
            Hahn, J. H. and Park, B.S.
            End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
            Unpublished (2005)
            Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel.: +82-31-299-1670
            Fax: +82-31-299-1672
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
            KBrS013D17
            Seq primer: T7
            Class: BAC ends.
            Location/Qualifiers
                1..29
                /organism="Brassica rapa subsp. pekinensis"
                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBrS013D17"
                /lab_host="E. coli DH10B"
                /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
                available at NIAB."

FEATURES             source
    source
        1..29
        /organism="Brassica rapa subsp. pekinensis"
        /mol_type="genomic DNA"
        /cultivar="Chiifu"
        /sub_species="pekinensis"
        /db_xref="taxon:51351"
        /clone="KBrS016B12"
        /lab_host="E. coli DH10B"
        /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
        /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
        ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
        available at NIAB."

Query Match      1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 649
AG193759
LOCUS      29 bp      DNA      linear      GSS 06-MAR-2004
DEFINITION AG193759 Pan troglodytes DNA, clone: RP43-071B06.T7, genomic survey
            sequence.
ACCESSION  AG193759
VERSION     AG193759.1 GI:4525935
KEYWORDS   GSS.
SOURCE     Pan troglodytes (chimpanzee)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Pan.
            1
            Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
            Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
            BAC end sequences of Library RP-43
            Unpublished
            2 (bases 1 to 29)
            Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
            Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
            Direct Submission
            Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail: redstone@mail.krribb.re.kr, URL: http://phs.grc.krribb.re.kr/,
            Tel: 82-42-866-7181, Fax: 82-42-860-4409)

Query Match      1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 648
DU835145
LOCUS      29 bp      DNA      linear      GSS 22-DEC-2005
DEFINITION KBrS016B12f KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBrS016B12, genomic survey
            sequence.
ACCESSION  DU835145
VERSION     DU835145.1 GI:83871741

```

COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI.

R.Site 2 : EcoRI.

Location/Qualifiers

1. .29

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-071B06.T7"

/sex="male"

/cell_type="lymphocytes"

/clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 650

TA334G090/c

LOCUS

DEFINITION T. brucei sheared genomic DNA clone 334g09, reverse sequence,
Genomic survey sequence.

ACCESSION AL491938

VERSION AL491938.1

KEYWORDS GI:11868238

SOURCE GSS.

ORGANISM Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

REFERENCE 1 (bases 1 to 29)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Meiville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

JOURNAL project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nleaved@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

LOCATION/Qualifiers

1. .29

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="334g09"

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737

Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 651

BG865511

LOCUS

DEFINITION 602783643F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4909811 5',

mrna sequence.

ACCESSION BG865511

VERSION BG865511.1

KEYWORDS GI:14216051

SOURCE EST.

ORGANISM Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 30)

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM10809 row: e column: 12

High quality sequence stop: 30.

FEATURES

Source

1. .30

/organism="Mus musculus"

/mol_type="mrna"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4909811"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP_SG2"

/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site: 1:

NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo

dt. Average insert size 1.3 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

Query Match 1.1%; Score 29; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 652

CN545845/c

LOCUS

DEFINITION EST 17789 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA

clone B3C500RL002E09 3', mRNA sequence.

ACCESSION CN545845

VERSION CN545845.1

KEYWORDS GI:46910470

SOURCE EST.

ORGANISM Vitis vinifera

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 30)

AUTHORS Abbal, P., Agase, A., Agase, A., Atanassova, R., Barrieu, F.,

Couure, C., Dedatdechamp, F., Delrot, S., Glissant, D., Grimpellet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

CN545845 30 bp mRNA linear EST 30-APR-2004
EST 17789 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3C500RL002E09 3', mRNA sequence.

ACCESSION CN545845

VERSION CN545845.1

KEYWORDS GI:46910470

SOURCE EST.

ORGANISM Vitis vinifera

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 30)

AUTHORS Abbal, P., Agase, A., Agase, A., Atanassova, R., Barrieu, F.,

Couure, C., Dedatdechamp, F., Delrot, S., Glissant, D., Grimpellet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7

FEATURES

source

Location/Qualifiers
1..30
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL002E09"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1.

RESULT 653

CZ914262/c
LOCUS CZ914262 31 bp DNA linear GSS 08-AUG-2005
DEFINITION 4013006B10.2EL_y1 4013 - RescueMu Grid O Zea mays genomic, genomic survey sequence.

ACCESSION CZ914262
VERSION CZ914262.1 GI:71930750
KEYWORDS GSS.
SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 31)

REFERENCE

Walbot V.

Maize genomic sequences found using engineered RescueMu transposon survey sequence.
Unpublished (2001)

TITLE

Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221

JOURNAL

Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013006 row: B column: 10
Class: transposon-tagged.
Features tagged.

FEATURES

source

Location/Qualifiers
1..31
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/Al88/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.1%; Score 29; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 654

CN546517/c
LOCUS CN546517 32 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18661 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS57R5007H05 3', mRNA sequence.

ACCESSION CN546517
VERSION CN546517.1 GI:46911142
KEYWORDS EST.
SOURCE Vitis vinifera

ORGANISM

Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.
1 (bases 1 to 32)

REFERENCE

AUTHORS

Abbal P., Agasse A., Ageorges A., Atanassova R., Barrieu F., Couture C., Dedaldecamp F., Delrot S., Glissant D., Grimplet J., Hamdi S., Romieu C. and Terrier N.

TITLE

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)

JOURNAL

COMMENT

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..32
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clones="B3CS57R5007H05"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

FEATURES

source

Query Match 1.1%; Score 29; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 29 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 655

```

DN955775/c
LOCUS       DN955775       32 bp     mRNA       linear       EST 04-MAY-2005
DEFINITION   It93f12.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.
ACCESSION   DN955775
VERSION     DN955775.1  GI:63027913
KEYWORDS    EST.
SOURCE      Gnetum gnemon
            Gnetum gnemon
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
            1 (bases 1 to 32)
REFERENCE    Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
            O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W.,
            Benfey,P., Coruzzi,G. and Stevenson,D.
            Expressed tag sequences from Gnetum female cone (NYBG)
            Unpublished (2003)
            Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Seq primer: -21M13UnivRev.
            Location/Qualifiers
                1..32
                /organism="Gnetum gnemon"
                /mol_type="mRNA"
                /db_xref="taxon:3382"
                /sex="female"
                /clone_lib="Gnetum female cone (NYBG)"
                /note="Organ: mature, unfertilized reproductive strobili;
                Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
                Completed 02/11/02, submitted for sequencing 02/12/02.
                Library: Stratagene ZAP Express cDNA Synthesis kit. The
                library was size-fractionated to enrich for large inserts.
                Sample: NYBG accession number #436/84"
Query Match      1.1%; Score 29; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
      |||
Db   32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 656
BU431802/c
LOCUS       BU431802       34 bp     mRNA       linear       EST 09-SEP-2002
DEFINITION   601654630r1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839742 3',
mRNA sequence.
ACCESSION   BU431802
VERSION     BU431802.1  GI:22770284
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
            1 (bases 1 to 34)
REFERENCE    NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Prepared by: The I.M.A.G.E. Consortium, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:

DN955775/c
LOCUS       DN955775       32 bp     mRNA       linear       EST 04-MAY-2005
DEFINITION   It93f12.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.
ACCESSION   DN955775
VERSION     DN955775.1  GI:63027913
KEYWORDS    EST.
SOURCE      Gnetum gnemon
            Gnetum gnemon
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
            1 (bases 1 to 32)
REFERENCE    Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
            O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W.,
            Benfey,P., Coruzzi,G. and Stevenson,D.
            Expressed tag sequences from Gnetum female cone (NYBG)
            Unpublished (2003)
            Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Seq primer: -21M13UnivRev.
            Location/Qualifiers
                1..32
                /organism="Gnetum gnemon"
                /mol_type="mRNA"
                /db_xref="taxon:3382"
                /sex="female"
                /clone_lib="Gnetum female cone (NYBG)"
                /note="Organ: mature, unfertilized reproductive strobili;
                Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
                Completed 02/11/02, submitted for sequencing 02/12/02.
                Library: Stratagene ZAP Express cDNA Synthesis kit. The
                library was size-fractionated to enrich for large inserts.
                Sample: NYBG accession number #436/84"
Query Match      1.1%; Score 29; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
      |||
Db   32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 656
BU431802/c
LOCUS       BU431802       34 bp     mRNA       linear       EST 09-SEP-2002
DEFINITION   601654630r1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839742 3',
mRNA sequence.
ACCESSION   BU431802
VERSION     BU431802.1  GI:22770284
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
            1 (bases 1 to 34)
REFERENCE    NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Prepared by: The I.M.A.G.E. Consortium, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:

```

```

http://image.llnl.gov
Plate: LLCM528 row: k column: 07
High quality sequence stop: 34.
Location/Qualifiers
    1..34
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:3839742"
    /tissue_type="glioblastoma"
    /lab_host="DH10B (T1 phage-resistant)"
    /clone_lib="NIH_MGC_57"
    /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
    SfiI (ggccctcgccg); Site_2: SfiI (ggccattatggcc);
    Double-stranded cDNA was prepared from cell line RNA. 5'
    and 3' adaptors were used in cloning as follows: 5'
    adaptor sequence: 5'-CACGCGCATATGCC-3' and 3' adaptor
    sequence: 5'-ATTCTAGAGCGGCGGCGGCGCATG-dT(30)BN-3'
    (where B = A, C, or G and N = A, C, G, or T). Average
    insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
    contained inserts by PCR. This library was enriched for
    full-length clones and was constructed by Clontech
    Laboratories (Palo Alto, CA)."
Query Match      1.1%; Score 29; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
      |||
Db   29 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 657
LOCUS       CV064432       35 bp     mRNA       linear       EST 24-AUG-2004
DEFINITION   WNEL10H12 Wheat EST endosperm library Triticum aestivum cDNA clone
WNEL10H12 5' similar to Unknown Function, mRNA sequence.
ACCESSION   CV064432
VERSION     CV064432.1  GI:51527609
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
            Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
            clade; Pooidae; Triticeae; Triticeae.
            1 (bases 1 to 35)
REFERENCE    Ali,S, Holloway,B. and Taylor,W.C.
            Normalisation of cereal endosperm EST libraries for structural and
            functional genomic analysis
            Plant Mol. Biol. Rep. 18, 123-132 (2000)
            Contact: Bill Taylor
            Commonwealth Scientific and Industrial Research Organisation
            Division of Plant Industry.
            CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
            Tel: 61 2 6246 5223
            Fax: 61 2 6246 5000
            Email: Bill.Taylor@csiro.au
            Seq primer: M13 reverse primer
            High quality sequence stop: 35.
            Location/Qualifiers
                1..35
                /organism="Triticum aestivum"
                /mol_type="mRNA"
                /cultivar="Hartog"
                /db_xref="taxon:4565"
                /clone="WNEL10H12"
                /tissue_type="endosperm"
                /dev_stage="developing endosperm tissue 6, 8, 10 dpa (days
                post_anthesis)"
                /lab_host="DH10B (Life Technology)"
                /clone_lib="Wheat EST endosperm library"
                /note="vector: _ZipLox; Site_1: Sal I; Site_2: Not I; mRNA

```

was prepared from endosperm tissues of the wheat cultivar Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa endosperm using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of ZipLox vector (Life Technology) after adding a Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."

Query Match 1.1%; Score 29; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 658
AM044046 36 bp mRNA linear EST 11-AUG-2005
LOCUS AM044046 Schistosoma mansoni lung schistosomulum Schistosoma
DEFINITION mansoni cDNA clone SmlC21b12.q1k, mRNA sequence.

ACCESSION AM044046
VERSION AM044046.1 GI:72292514

KEYWORDS EST.
SOURCE Schistosoma mansoni

ORGANISM Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.

REFERENCE 1 (bases 1 to 36)

AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,

Mikolaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.,

Microarray analysis identifies genes preferentially expressed in

the lung schistosomulum of Schistosoma mansoni

Unpublished (2005)

JOURNAL Contact: Ivens AC

COMMENT Pathogen Microarrays Group

Wellcome Trust Sanger Institute

Hinxton, CB10 1SA, UNITED KINGDOM.

LOCATION/Qualifiers

1..36

/organism="Schistosoma mansoni"

/mol_type="mRNA"

/db_xref="taxon:6183"

/clone="SmlC21b12.q1k"

/dev_stages="lung schistosomulum"

/clone_lib="Schistosoma mansoni lung schistosomulum"

/note="Country: Puerto Rico"

Query Match 1.1%; Score 29; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 8 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 36

RESULT 659
CF318239 32 bp mRNA linear EST 15-AUG-2003
LOCUS HD--08-E17.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--08-E17, mRNA sequence.

ACCESSION CF318239

VERSION CF318239.1 GI:33690000

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1 (bases 1 to 32)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

LARGE-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..32
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--08-E17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
line."

Query Match 1.0%; Score 28.8; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 4.1e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 660

AZ627842/c

LOCUS

DEFINITION

1M0474G03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic

clone UUGC1M0474G03 F, genomic survey sequence.

ACCESSION AZ627842

VERSION AZ627842.1 GI:11750128

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Murinae; Mus.

REFERENCE 1 (bases 1 to 32)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5066

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0474 row: G column: 03

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 32.

Location/Qualifiers

FEATURES

```

source
1. .32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474G03"
/sex="Male"
/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 28.8; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 4.1e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 32 AAAAAAAAAAAAAAAAAAGTAAAAAAAAAAAAA 1

RESULT 661
AJ800678/c
LOCUS
DEFINITION
AJ800678 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018_4_11_b17, mRNA sequence.
ACCESSION
VERSION
AJ800678.1 GI:51116006
KEYWORDS
SOURCE
Antirrhinum majus (snapdragon)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamials; Lamiales; Plantaginaceae; Antirrhineae;
Antirrhinum.
REFERENCE
1 (bases 1 to 34)
AUTHORS
Bey M., Stueber K., Fellenberg K., Schwarz-Sommer Z., Sommer H.,
Saedler H. and Zachgo S.
TITLE
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
DEFICIENS
JOURNAL
Plant Cell 16 (12), 3197-3215 (2004)
PUBMED
15539471
COMMENT
Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.

FEATURES
source
1. .34
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_4_11_b17"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

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```

Query Match 1.0%; Score 28.8; DB 1; Length 34;
Best Local Similarity 93.8%; Pred. No. 4.2e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 34 AACAAATATAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 662
AM043639
LOCUS
DEFINITION
AM043639 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC23b07.qik, mRNA sequence.
ACCESSION
VERSION
AM043639.1 GI:72290911
KEYWORDS
EST.
SOURCE
Schistosoma mansoni
ORGANISM
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeiida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 36)
AUTHORS
Dillon G.P., Feltwell T., Skelton J.P., Ashton P.D., Coulson P.S.,
Nikolaïdou-Katsaridou N., Quail M.A., Wilson R.A. and Ivens A.C.
TITLE
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL
Unpublished (2005)
COMMENT
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
LOCATION/Qualifiers
1. .36
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC23b07.qik"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="country: Puerto Rico"

Query Match 1.0%; Score 28.8; DB 1; Length 36;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2701 TTGTGACTAAAAAAAAAAAAAAAAAAAAAAAAA 2732
Db 5 TTTTATTATAAAAAAAAAAAAAAAAAAAAAA 36

RESULT 663
CN546288/c
LOCUS
DEFINITION
CN546288 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS1XGB015D07.3, mRNA sequence.
ACCESSION
VERSION
CN546288.1 GI:46910913
KEYWORDS
EST.
SOURCE
Vitis vinifera
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Abbal P., Agasse A., Georges A., Atanassova R., Barrieu F.,
Couture C., Dedaïdechamp F., Delrot S., Glissant D., Grimplet J.,
Hamdi S., Romieu C. and Terrier N.
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche

```

Agronomie
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7

Location/Qualifiers

1. .30
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3C51XGB015D07"
/dev_stage="green stage"
/clone_lib="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2, Site_1: SfiA; Site_2: SfiB; Oriented library"

FEATURES

source

Query Match 1.0%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 4.2e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACA 1

RESULT 664

AZ443322

LOCUS

IM0237120R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0237120 R, genomic survey sequence.

ACCESSION

AZ443322

VERSION

AZ443322.1

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 30)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0237 row: L column: 20

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

1. .30

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0237L20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

FEATURES

source

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 4.2e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATAAA 30

RESULT 665

AZ458127/c

LOCUS

IM0261124R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0261124 R, genomic survey sequence.

ACCESSION

AZ458127

VERSION

AZ458127.1

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 30)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0261 row: I column: 24

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

1. .30

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0261124"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

FEATURES

source

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match          1.0%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 4.2e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 666
LOCUS C2917310
DEFINITION 4021005807.2EL_Y1 4021 - RescueMu Grid V Zea mays genomic, Genomic
survey sequence.
ACCESSION C2917310
VERSION C2917310.1 GI:71936005
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 30)
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
JOURNAL clade; Panicoideae; Andropogoneae; Zea.
COMMENT Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021005 row: B column: 07
Class: transposon-tagged.
FEATURES
    source
        Location/Qualifiers
            1..30
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /cultivar="mixed background W23/A188/B73/K55"
                /db_xref="taxon:4577"
                /tissue_type="leaf"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="4021 - RescueMu Grid V"
                /note="Organ: leaf; Vector: RescueMu (engineered from
                pluescript backbone); Site 1: BamHI, Site 2: BglII;
                RescueMu is a 4.9 Kb, modified maize Mu transposon
                designed to allow plasmid rescue from total genomic DNA.
                Mu elements insert preferentially into transcription
                units. For more information on RescueMu, go to the web
                site 'http://www.mutransposon.org/project/RescueMu/'. Grid

```

V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

```

Query Match          1.0%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 4.2e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 667
LOCUS DU833997/c
DEFINITION DU833997 30 bp DNA linear GSS 22-DEC-2005
subsp. pekinensis genomic clone KBRs013D15, genomic survey
sequence.
ACCESSION DU833997
VERSION DU833997.1 GI:83870593
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
REFERENCE 1 (bases 1 to 30)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.90.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBRs013D15
Seq primer: T7
Class: BAC ends.
FEATURES
    source
        Location/Qualifiers
            1..30
                /organism="Brassica rapa subsp. pekinensis"
                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBRs013D15"
                /lab_host="E. coli DH10B"
                /clone_lib="KBRs, Brassica rapa Sau3AI BAC library"
                /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                ssp pekinensis var. Chiifu BAC library (KBRs BAC) is
                available at NIAB."

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAACAAAAA 1

RESULT 668
LOCUS CN546007/c
DEFINITION CN546007 EST 17956 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA

```

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clone B3CS00RL007D07 3', mRNA sequence.
ACCESSION   CN546007
VERSION     CN546007.1  GI:46910632
KEYWORDS    EST.
SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera
REFERENCE   1. (bases 1 to 32)
AUTHORS     Abbal, P., Agase, A., Ageorges, A., Atanasova, R., Barrieu, F.,
            Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
            Hamdi, S., Romieu, C. and Terrier, N.
TITLE       Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; Vitaceae; Vitis.
JOURNAL     1. (bases 1 to 32)
COMMENT     Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
            Unpublished (2002)
            Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.
            Location/Qualifiers
                1. 32
                /organism="Vitis vinifera"
                /mol_type="mRNA"
                /cultiVar="Cabernet Sauvignon"
                /db_xref="taxon:23760"
                /clone="B3CS00RL007D07"
                /dev_stage="ripening stage"
                /clone_lib="Ripe Grape Skin Triplex2 Library"
                /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
                SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 28.4; DB 1; Length 32;
Best Local Similarity 96.7%; Pred. No. 4.3e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

FEATURES
source
LOCUS       CN546531
DEFINITION  CN546531
ACCESSION   CN546531
VERSION     CN546531.1  GI:46911156
KEYWORDS    EST.
SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera
REFERENCE   1. (bases 1 to 32)
AUTHORS     Abbal, P., Agase, A., Ageorges, A., Atanasova, R., Barrieu, F.,
            Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
            Hamdi, S., Romieu, C. and Terrier, N.
TITLE       Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; Vitaceae; Vitis.
JOURNAL     1. (bases 1 to 32)
COMMENT     Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
            Unpublished (2002)
            Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.
            Location/Qualifiers
                1. 32
                /organism="Vitis vinifera"
                /mol_type="mRNA"
                /cultiVar="Cabernet Sauvignon"
                /db_xref="taxon:23760"
                /clone="B3CS00RL007D07"
                /dev_stage="ripening stage"
                /clone_lib="Ripe Grape Skin Triplex2 Library"
                /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
                SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 28.4; DB 1; Length 32;
Best Local Similarity 96.7%; Pred. No. 4.3e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

FEATURES
source
LOCUS       CN546531
DEFINITION  CN546531
ACCESSION   CN546531
VERSION     CN546531.1  GI:46911156
KEYWORDS    EST.
SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera
REFERENCE   1. (bases 1 to 32)
AUTHORS     Abbal, P., Agase, A., Ageorges, A., Atanasova, R., Barrieu, F.,
            Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
            Hamdi, S., Romieu, C. and Terrier, N.
TITLE       Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; Vitaceae; Vitis.
JOURNAL     1. (bases 1 to 32)
COMMENT     Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
            Unpublished (2002)
            Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.
            Location/Qualifiers
                1. 32
                /organism="Vitis vinifera"
                /mol_type="mRNA"
                /cultiVar="Cabernet Sauvignon"
                /db_xref="taxon:23760"
                /clone="B3CS00RL007D07"
                /dev_stage="ripening stage"
                /clone_lib="Ripe Grape Skin Triplex2 Library"
                /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
                SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 28.4; DB 1; Length 32;
Best Local Similarity 96.7%; Pred. No. 4.3e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

FEATURES
source
LOCUS       CN546531
DEFINITION  CN546531
ACCESSION   CN546531
VERSION     CN546531.1  GI:46911156
KEYWORDS    EST.
SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera
REFERENCE   1. (bases 1 to 32)
AUTHORS     Abbal, P., Agase, A., Ageorges, A., Atanasova, R., Barrieu, F.,
            Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
            Hamdi, S., Romieu, C. and Terrier, N.
TITLE       Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; Vitaceae; Vitis.
JOURNAL     1. (bases 1 to 32)
COMMENT     Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
            Unpublished (2002)
            Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.
            Location/Qualifiers
                1. 32
                /organism="Vitis vinifera"
                /mol_type="mRNA"
                /cultiVar="Cabernet Sauvignon"
                /db_xref="taxon:23760"
                /clone="B3CS00RL007D07"
                /dev_stage="ripening stage"
                /clone_lib="Ripe Grape Skin Triplex2 Library"
                /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
                SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 28.4; DB 1; Length 33;
Best Local Similarity 96.7%; Pred. No. 4.4e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

FEATURES
source
LOCUS       CV725332
DEFINITION  CV725332
ACCESSION   CV725332
VERSION     CV725332.1  GI:55412956
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
REFERENCE   1. (bases 1 to 33)
AUTHORS     Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
            Location/Qualifiers
                1. 33
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultiVar="Nackdong"
                /db_xref="taxon:39947"
                /clone="14Salt--02-F20"
                /tissue_type="leaf"
                /dev_stage="14 days after germination"
                /lab_hosts="E.coli SOLR"
                /clone_lib="Salt treated rice leaf lambda phage cDNA
                library (14Salt)"
                /note="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
                cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
                with EcoRI and 3' end with XhoI site."

Query Match      1.0%; Score 28.4; DB 1; Length 33;
Best Local Similarity 96.7%; Pred. No. 4.4e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736

```

```

Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
            Location/Qualifiers
                1. 33
                /organism="Vitis vinifera"
                /mol_type="mRNA"
                /cultiVar="Cabernet Sauvignon"
                /db_xref="taxon:29760"
                /clone="B3CS58RB008A08"
                /dev_stage="ripe stage"
                /clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
                /note="Organ: Fruit without seeds; Vector: Lambda
                Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 28.4; DB 1; Length 33;
Best Local Similarity 96.7%; Pred. No. 4.4e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

FEATURES
source
LOCUS       CV725332/C
DEFINITION  CV725332
ACCESSION   CV725332
VERSION     CV725332.1  GI:55412956
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
REFERENCE   1. (bases 1 to 33)
AUTHORS     Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
            Location/Qualifiers
                1. 33
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultiVar="Nackdong"
                /db_xref="taxon:39947"
                /clone="14Salt--02-F20"
                /tissue_type="leaf"
                /dev_stage="14 days after germination"
                /lab_hosts="E.coli SOLR"
                /clone_lib="Salt treated rice leaf lambda phage cDNA
                library (14Salt)"
                /note="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
                cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
                with EcoRI and 3' end with XhoI site."

Query Match      1.0%; Score 28.4; DB 1; Length 33;
Best Local Similarity 96.7%; Pred. No. 4.4e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736

```


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 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES

Location/Qualifiers

1..35

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS00RL009B01"

/dev_stage="ripening stage"

/clone_lib="Ripe Grape Skin Triplex2 Library"

/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28.4; DB 1; Length 35;

Best Local Similarity 96.7%; Pred. No. 4.5e+02;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 674

CN546416/c

LOCUS

DEFINITION CN546416 35 bp mRNA linear EST 30-APR-2004
 CDNA clone B3CS1XGB016G05 3', mRNA sequence.

ACCESSION CN546416

VERSION

KEYWORDS

SOURCE

ORGANISM

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

1 (bases 1 to 35)

Abbal,P., Agasse,A., Agorces,A., Atanassova,R., Barrieu,F.,

Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,

Hamdi,S., Ronieu,C. and Terrier,N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

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France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..35

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS1XGB016G05"

/dev_stage="green stage"

/clone_lib="Green Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28.4; DB 1; Length 35;

Best Local Similarity 96.7%; Pred. No. 4.5e+02;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 675

CN546519/c

LOCUS

DEFINITION CN546519 35 bp mRNA linear EST 30-APR-2004
 CDNA clone B3CS57RB007H07 3', mRNA sequence.

ACCESSION CN546519

VERSION

KEYWORDS

SOURCE

ORGANISM

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

1 (bases 1 to 35)

Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,

Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,

Hamdi,S., Ronieu,C. and Terrier,N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

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France

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Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..35

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS57RB007H07"

/dev_stage="ripe stage"

/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28.4; DB 1; Length 35;

Best Local Similarity 96.7%; Pred. No. 4.5e+02;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 676

CN546666/c

LOCUS

DEFINITION CN546666 35 bp mRNA linear EST 30-APR-2004
 vifera CDNA clone B3CS37TB007E01 3', mRNA sequence.

ACCESSION CN546666

VERSION

KEYWORDS

SOURCE

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

1 (bases 1 to 35)

Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,

Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,

Hamdi,S., Ronieu,C. and Terrier,N.

TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7

FEATURES
 source
 1. .35
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CSJ7TB007E01"
 /dev_stage="veraison stage"
 /clone_lib="Turning Grape Berry Lambda Triplex2 Library"
 /notes="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28.4; DB 1; Length 35;
Best Local Similarity 96.7%; Pred. No. 4.5e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
 |||||
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 677
AJ791259/c
LOCUS AJ791259
DEFINITION AJ791259 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018_2_08 d21, mRNA sequence.
ACCESSION AJ791259
VERSION AJ791259.1 GI:51061461
KEYWORDS EST.
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Antirrhinum majus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum
REFERENCE 1 (bases 1 to 33)
AUTHORS Bey.M., Stueber.K., Fellenberg.K., Schwarz-Sommer,Z., Sommer.H., Saedler.H. and Zachgo.S.
TITLE Characterization of Antirrhinum Petal Development and Identification of Target Genes of the Class B MADS Box Gene DEFICIENS
JOURNAL Plant Cell 16 (12), 3197-3215 (2004)
PUBLISHED 15539471
COMMENT Contact: Schwarz-Sommer Z
 Molekulare Pflanzen-genetik
 MPI fuer Zuechtungs-forschung
 Carl-von-Linne Weg 10, D-50829, Germany.
 Location/Qualifiers
 1. .33
 /organism="Antirrhinum majus"
 /mol_type="mRNA"
 /db_xref="taxon:4151"
 /clone="018_2_08_d21"
 /tissue_type="whole plant"
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Query Match 1.0%; Score 28.2; DB 1; Length 33;
Best Local Similarity 90.9%; Pred. No. 4.5e+02;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7

FEATURES
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 1. .35
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CSJ7TB007E01"
 /dev_stage="veraison stage"
 /clone_lib="Turning Grape Berry Lambda Triplex2 Library"
 /notes="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28.4; DB 1; Length 35;
Best Local Similarity 96.7%; Pred. No. 4.5e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
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Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 677
AJ791259/c
LOCUS AJ791259
DEFINITION AJ791259 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018_2_08 d21, mRNA sequence.
ACCESSION AJ791259
VERSION AJ791259.1 GI:51061461
KEYWORDS EST.
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Antirrhinum majus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum
REFERENCE 1 (bases 1 to 33)
AUTHORS Bey.M., Stueber.K., Fellenberg.K., Schwarz-Sommer,Z., Sommer.H., Saedler.H. and Zachgo.S.
TITLE Characterization of Antirrhinum Petal Development and Identification of Target Genes of the Class B MADS Box Gene DEFICIENS
JOURNAL Plant Cell 16 (12), 3197-3215 (2004)
PUBLISHED 15539471
COMMENT Contact: Schwarz-Sommer Z
 Molekulare Pflanzen-genetik
 MPI fuer Zuechtungs-forschung
 Carl-von-Linne Weg 10, D-50829, Germany.
 Location/Qualifiers
 1. .33
 /organism="Antirrhinum majus"
 /mol_type="mRNA"
 /db_xref="taxon:4151"
 /clone="018_2_08_d21"
 /tissue_type="whole plant"
 /clone_lib="Antirrhinum majus whole plant"

Query Match 1.0%; Score 28.2; DB 1; Length 33;
Best Local Similarity 90.9%; Pred. No. 4.5e+02;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7

FEATURES
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 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CSJ7TB007E01"
 /dev_stage="veraison stage"
 /clone_lib="Turning Grape Berry Lambda Triplex2 Library"
 /notes="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28.4; DB 1; Length 35;
Best Local Similarity 96.7%; Pred. No. 4.5e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
 |||||
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 677
AJ791259/c
LOCUS AJ791259
DEFINITION AJ791259 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018_2_08 d21, mRNA sequence.
ACCESSION AJ791259
VERSION AJ791259.1 GI:51061461
KEYWORDS EST.
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Antirrhinum majus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum
REFERENCE 1 (bases 1 to 33)
AUTHORS Bey.M., Stueber.K., Fellenberg.K., Schwarz-Sommer,Z., Sommer.H., Saedler.H. and Zachgo.S.
TITLE Characterization of Antirrhinum Petal Development and Identification of Target Genes of the Class B MADS Box Gene DEFICIENS
JOURNAL Plant Cell 16 (12), 3197-3215 (2004)
PUBLISHED 15539471
COMMENT Contact: Schwarz-Sommer Z
 Molekulare Pflanzen-genetik
 MPI fuer Zuechtungs-forschung
 Carl-von-Linne Weg 10, D-50829, Germany.
 Location/Qualifiers
 1. .33
 /organism="Antirrhinum majus"
 /mol_type="mRNA"
 /db_xref="taxon:4151"
 /clone="018_2_08_d21"
 /tissue_type="whole plant"
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Query Match 1.0%; Score 28.2; DB 1; Length 33;
Best Local Similarity 90.9%; Pred. No. 4.5e+02;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
 |||||
Db 33 CCAAAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 678
CF335736/c
LOCUS CF335736
DEFINITION CF335736 33 bp mRNA linear EST 18-AUG-2003
 JMT--05-I12.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--05-I12, mRNA sequence.
ACCESSION CF335736
VERSION CF335736.1 GI:33819839
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 33)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1. .33
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--05-I12"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 1.0%; Score 28.2; DB 1; Length 33;
Best Local Similarity 90.9%; Pred. No. 4.5e+02;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
 |||||
Db 33 AAAAAAAAAAACCAACCAAAAAAAAAAAAAAAAAA 1

RESULT 679
CZ919845
LOCUS CZ919845
DEFINITION CZ919845 33 bp DNA linear GSS 08-AUG-2005
 4021015A06.2EL y1 4021 - RescueMu Grid V Zea mays genomic survey sequence.
ACCESSION CZ919845
VERSION CZ919845.1 GI:71940731
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 33)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon

and Dixon, L.
Development of a porcine cDNA microarray
Unpublished (2004)
Contact: Hopwood PA
Dept. of Preclinical Veterinary Sciences
Royal School for Veterinary Studies
Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM
Sequencing was performed by ARK Genomics. This clone is available
from ARK- Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS,
UK. See www.ark-genomics.org or contact info@arkgenomics.org.

FEATURES
source
1. .35
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001822c_A11"
/tissue_type="muscle"
/cell_type="macrophage"
/clone_lib="muscle - muscle minus alveolar macrophage"

Query Match 1.0%; Score 28.2; DB 1; Length 35;
Best Local Similarity 90.9%; Pred. No. 4.6e+02;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2701 TTGTACTAAAAA 28 bp mRNA linear EST 28-JUN-2004
||||| 2733
Db 33 TTTTITTTTAAAAA 1

RESULT 683
AJ666435/c
LOCUS
DEFINITION
AJ666435 CSEQRAN09 Sus scrofa cDNA clone C0000033_L21, mRNA
sequence.
ACCESSION
AJ666435
VERSION
AJ666435.1 GI:49350886
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE
1 (bases 1 to 28)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector: pBluescriptII(KS+) R. Site.1:
EcoRI R. Site.2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
source
1. .28
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_L21"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAA 28 bp mRNA linear EST 11-AUG-2005
||||| 2736
Db 28 AAAAAAAAAA 1

RESULT 684
AM043789/c
LOCUS
DEFINITION
AM043789 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC19g02.q1k, mRNA sequence.
ACCESSION
AM043789
VERSION
AM043789.1 GI:72291602
KEYWORDS
EST.
SOURCE
Schistosoma mansoni
ORGANISM
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 28)
Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.,
Nikolaïdou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
source
1. .28
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC19g02.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAA 28 bp mRNA linear EST 11-AUG-2005
||||| 2736
Db 28 AAAAAAAAAA 1

RESULT 685
AM043903/c
LOCUS
DEFINITION
AM043903 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC19b04.q1k, mRNA sequence.
ACCESSION
AM043903
VERSION
AM043903.1 GI:72292227
KEYWORDS
EST.
SOURCE
Schistosoma mansoni
ORGANISM
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 28)
Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.,
Nikolaïdou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
source
1. .28
/organism="Schistosoma mansoni"
/mol_type="mRNA"


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/db_xref="taxon:6183"
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/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="country: Puerto Rico"

Query Match      1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
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Db  28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 686
AM043968
LOCUS      28 bp mRNA linear EST 11-AUG-2005
DEFINITION
  AM043968 Schistosoma mansoni lung schistosomulum Schistosoma
  mansoni cDNA clone SmlC20h11.q1k, mRNA sequence.
ACCESSION
  AM043968
VERSION
  AM043968.1 GI:72292357
KEYWORDS
  EST.
SOURCE
  Schistosoma mansoni
  Schistosoma mansoni
  Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
  Strigeida; Schistosomatidae; Schistosomatidae; Schistosoma.
  1 (bases 1 to 28)
AUTHORS
  Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
  Nikolaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE
  Microarray analysis identifies genes preferentially expressed in
  the lung schistosomulum of Schistosoma mansoni
JOURNAL
  Unpublished (2005)
COMMENT
  Contact: Ivens AC
  Pathogen Microarrays Group
  Wellcome Trust Sanger Institute
  Hinxton, CB10 1SA, UNITED KINGDOM.
  Location/Qualifiers
  1..28
  /organism="Schistosoma mansoni"
  /mol_type="mRNA"
  /db_xref="taxon:6183"
  /clone="SmIC20h11.q1k"
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  /clone_lib="Schistosoma mansoni lung schistosomulum"
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FEATURES
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Query Match      1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
      |||||||
Db  1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 687
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LOCUS      28 bp mRNA linear EST 20-SEP-2005
DEFINITION
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  mansoni cDNA clone SmlC28d06.q1k, mRNA sequence.
ACCESSION
  AM044512
VERSION
  AM044512.1 GI:75966804
KEYWORDS
  EST.
SOURCE
  Schistosoma mansoni
  Schistosoma mansoni
  Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
  Strigeida; Schistosomatidae; Schistosomatidae; Schistosoma.
  1 (bases 1 to 28)
AUTHORS
  Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
  Nikolaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE
  Microarray analysis identifies genes preferentially expressed in
  the lung schistosomulum of Schistosoma mansoni

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JOURNAL      Unpublished (2005)
COMMENT
  Contact: Ivens AC
  Pathogen Microarrays Group
  Wellcome Trust Sanger Institute
  Hinxton, CB10 1SA, UNITED KINGDOM.
  Location/Qualifiers
  1..28
  /organism="Schistosoma mansoni"
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  /dev_stage="lung schistosomulum"
  /clone_lib="Schistosoma mansoni lung schistosomulum"
  /note="country: Puerto Rico"

Query Match      1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
      |||||||
Db  28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 688
CF282351/c
LOCUS      28 bp mRNA linear EST 14-AUG-2003
DEFINITION
  14ETL--09-N05.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
  Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-N05,
  mRNA sequence.
ACCESSION
  CF282351
VERSION
  CF282351.1 GI:33659738
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 28)
REFERENCE
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
JOURNAL
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
  1..28
  /organism="Oryza sativa (japonica cultivar-group)"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:39947"
  /clone="14ETL--09-N05"
  /tissue_type="leaf"
  /dev_stage="14 days after germination"
  /lab_hosts="E.coli DH10B"
  /clone_lib="Rice etiolated leaf plasmid cDNA library
  (14ETL)"
  /note="vector: pCR4-TOP0; Site 1: EcoRI; mRNA was capped
  with oligoribonucleotides and then used as templates for
  RT-PCR."

Query Match      1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
      |||||||
Db  28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 689
CF321885/c

LOCUS
DEFINITION

CF321885 28 bp mRNA linear EST 15-AUG-2003
HD--13-E16-g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--13-E16, mRNA sequence.

ACCESSION
VERSION

CF321885.1 GI:33693646

SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 28)

REFERENCE
AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE
JOURNAL

Large-scale Sequencing Analysis of Rice ESTs

COMMENT

Unpublished (2003)
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Contact: Nahm B.H.

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1..28
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--13-E16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match

Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736

Db

28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 690
CF330748/c

LOCUS
DEFINITION

CF330748 28 bp mRNA linear EST 18-AUG-2003
NACL--06-J14.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--06-J14, mRNA
sequence.

ACCESSION
VERSION

CF330748.1 GI:33809717

SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 28)

REFERENCE
AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL
COMMENT

Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1..28
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--06-J14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match

Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736

Db

28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 691
CF330938

LOCUS

DEFINITION

CF330938 28 bp mRNA linear EST 18-AUG-2003
NACL--06-N19.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--06-N19, mRNA
sequence.

ACCESSION
VERSION

CF330938

KEYWORDS
SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 28)

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE
JOURNAL

Large-scale Sequencing Analysis of Rice ESTs

COMMENT

Unpublished (2003)
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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1..28
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--06-N19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

The library was size-fractionated to enrich for large inserts."

Query Match 1.0%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. NO. 4.2e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 695
 AZ399637/c
 LOCUS
 DEFINITION
 AZ399637
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0165 row: N column: 04
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 /clone="UUGC1M0165N04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into

FEATURES
 source

chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. NO. 4.2e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 696
 AZ401766
 LOCUS
 DEFINITION
 AZ401766
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
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 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0168 row: O column: 08
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0168O08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
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 (http://www.jax.org/resources/documents/dnares/). The DNA
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 inducible derivative of plasmid R1. The vector was ligated
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FEATURES
 source

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
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 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 697
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 LOCUS AZ471744 28 bp DNA linear GSS 04-OCT-2000
 DEFINITION IM0286K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0286K08 R, genomic survey sequence.
 ACCESSION AZ471744
 VERSION AZ471744.1 GI:10629965
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0286 row: K column: 08
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
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 /organism="Mus musculus"
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0286K08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

FEATURES
 source

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
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 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 698
 AZ493138
 LOCUS AZ493138 28 bp DNA linear GSS 05-OCT-2000
 DEFINITION IM0327F02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0327F02 R, genomic survey sequence.
 ACCESSION AZ493138
 VERSION AZ493138.1 GI:10666359
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0327 row: F column: 02
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 High quality sequence stop: 28.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0327F02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

FEATURES
 source

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 699
AZ653365/c
LOCUS
DEFINITION
28 bp DNA linear GSS 14-DEC-2000
1M0527E02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0527E02 F, genomic survey sequence.

ACCESSION
AZ653365
VERSION
GI:11790511

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhauser,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0527 row: E column: 02

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"

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/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0527E02"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

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inducible derivative of plasmid R1. The vector was ligated

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chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 700
AZ785035/c

LOCUS

DEFINITION

28 bp DNA linear GSS 16-FEB-2001

2M0028J01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0028J01 R, genomic survey sequence.

ACCESSION

AZ785035

VERSION

AZ785035.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 28)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D.,Weiss,R.

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Unpublished (2000)

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0028 row: J column: 01

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

1..28

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0028J01"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

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inducible derivative of plasmid R1. The vector was ligated

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adaptored vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 701
A2824519/c
LOCUS
DEFINITION 28 bp DNA linear GSS 20-FEB-2001
clone UUGC2M0099109 F, genomic survey sequence.

ACCESSION A2824519
VERSION A2824519.1 GI:12994427

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 28)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0039 row: I column: 09

Seq primer: CTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0099109"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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adaptored vector DNA, and transformed into

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and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 702

A2833425

LOCUS

DEFINITION 28 bp DNA linear GSS 20-FEB-2001
clone UUGC2M0115D04 R, genomic survey sequence.

ACCESSION A2833425

VERSION A2833425.1 GI:13003333

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 28)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0115 row: D column: 04

Seq primer: CACACAGGAACACCTATGACC

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

FEATURES

source

1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0115D04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
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Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 703
AZ866569/c
LOCUS
DEFINITION 28 bp DNA linear GSS 21-FEB-2001
clone UUGC2M0177B08 F, genomic survey sequence.

ACCESSION AZ866569
VERSION
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 28)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0177 row: B column: 08

Seq primer: CGTGTAAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

FEATURES

source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0177B08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 704
CZ912316/c

LOCUS
DEFINITION 28 bp DNA linear GSS 08-AUG-2005
4012010A02.1EL_Y1 4012 - RescueMu Grid BB Zea mays genomic, genomic
survey sequence.

ACCESSION CZ912316
VERSION
KEYWORDS
SOURCE GSS.
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 28)

AUTHORS Walbot,V.

TITLE Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)

JOURNAL Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4012010 row: A column: 02

Class: transposon-tagged.

FEATURES

source

1..28
/organism="Zea mays"
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/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4012 - RescueMu Grid BB"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.utransposon.org/project/RescueMu/'. Grid
BB was grown at UC Berkeley in 2001. DNA was extracted
from leaf strips, double digested using BamHI and BglII,
and ligated to form circular plasmids. DH10B cells were
transformed and then screened on LB plates with
ampicillin."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 705

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CZ913960
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DEFINITION  4013005A02.1EL_x1 4013 - RescuedMu Grid O Zea mays genomic, genomic
survey sequence.
ACCESSION  CZ913960
VERSION    CZ913960.1  GI:71930279
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 28)
AUTHORS   Walbot V.
TITLE     Maize genomic sequences found using engineered RescuedMu transposon
JOURNAL   Unpublished (2001)
COMMENT   Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Very probable ligation site of ends cut by single endonuclease.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 4013005 row: A column: 02
            Class: transposon-tagged.
            Location/Qualifiers
                1..28
                /organism="Zea mays"
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                /tissue_type="leaf"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="4013 - RescuedMu Grid O"
                /note="Organ: leaf; Vector: RescuedMu (engineered from
                pBluescript backbone); Site_1: BamHI; Site_2: BglII;
                RescuedMu is a 4.9 kb, modified maize transposon
                designed to allow plasmid rescue from total genomic DNA.
                Mu elements insert preferentially into transcription
                units. For more information on RescuedMu, go to the web
                site 'http://www.mutransposon.org/project/RescuedMu/'. Grid
                O was grown at Stanford in 2001. DNA was extracted from
                leaf strips, double digested using BamHI and BglII, and
                ligated to form circular plasmids. DH10B cells were
                transformed and then screened on LB plates with
                ampicillin."

FEATURES             source
    source
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        Best Local Similarity 100.0%; Pred. No. 4.2e+02;
        Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db  1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 706
DU828712/c
LOCUS       DU828712                28 bp    DNA    linear    GSS 22-DEC-2005
DEFINITION  KBrS003K05R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS003K05, genomic survey
sequence.
ACCESSION  DU828712
VERSION    DU828712.1  GI:83865308
KEYWORDS   GSS.
SOURCE     Brassica rapa subsp. pekinensis
ORGANISM   Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 28)
AUTHORS   Yang T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J. H. and Park,B.S.
TITLE     End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL   Unpublished (2005)
COMMENT   Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1672
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
            KBrS016F07
            Seq primer: T7
            Class: BAC ends.
            Location/Qualifiers
                1..28

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db  1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 707
DU835260
LOCUS       DU835260                28 bp    DNA    linear    GSS 22-DEC-2005
DEFINITION  KBrS016F07F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS016F07, genomic survey
sequence.
ACCESSION  DU835260
VERSION    DU835260.1  GI:83871856
KEYWORDS   GSS.
SOURCE     Brassica rapa subsp. pekinensis
ORGANISM   Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 28)
AUTHORS   Yang T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J. H. and Park,B.S.
TITLE     End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL   Unpublished (2005)
COMMENT   Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1672
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
            KBrS016F07
            Seq primer: T7
            Class: BAC ends.
            Location/Qualifiers
                1..28

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REFERENCE
AUTHORS   Yang T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J. H. and Park,B.S.
TITLE     End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL   Unpublished (2005)
COMMENT   Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1672
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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            Class: BAC ends.
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                /lab_host="E. coli DH10B"
                /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
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                available at NIAB."

FEATURES             source
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Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db  28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 707
DU835260
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DEFINITION  KBrS016F07F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS016F07, genomic survey
sequence.
ACCESSION  DU835260
VERSION    DU835260.1  GI:83871856
KEYWORDS   GSS.
SOURCE     Brassica rapa subsp. pekinensis
ORGANISM   Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 28)
AUTHORS   Yang T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J. H. and Park,B.S.
TITLE     End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL   Unpublished (2005)
COMMENT   Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1672
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
            KBrS016F07
            Seq primer: T7
            Class: BAC ends.
            Location/Qualifiers
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/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
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Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 708
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LOCUS KBrS016P17F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016P17, genomic survey sequence.
DEFINITION
ACCESSION DU835584
VERSION DU835584.1 GI:83872180
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 28)
AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBrS016P17
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
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/sub_species="pekinensis"
/db_xref="taxon:51351"
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/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 708
DU835584 28 bp DNA linear GSS 22-DEC-2005
LOCUS KBrS016P17F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016P17, genomic survey sequence.
DEFINITION
ACCESSION DU835584
VERSION DU835584.1 GI:83872180
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 28)
AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBrS016P17
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
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/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 709
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LOCUS KBrS082B24F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS082B24, genomic survey sequence.
DEFINITION
ACCESSION DU835584
VERSION DU835584.1 GI:84766449
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 28)
AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone KBrS082B24
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..28
/organism="Brassica rapa subsp. pekinensis"
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/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS082B24"
/lab_host="E. coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 710
TA291A01Q 28 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 291a01, reverse sequence, genomic survey sequence.
DEFINITION
ACCESSION AL486613
VERSION AL486613.1 GI:11853602
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 28)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submission

```

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@igr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

Location/Qualifiers
1..28
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="291a01"

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28
|||||

RESULT 711
LOCUS TA379D11P 28 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 379d11, forward sequence, genomic survey sequence.

ACCESSION AL497637
VERSION AL497637.1 GI:11873359
KEYWORDS GSS.

SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 28)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@igr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

Location/Qualifiers
1..28
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="379d11"

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||

Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 712
LOCUS CN545883/c

DEFINITION EST 17827 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00RL006A02 3', mRNA sequence.

ACCESSION CN545883
VERSION CN545883.1 GI:46910508
KEYWORDS EST.

SOURCE Vitis vinifera
ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 29)

AUTHORS Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldecamp, F., Delrot, S., Gliseant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: 17.

FEATURES

Location/Qualifiers
1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006A02"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||

Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2
|||||

RESULT 713
LOCUS CZ912823/c

DEFINITION CZ912823 4012012A03.2EL.y1 4012 - Rescued Grid BB Zea mays genomic, genomic survey sequence.

ACCESSION CZ912823
VERSION CZ912823.1 GI:71928421
KEYWORDS GSS.

SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 29)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4012012 row: A column: 03
Class: transposon-tagged.
FEATURES
source
Location/Qualifiers
1..29
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4012 - RescueMu Grid BB"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'.
Gri
BB was grown at UC Berkeley in 2001. DNA was extracted
from leaf strips, double digested using BamHI and BglII,
and ligated to form circular plasmids. DH10B cells were
transformed and then screened on LB plates with
ampicillin."
Query Match 1.0%; Score 28; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 2707 CTAAAAA.....AAAAAAAAAAAAAAAAAAAA 2734
Db 28 CTAAAAA.....AAAAAAAAAAAAAAAAAAAA 1
RESULT 714
CZ914240
LOCUS
DEFINITION
CZ914240 29 bp DNA linear GSS 08-AUG-2001
survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 29)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.

```

Reverse complemented post-ligation sequence from source sequence.
Plate: 4013006 row: B column: 03
Class: transposon-tagged.

FEATURES
source
1..29
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.0%; Score 28; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.3e-02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 715
CN545968/c
LOCUS
DEFINITION
EST 17916 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL007A02 3', mRNA sequence.
CN545968
CN545968.1 GI:46910593
EST.
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedalechamp,F., Delrot,S., Glissant,D., Grimpet,J.,
Hamdi,S., Romeu,C. and Terrier,N
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1..30
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL007A02"
/dev_stage="ripening stage"

FEATURES
source

/clone.lib="Ripe Grape Skin Triplex2 Library"
 /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
 SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred.No. 4.4e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
 |||||
 Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 716
 CN546523 30 bp mRNA linear EST 30-APR-2004
 LOCUS EST 18667 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
 DEFINITION cDNA clone B3CS57RB007H12 3', mRNA sequence.

ACCESSION CN546523
 VERSION CN546523.1 GI:46911148
 KEYWORDS EST.

SOURCE

ORGANISM

Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.

REFERENCE 1. (bases 1 to 30)

AUTHORS

Abbal.P., Agasse.A., Ageorges.A., Atanasova.R., Barrieu.F.,
 Couture.C., Dedaldecamp.F., Delrot.S., Glissant.D., Grimplet,J.,
 Hamdi.S., Romieu.C. and Terrier.N.
 TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages

JOURNAL

Unpublished (2002)

COMMENT

Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES

source

1..30
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS57RB007H12"
 /dev_stages="ripe stage"
 /clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda
 Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred.No. 4.4e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
 |||||
 Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 717
 C2919540 30 bp DNA linear GSS 08-AUG-2005
 LOCUS C2919540
 DEFINITION 4021013F10.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic
 survey sequence.

ACCESSION C2919540
 VERSION C2919540.1 GI:71940164
 KEYWORDS GSS.

SOURCE

Zea mays

ORGANISM

Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1. (bases 1 to 30)

AUTHORS

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered RescueMu transposon
 Walbot,V.
 Unpublished (2001)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 4021013 row: F column: 10
 Class: transposon-tagged.

Location/Qualifiers

source

1..30
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lib_host="DH10B"
 /clone_lib="4021 - RescueMu Grid V"
 /note="Organ: leaf; Vector: RescueMu (engineered from
 pBluescript backbone); Site 1: BamHI; Site 2: BglII;
 RescueMu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on RescueMu, go to the web
 site 'http://www.mutransposon.org/project/RescueMu/'. Grid
 V was grown at University of Arizona in 2003. DNA was
 extracted from leaf strips, double digested using BamHI
 and BglII, and ligated to form circular plasmids. DH10B
 cells were transformed and then screened on LB plates with
 ampicillin."

Query Match 1.0%; Score 28; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred.No. 4.4e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 718
 AW245279/c 31 bp mRNA linear EST 07-JAN-2000
 LOCUS AW245279
 DEFINITION 2820044.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820044 3',
 mRNA sequence.

ACCESSION AW245279

VERSION AW245279.1 GI:6588272

KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1. (bases 1 to 31)

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs: 2820044.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project
 Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center
 PHRED: cross match from University of Washington Genome Center
 TRIMMING: Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu/LowQuality> Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 31 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
 Plate: LLCM3 row: C column: 21.
 Location/Qualifiers

FEATURES

source

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1. .31
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820044"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match 1.0%; Score 28; DB 1; Length 31;
 Best Local Similarity 90.3%; Pred. No. 4.5e+02;
 Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
 |||||
 Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 719

CV057897

LOCUS
 DEFINITION CV057897 31 bp mRNA linear EST 24-AUG-2004
 BNEL32a8 Barley EST endospERM library Hordeum vulgare subsp. vulgare cDNA clone BNEL32a8 5' similar to Unknown Function, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade; Poideae; Triticeae; Hordeum.

REFERENCE

AUTHORS

Ali S. Holloway, B. and Taylor, W.C.
 Normalisation of cereal endospERM EST libraries for structural and functional genomic analysis

JOURNAL

COMMENT

Plant Mol. Biol. Rep. 18, 123-132 (2000)
 Contact: Bill Taylor
 Commonwealth Scientific and Industrial Research Organisation
 Division of Plant Industry
 CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
 Tel: 61 2 6246 5223
 Fax: 61 2 6246 5000
 Email: Bill.Taylor@csiro.au
 Seq primer: M13 reverse primer
 High quality sequence stop: 31.
 Location/Qualifiers

FEATURES

source

```

1. .31
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820044"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
```

```

/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Himalaya"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="BNEL32a8"
/tissue_type="endospERM"
/dev_stage="developing endospERM tissue 10, 12, 15 dpa (days post anthesis)"
/lab_host="DH10B (Life Technology)"
/clone_lib="Barley EST endospERM library"
/note="Vector: ZipLox; Site 1: Sal I; Site 2: Not I; mRNA was prepared from endospERM tissues of the barley cultivar Himalaya. cDNA was synthesised from pooled 10, 12, and 15 dpa endospERM using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of ZipLox vector (Life Technology) after adding a Sal I-Xho I adaptor (Stratagene). Constructed by Shanjahan Ali and Bill Taylor."
```

Query Match 1.0%; Score 28; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 720

AM046790

LOCUS

DEFINITION AM046790 32 bp mRNA linear EST 11-AUG-2005
 mansoni cDNA clone SmlC27e08.q1k, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Schistosoma mansoni
 Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidae; Schistosomatoidea; Schistosomidae; Schistosoma.

REFERENCE

AUTHORS

Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
 Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
 Unpublished (2005)

JOURNAL

COMMENT

Contact: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES

source

```

1. .32
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC27e08.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="Country: Puerto Rico"
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Query Match 1.0%; Score 28; DB 1; Length 32;
 Best Local Similarity 96.6%; Pred. No. 4.5e+02;
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 721

CD577661

LOCUS

CD577661 32 bp mRNA linear EST 15-JUN-2004


```

DEFINITION Iqori.A02.Q3.007 ESTs from wild-caught Anopheles funestus
populations Anopheles funestus cDNA 5', mRNA sequence.
ACCESSION CD577661.1 GI:48718676
VERSION CD577661.1 GI:48718676
KEYWORDS EST.
SOURCE Anopheles funestus
ORGANISM Anopheles funestus
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
REFERENCE 1 (bases 1 to 32)
AUTHORS Besansky,N.J., Serazin,A.C. and Dana,A.
TITLE Towards the transcriptome of Anopheles funestus: a molecular
snapshot
JOURNAL Unpublished (2003)
COMMENT Contact: Andrew Serazin
Collins/Besansky Lab
Center for Tropical Disease Research and Training, University of
Notre Dame
317 Galvin Life Science, Notre Dame, IN 46556, USA
Tel: 5746319321
Email: nbesansk@nd.edu
These sequences may be of either nuclear or mitochondrial origin.
FEATURES
Location/Qualifiers
1..32
/organism="Anopheles funestus"
/mol_type="mRNA"
/strain="West African"
/db_xref="taxon:62324"
/sex="male and female"
/dev_stage="embryo, larvae, pupae, and adult"
/clone_lib="ESTs from wild-caught Anopheles funestus
populations"
/note="Vector: LambdaTriplex2"

Query Match 1.0%; Score 28; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 722
AZ397471 32 bp DNA linear GSS 03-OCT-2000
LOCUS IM0162P23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0162P23 F, genomic survey sequence.
ACCESSION AZ397471
VERSION AZ397471
KEYWORDS GSS.
SOURCE AZ397471.1 GI:10512543
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Mammalogathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 32)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

```

```

Insert Length: 10000 Std Error: 0.00
Plate: 0162 row: P column: 23
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0162P23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (G14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 723
AV743346 33 bp mRNA linear EST 17-OCT-2000
LOCUS AV743346 CB Homo sapiens cDNA clone CEMABD12 5', mRNA sequence.
DEFINITION AV743346
ACCESSION AV743346
VERSION AV743346.1 GI:10860927
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 33)
AUTHORS Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
Chen,S., Mao,M. and Chen,Z.
TITLE Homo sapiens CB library cDNA clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mbshi@ms.stn.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
FEATURES
Location/Qualifiers
1..33

```

```

insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match          1.0%; Score 27.8; DB 1; Length 31;
Best Local Similarity 93.5%; Pred. No. 4.6e+02;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 AAAAAAAAACAAAAAAAAAAAAAAAAAACAAAAAAAAAAAA 1

RESULT 725
LOCUS CX014884
DEFINITION io77d03.g1 Whole Heart Library (DOEST5) Canis familiaris cDNA,
mRNA sequence.
ACCESSION CX014884
VERSION CX014884.1 GI:56397295
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 31)
AUTHORS Ballija,V.S., Nascimento L.U. and McCombie,W.R.
TITLE ESTs from Canis familiaris whole heart (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org.

FEATURES
source
    1..31
        /organism="Canis familiaris"
        /mol_type="mRNA"
        /db_xref="taxon:9615"
        /sex="Unknown"
        /dev_stage="3 month old normal canine"
        /lab_host="XL10 Gold"
        /clone_lib="Whole Heart Library (DOEST5)"
        /note="Organ: Heart; Vector: pBluescript II SK; Site: 1:
        EcoRI; Site 2: XhoI; Library constructed using pBluescript
        XR kit from Stratagene. Cloned cDNA was size selected
        between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
        Medical Genetics, School of Veterinary Medicine,
        University of Pennsylvania, 3800 Spruce Street,
        Philadelphia, PA 19104-6051"

Query Match          1.0%; Score 27.8; DB 1; Length 31;
Best Local Similarity 93.5%; Pred. No. 4.6e+02;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 AAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 726
LOCUS CV727574/c
DEFINITION CV727574
            33 bp mRNA linear EST 04-NOV-2004
            14Salt--05-M13.g1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
            14Salt--05-M13, mRNA sequence.
ACCESSION CV727574
VERSION CV727574.1 GI:55415198
KEYWORDS EST.

```

```

SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..33
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--05-M13"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match 1.0%; Score 27.8; DB 1; Length 33;
Best Local Similarity 93.5%; Pred. No. 4.7e+02;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2705 TACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
| | | | | | | | | | | | | | | | | | | | | |
Db 31 TCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 727
AJ656734 34 bp mRNA linear EST 28-JUN-2004
LOCUS
DEFINITION
AJ656734 KN277 Sus scrofa cDNA clone C0005194_F08, mRNA sequence.
ACCESSION
AJ656734.1 GI:49340766
VERSION
EST.
KEYWORDS
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 34)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
JOURNAL
COMMENT
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBluescriptII(SK+). R. Site1: EcoRI
R. Site2: NotI 5'. Seq Primer M13F Normalised library constructed
from pooled early embryos, from 8- cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,
www.ukargenomics.org.
Location/Qualifiers

FEATURES
source
1..34
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005194_F08"
/tissue_type="embryo"
/clone_lib="KN277"
/notes="Vector: pBluescriptII(SK+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
to blastocysts."
Query Match 1.0%; Score 27.6; DB 1; Length 34;
Best Local Similarity 88.2%; Pred. No. 4.9e+02;
Matches 30; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TAAAAAATTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 728
BQ594010/c
LOCUS
DEFINITION
BQ594010 BQ12759-024-025-L15-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-025-L15 5-PRIME, mRNA sequence.
ACCESSION
BQ594010
VERSION
BQ594010.1 GI:26123593
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 34)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 34 Std Error: 0.00
Plate: 25 row: L column: 15
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers

FEATURES
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1..34
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:192840"
/db_xref="taxon:161934"
/clone="024-025-L15"
/tissue_type="developing root"
/lab_host="EMDH108"
/clone_lib="MP1Z-ADIS-024-developing root"
/notes="Vector: pCMVSPORT6; Site1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

```

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Query Match      1.0%; Score 27.6; DB 1; Length 34;
Best Local Similarity 88.2%; Pred. No. 4.9e+02;
Matches 30; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
DB 34 AAAAAAAAAAGGGGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 729
BQ590537/c
LOCUS
DEFINITION
29 bp mRNA linear EST 06-DEC-2002
CDNA clone 024-019-C03-T7 MP1Z-ADIS-024-storage root Beta vulgaris
BQ590537
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Beta vulgaris

REFERENCE
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
1 (bases 1 to 29)
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert length: 29 Std Error: 0.00
Plate: 19 row: C column: 03
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES
source
1..29
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189579"
/db_xref="taxon:161934"
/clone="024-019-C03"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwiltener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.0%; Score 27.4; DB 1; Length 29;
Best Local Similarity 96.6%; Pred. No. 4.7e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
DB 29 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 730
BQ590537/c
LOCUS
DEFINITION
29 bp mRNA linear EST 30-APR-2004
CDNA clone B3CS00GL004F12 3', mRNA sequence.
BQ590537
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera

REFERENCE
AUTHORS
Abbal,P., Agasse,A., Agasse,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaidechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
1 (bases 1 to 29)
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
PUBMED
Unpublished (2002)
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche

Query Match      1.0%; Score 27.4; DB 1; Length 29;
Best Local Similarity 96.6%; Pred. No. 4.7e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
DB 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 731
CN545616/c
LOCUS
DEFINITION
29 bp mRNA linear EST 30-APR-2004
CDNA clone B3CS00RU004B01 3', mRNA sequence.
CN545616
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera

REFERENCE
AUTHORS
Abbal,P., Agasse,A., Agasse,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaidechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
1 (bases 1 to 29)
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
PUBMED
Unpublished (2002)
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche

```

Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES

Location/Qualifiers

1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL004B01"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 27.4; DB 1; Length 29;

Best Local Similarity 96.6%; Pred. No. 4.7e+02; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTAACAAAAA 2735

Db 29 CCAAAAAAAAAA 1

RESULT 732

CN546518/c

LOCUS

DEFINITION EST 18662 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera

CDNA clone B3CS57RB007H06 3', mRNA sequence.

CN546518

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 29)

AUTHORS Abbal P., Agase A., Ageorges A., Atanassova, R., Barrieu, F.,

Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,

Hamdi, S., Komieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,

France

Tel: 00-33- (0)5-57-12-25-50

Fax: 00-33- (0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

FEATURES

source

Location/Qualifiers

1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007H06"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 27.4; DB 1; Length 29;

Best Local Similarity 96.6%; Pred. No. 4.7e+02; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAA 2737

Db 29 AAAAAAAAAA 1

RESULT 733

AZ825156

LOCUS

DEFINITION

clone UUGC2M0100N08 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0100 row: N column: 08

Seq primer: CGTTGTTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

1..29

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0100N08"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi4732114|gb|AF129072.1) a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.0%; Score 27.4; DB 1; Length 29;

Best Local Similarity 96.6%; Pred. No. 4.7e+02;

Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

VERSION	D0834266.1	GI:83870862
KEYWORDS	GSS.	
SOURCE	Brassica rapa subsp. pekinensis	
ORGANISM	Brassica rapa subsp. pekinensis	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.	
AUTHORS	1 (bases 1 to 29) Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S.	
TITLE	End sequence of Brassica rapa Sau3AI (KBrS) BAC clone	
JOURNAL	Unpublished (2005)	
COMMENT	Contact: Beom-Seok Park Brassica Genomics Team National Institute of Agricultural Biotechnology 225 Seodun-Dong, Suwon, 441-707, Korea Tel: +82-31-299-1670 Fax: +82-31-299-1672 Email: pbeom@da.wo.kr BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBrS013N05	
FEATURES	Seq primer: T7 Class: BAC ends.	
source	Location/Qualifiers	
	1..29	
	/organism="Brassica rapa subsp. pekinensis"	
	/mol_type="genomic DNA"	
	/cultivar="Chiifu"	
	/sub_species="pekinensis"	
	/db_xref="taxon:51351"	
	/clone="KBrS013N05"	
	/lab_host="E. coli DH10B"	
	/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"	
	/note="Vector: pCUGTBAC1; site_1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."	
Query Match	1.0%;	Score 27.4; DB 1; Length 29;
Best Local Similarity	96.6%;	Pred. No. 4.7e+02;
Matches	28; Conservative	0; Mismatches 1; Indels 0; Gaps 0
Qy	2709	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db	29	AAAAAAAAAAAAAAAAAAAAAAAAATATA 1
RESULT 736		
AL038672		
LOCUS	AL038672	30 bp mRNA linear EST 06-JUL-2000
DEFINITION	DKFZ566J1346_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone	
ACCESSION	AL038672	
VERSION	AL038672.1	GI:49682180
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 30)	
AUTHORS	Ottewaelde, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wlemann, S.	
TITLE	EST (Ottewaelde, et al.)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: MIPS	
FEATURES	MIPS	
source	Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.	
	Location/Qualifiers	
	1..30	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	

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/clone="DKFZp566J1346"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 1.0%; Score 27.4; DB 1; Length 30;
Best Local Similarity 96.6%; Pred. No. 4.8e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db 2 TAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAA 30

RESULT 737
LOCUS AU267300 30 bp mRNA linear EST 26-APR-2004
DEFINITION AU267300 VS Dictyostellium discoideum cDNA clone VSH345 5', mRNA
sequence.
ACCESSION AU267300
VERSION AU267300.1 GI:20526098
KEYWORDS EST.
SOURCE Dictyostellium discoideum
ORGANISM Dictyostellium discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
REFERENCE 1 (bases 1 to 30)
AUTHORS Urushihara,H., Morio,T., Saito,T., Kohara,Y., Koriki,E., Ochial,H.,
Maeda,M., Williams,J.G., Takeuchi,I. and Tanaka,Y.
TITLE Analyses of cDNAs from growth and slug stages of Dictyostellium
discoideum
JOURNAL Nucleic Acids Res. 32 (5), 1647-1653 (2004)
PUBMED 15010511
CONTACT: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES
source
Location/Qualifiers
1..30
/organism="Dictyostellium discoideum"
/mol_type="mRNA"
/strains="AX4"
/db_xref="taxon:44689"
/clone="VSH345"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 1.0%; Score 27.4; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAATNAAAAAAAAA 30

RESULT 738
CN546316/c
LOCUS CN546316 30 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18268 Green Grape Berry Lambda Triplex2 Library vitis vinifera
cDNA clone B3CS1XGB015F11 3', mRNA sequence.
ACCESSION CN546316
VERSION CN546316.1 GI:46910941
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

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```

rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS1XGB015F11"
/dev_stage="green stage"
/clone_lib="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiI; Site_2: SfiI; Oriented library"

Query Match 1.0%; Score 27.4; DB 1; Length 30;
Best Local Similarity 96.6%; Pred. No. 4.8e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 739
DR31A1ST 30 bp DNA linear GSS 22-NOV-2002
LOCUS DR31A1ST
DEFINITION Danio rerio genomic clone DKEY-31A15, genomic survey sequence.
ACCESSION AL987581
VERSION AL987581.1 GI:25176586
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 30)
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-31A15"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"

Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES
source
Location/Qualifiers
1..30
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-31A15"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"

Query Match 1.0%; Score 27.4; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

REFERENCE
AUTHORS
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Ronieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
Location/Qualifiers
1..30
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS1XGB015F11"
/dev_stage="green stage"
/clone_lib="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiI; Site_2: SfiI; Oriented library"

Query Match 1.0%; Score 27.4; DB 1; Length 30;
Best Local Similarity 96.6%; Pred. No. 4.8e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 739
DR31A1ST 30 bp DNA linear GSS 22-NOV-2002
LOCUS DR31A1ST
DEFINITION Danio rerio genomic clone DKEY-31A15, genomic survey sequence.
ACCESSION AL987581
VERSION AL987581.1 GI:25176586
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 30)
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-31A15"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"

Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES
source
Location/Qualifiers
1..30
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-31A15"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"

Query Match 1.0%; Score 27.4; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 740
CN545916/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1..31
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006D01"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 27.4; DB 1; Length 31;
Best Local Similarity 96.6%; Pred. No. 4.8e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 31 AAAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 741
AZ759642/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0552 row: E column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1..33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0552E03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 27.4; DB 1; Length 33;
Best Local Similarity 96.6%; Pred. No. 5e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db 32 TAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 742
DN988790/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

DN988790
ZEBRA_2R_2-II_02_ZEBRA_2R_2-II_02_G01.abi Bermuda grass line Zebra
subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone
ZEBRA_2R_2-II_02_ZEBRA_2R_2-II_02_G01.abi, mRNA sequence.
DN988790
Cynodon dactylon (Bermuda grass)
Cynodon dactylon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.
1 (bases 1 to 34)
Melmaiee,K., Elavarthi,S. and Guenzi,A.C.

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 740
CN545916/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

CN545916
EST 17860 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL006D01 3', mRNA sequence.
CN545916
GI:46910541
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 31)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedalchamps,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Tertier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7
Location/Qualifiers
1..31
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006D01"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 27.4; DB 1; Length 31;
Best Local Similarity 96.6%; Pred. No. 4.8e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 31 AAAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 741
AZ759642/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

AZ759642
IM0552E03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0552E03 R, genomic survey sequence.
AZ759642
GI:12866639
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 33)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,

```

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TITLE
Identification of differentially expressed genes associated with
cold acclimation using suppression subtraction hybridization (SSH)
and cDNA microarrays
JOURNAL
Unpublished (2005)
COMMENT
Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405-744-6039
Email: acg@mail.pss.okstate.edu
PCR PRIMERS
FORWARD: M13 forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward
Location/Qualifiers
1. .34
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="Zebra"
/db_xref="taxon:28909"
/clone="ZEBRA_2R_2-II_02_ZEBRA_2R_2-II_02_G01.ab1"
/tissue_type="Crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass line Zebra subtracted cold
acclimated cDNA library"
/notes="Vector: Qisgen's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."

Query Match 1.0%; Score 27.4; DB 1; Length 34;
Best Local Similarity 96.6%; Pred. No. 5.1e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2706 ACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
Db 34 ACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 743
CF298526/c
LOCUS
DEFINITION
32 bp mRNA linear EST 15-AUG-2003
7LEAF--01-P04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--01-P04, mRNA
sequence.
ACCESSION
CF298526
VERSION
CF298526.1 GI:33670287
KEYWORDS
EST.
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.
FEATURES
source
1. .32
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--04-H03"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.0%; Score 27.2; DB 1; Length 32;
Best Local Similarity 90.6%; Pred. No. 5.1e+02;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 32 AAAAAAAAAACATTAAAAAAAAAAAAAAAAA 1

RESULT 745
AW250841/c
LOCUS
DEFINITION
32 bp mRNA linear EST 07-JAN-2000
7LEAF--01-P04.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--04-H03, mRNA sequence.
ACCESSION
CF334956
VERSION
CF334956.1 GI:33818248
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.
FEATURES
source
1. .32
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--04-H03"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

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/clone="7LEAF--01-P04"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 27.2; DB 1; Length 32;
Best Local Similarity 90.6%; Pred. No. 5.1e+02;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 32 AAAAAAAAAACATTAAAAAAAAAAAAAAAAA 1

RESULT 744
CF334956/c
LOCUS
DEFINITION
32 bp mRNA linear EST 18-AUG-2003
JMT--04-H03.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--04-H03, mRNA sequence.
ACCESSION
CF334956
VERSION
CF334956.1 GI:33818248
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.
FEATURES
source
1. .32
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--04-H03"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.0%; Score 27.2; DB 1; Length 32;
Best Local Similarity 90.6%; Pred. No. 5.1e+02;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 32 AAAAAAAAAACATTAAAAAAAAAAAAAAAAA 1

RESULT 745
AW250841/c
LOCUS
DEFINITION
32 bp mRNA linear EST 07-JAN-2000
7LEAF--01-P04.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--04-H03, mRNA sequence.
ACCESSION
CF334956
VERSION
CF334956.1 GI:33818248
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.
FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

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DEFINITION      2821274.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821274 3',
                  mRNA sequence.
ACCESSION      AW250841
VERSION        AW250841.1 GI:6593834
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.
REFERENCE      NIH-MGC http://mgc.nci.nih.gov/
AUTHORS       National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE         Unpublished (1999)
JOURNAL
COMMENT       Other_ESTs: 2821274.5prime
                Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
                Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
                Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
                project Clone distribution: MGC clone distribution information can
                be found through the I.M.A.G.E. Consortium/LNL at:
                www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
                Scores: PHRED from University of Washington Genome Center
                Trimming: cross match from University of Washington Genome Center
                PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
                Drosophila Genome Project. University of Washington Center
                http://www.genome.washington.edu Low Quality Sequence: 32
                contiguous PHRED high quality bases followed vector sequence. Very
                Low Quality Sequence: Trace file contained 32 contiguous distinct
                peaks following vector sequence. Polyadenylation: Based upon the
                presence of a XhoI site followed by a run of 14 or more T residues
                at the beginning of the sequence, this cDNA insert was
                polyadenylated.
                Plate: LLCM6 row: G column: 3
                High quality sequence stop: 32.
FEATURES       Location/Qualifiers
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                /organism="Homo sapiens"
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                /db_xref="taxon:9606"
                /clone="IMAGE:2821274"
                /tissue_type="small cell carcinoma"
                /cell_line="MGC3"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH MGC 7"
                /notes="Organ: lung; Vector: pOTB7; site 1: XhoI; site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
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Query Match      1.0%; Score 27.2; DB 1; Length 32;
Best Local Similarity 90.6%; Pred. No. 5.1e+02;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
      |||
      32 AAAAAAAAAAAAAAAAAATCCAAAAAAAAAAAA 1
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RESULT 746
CZ467504
LOCUS          CZ467504          32 bp  DNA  linear  GSS 29-APR-2005
DEFINITION    c01856-3prime Exelixis piggyBac PB insertions Drosophila
                melanogaster genomic Sequence recovered from 3' end of piggyBac,
                genomic survey sequence.
ACCESSION     CZ467504
VERSION       CZ467504.1 GI:62961517
KEYWORDS      GSS.
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SOURCE          Drosophila melanogaster (fruit fly)
ORGANISM        Drosophila melanogaster
                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 32)
AUTHORS        Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
                Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
                Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
                Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
                Laufer,A., Mazotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
                Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,P.,
                Swimmer,C., Kopczyński,C., Duyk,G., Winberg,W.L. and Margolis,J.
                A complementary transposon tool kit for Drosophila melanogaster
                using P and piggyBac
                Nat. Genet. 36 (3), 283-287 (2004)
JOURNAL         14981521
COMMENT        Contact: Roger A Hoskins
                Berkeley Drosophila Genome Project
                Lawrence Berkeley National Laboratory
                Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
                Tel: 510 486 4015
                Fax: 510 486 6798
                Email: RHoskins@lbl.gov
                Sequence recovery method was inverse PCR.
                Sequence orientation is forward strand relative to 5' end of
                piggyBac element.
                This insertion position is unspecified in the 32 bases.
                The insertion position refers to the first base of the 4 base TTAA
                target recognition sequence.
                Class: transposon insertion site.
                Location/Qualifiers
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                /organism="Drosophila melanogaster"
                /mol_type="genomic DNA"
                /strain="isogenic w- strain"
                /db_xref="taxon:7227"
                /clone_lib="Exelixis piggyBac PB insertions"
                /note="Vector: piggyBac PB (GenBank accession number
                AY515146); An isogenic w- Drosophila melanogaster strain
                was mutagenized by remobilization of transposable
                elements. We remobilized the PB element using
                Hep70:piggyBac transposase from a single ammunition
                element on either the X or third chromosome. We induced
                transposase expression by immersing bottles in a
                circulating 37°C water bath for a daily (days 3-10 after
                egg-laying) 1-h heat shock. We outcrossed the resulting
                dysgenic males to an isogenic w- strain. New insertions
                were identified on the basis of a change in eye color
                (third chromosome ammunition) or the appearance of w+ male
                progeny (X chromosome ammunition). All lines were mapped
                to a chromosome by standard genetic methods, examined for
                homozygous viability, and used for recovery of flanking
                genomic sequence by inverse PCR."
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Query Match      1.0%; Score 27.2; DB 1; Length 32;
Best Local Similarity 90.6%; Pred. No. 5.1e+02;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
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      1 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAAA 32
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RESULT 747
AM048211/c
LOCUS          AM048211          27 bp  mRNA  linear  EST 20-SEP-2005
DEFINITION    AM048211 Schistosoma mansoni lung schistosomulum Schistosoma
                mansoni cDNA clone SmlC29a09.gik, mRNA sequence.
ACCESSION     AM048211
VERSION       AM048211.1 GI:75968183
KEYWORDS      EST.
SOURCE        Schistosoma mansoni
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ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE
AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
FEATURES
source
1. .27
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC29a09.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="country: Puerto Rico"

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 748
CF291968/c
LOCUS CF291968
DEFINITION 14ROOT--02-J21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-J21, mRNA
sequence.
ACCESSION CF291968
VERSION CF291968.1 GI:33661001
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
source
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE
AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
FEATURES
source
1. .27
/organism="Schistosoma mansoni"
/mol_type="mRNA"
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/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="country: Puerto Rico"

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 748
CF291968/c
LOCUS CF291968
DEFINITION 14ROOT--02-J21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-J21, mRNA
sequence.
ACCESSION CF291968
VERSION CF291968.1 GI:33661001
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
source
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE
AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
FEATURES
source
1. .27
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC29a09.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
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Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 750
CF330557/c
LOCUS CF330557
DEFINITION NACL--06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--06-F04, mRNA
sequence.
ACCESSION CF330557
VERSION CF330557.1 GI:33809352
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

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Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 749
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LOCUS CF329725
DEFINITION CF329725 27 bp mRNA linear EST 18-AUG-2003
NACL--05-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--05-C12, mRNA
sequence.
ACCESSION CF329725
VERSION CF329725.1 GI:33807665
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
source
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/mol_type="mRNA"
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RT-PCR."

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 750
CF330557/c
LOCUS CF330557
DEFINITION NACL--06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--06-F04, mRNA
sequence.
ACCESSION CF330557
VERSION CF330557.1 GI:33809352
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

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REFERENCE
 1 (bases 1 to 27)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE
 Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL
 Unpublished (2003)
 COMMENT
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
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 1. .27
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
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 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL-06-F04"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."
 Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 751
 CF335229/c
 LOCUS
 DEFINITION
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 27)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE
 Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL
 Unpublished (2003)
 COMMENT
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
 source
 1. .27
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--04-N08"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid

CDNA library (JMT)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."
 Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 752
 AW327923
 LOCUS
 DEFINITION
 dr02g08.x1 NIH MGC_3 Homo sapiens cDNA clone IMAGE:2847159 5', mRNA
 sequence.
 ACCESSION
 AW327923
 VERSION
 AW327923.1 GI:6798418
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.
 1 (bases 1 to 27)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Edge Biosystems
 CDNA Sequencing by: NIH Intramural Sequencing Center (NISC)
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Plate: LLCM0029 row: M column: 16
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers
 1. .27
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2847159"
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 /clone_lib="NIH_MGC_3"
 /note="Organ: Lymph; Vector: pOTB7a; Library prepared by
 Edge Biosystems."

FEATURES
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 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2847159"
 /tissue_type="Burkitt lymphoma"
 /cell_line="MGC4"
 /clone_lib="NIH_MGC_3"
 /note="Organ: Lymph; Vector: pOTB7a; Library prepared by
 Edge Biosystems."
 Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 753
 CN545326/c
 LOCUS
 DEFINITION
 EST 17270 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
 clone B3CS00GL006G12 3', mRNA sequence.
 ACCESSION
 CN545326
 VERSION
 CN545326.1 GI:46909951
 KEYWORDS
 EST.
 SOURCE
 Vitis vinifera

ORGANISM	Vitis vinifera			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.			
AUTHORS	1 (bases 1 to 27) Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F., Couture,C., Dedaldéchamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.			
TITLE	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Hamdi S. UMR 619 - Equipe Biologie de la Vigne Université de Bordeaux I, Institut National de la Recherche Agronomique 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France Tel: 00-33-(0)5-57-12-25-50 Fax: 00-33-(0)5-57-12-25-48 Email: s.hamdi@bordeaux.inra.fr			
FEATURES	Seq primer: T7.			
source	Location/Qualifiers			
	1..27			
	/organism="Vitis vinifera"			
	/mol_type="mRNA"			
	/cultivar="Cabernet Sauvignon"			
	/db_xref="taxon:29760"			
	/clone="B3CS00GL006G12"			
	/dev_stage="Green stage"			
	/clone_lib="Green Grape Skin Triplex2 Library"			
	/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"			
Query Match	1.0%; Score 27; DB 1; Length 27;			
Best Local Similarity	100.0%; Pred.No. 4.8e+02;			
Matches	27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	2709	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2735	
Db	27	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1	
RESULT 754	CN545492			
LOCUS	EST 17436 Green Grape Skin Triplex2 Library Vitis vinifera CDNA			
DEFINITION	Clone B3CS00GL005G05 3', mRNA sequence.			
ACCESSION	CN545492			
VERSION	CN545492.1 GI:46910117			
KEYWORDS	EST.			
SOURCE	Vitis vinifera			
ORGANISM	Vitis vinifera			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.			
AUTHORS	1 (bases 1 to 27) Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F., Couture,C., Dedaldéchamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.			
TITLE	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Hamdi S. UMR 619 - Equipe Biologie de la Vigne Université de Bordeaux I, Institut National de la Recherche Agronomique 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France Tel: 00-33-(0)5-57-12-25-50 Fax: 00-33-(0)5-57-12-25-48 Email: s.hamdi@bordeaux.inra.fr			
FEATURES	Seq primer: T7.			
	Location/Qualifiers			


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Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
      |||||||
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 759
CN546052/c 27 bp mRNA linear EST 30-APR-2004
LOCUS EST 18004 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
DEFINITION clone B3CS00RL007H09 3', mRNA sequence.
ACCESSION CN546052
VERSION EST
KEYWORDS CN546052.1 GI:46910677
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
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Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
Location/Qualifiers
source 1..27
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS1XGB015C02"
/dev_stage="green stage"
/clone_lib="Green Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
      |||||||
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 761
CN546337/c 27 bp mRNA linear EST 30-APR-2004
LOCUS EST 18289 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION cDNA clone B3CS1XGB015H08 3', mRNA sequence.
ACCESSION CN546337
VERSION EST
KEYWORDS CN546337.1 GI:46910962
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
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Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
Location/Qualifiers
source 1..27
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL007H09"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
      |||||||
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 760
CN546271/c 27 bp mRNA linear EST 30-APR-2004
LOCUS EST 18223 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION cDNA clone B3CS1XGB015C02 3', mRNA sequence.
ACCESSION CN546271
VERSION EST
KEYWORDS CN546271.1 GI:46910896
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.

```

```

TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
JOURNAL or seeds) at Various Developmental Stages
COMMENT Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
Location/Qualifiers
source 1..27
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS1XGB015C02"
/dev_stage="green stage"
/clone_lib="Green Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
      |||||||
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 761
CN546337/c 27 bp mRNA linear EST 30-APR-2004
LOCUS EST 18289 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION cDNA clone B3CS1XGB015H08 3', mRNA sequence.
ACCESSION CN546337
VERSION EST
KEYWORDS CN546337.1 GI:46910962
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
Location/Qualifiers
source 1..27
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/db_xref="taxon:29760"
/clone="B3CS1XGB015H08"
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/clone_lib="Green Grape Berry Lambda Triplex2 Library"

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/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

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Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 762
CN546559/c
LOCUS
DEFINITION
CN546559 27 bp mRNA linear EST 30-APR-2004
CDNA clone B3CS58RB008C12 3', mRNA sequence.
ACCESSION
CN546559
VERSION
CN546559.1 GI:46911184
KEYWORDS
EST.
SOURCE
Vitis vinifera
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE
AUTHORS
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..27
/organism="Vitis vinifera"
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/cultivar="Cabernet Sauvignon"
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Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 764
CN546574/c
LOCUS
DEFINITION
CN546574 27 bp mRNA linear EST 08-JUN-2005
ik79h10.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION
CN546574
VERSION
CN546574.1 GI:67050778
KEYWORDS
EST.
SOURCE
Ginkgo biloba (maidenhair tree)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
REFERENCE
AUTHORS
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE
Expressed tag sequences from Ginkgo female leaf (NYBG)
JOURNAL
Unpublished (2005)
COMMENT
Contact: W. Richard McCombie
Email: mcombie@cshl.org
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..27
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/sex="female"

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Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 763
CN546574/c
LOCUS
DEFINITION
CN546574 27 bp mRNA linear EST 30-APR-2004
CDNA clone B3CS58RB008C12 3', mRNA sequence.
ACCESSION
CN546574
VERSION
CN546574.1 GI:46911199
KEYWORDS
EST.
SOURCE
Vitis vinifera
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE
AUTHORS
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
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France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
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/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58RB008C12"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE
AUTHORS
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hamdi S.
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France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..27
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58RB008C12"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 764
CN546574/c
LOCUS
DEFINITION
CN546574 27 bp mRNA linear EST 08-JUN-2005
ik79h10.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION
CN546574
VERSION
CN546574.1 GI:67050778
KEYWORDS
EST.
SOURCE
Ginkgo biloba (maidenhair tree)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
REFERENCE
AUTHORS
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE
Expressed tag sequences from Ginkgo female leaf (NYBG)
JOURNAL
Unpublished (2005)
COMMENT
Contact: W. Richard McCombie
Email: mcombie@cshl.org
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..27
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"

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/clone.lib="Ginkgo female leaf (NVBG)"
 /note="Organ: leaf; Vector: :pBK-CMV; Site:1: XhoI;
 Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
 The library was size-fractionated to enrich for large
 inserts."

Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
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 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 765
 AZ344642/c
 LOCUS
 DEFINITION 27 bp DNA linear GSS 29-SEP-2000
 clone UUGC1M0078H15 R, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 27)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,W., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0078 row: H column: 15
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends

High quality sequence stop: 27.

FEATURES

source

1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0078H15"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 766
 AZ401672/c

LOCUS
 DEFINITION 27 bp DNA linear GSS 03-OCT-2000
 clone UUGC1M0168K04 R, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS

1 (bases 1 to 27)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0168 row: K column: 04
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends

High quality sequence stop: 27.

FEATURES

source

1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0168K04"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 769
 AZ580921/c
 LOCUS
 DEFINITION 27 bp DNA linear GSS 13-DEC-2000
 clone UUGC1M0369E24 F, genomic survey sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0369 row: E column: 24
 Seq primer: CGTTGTAAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 27.

FEATURES
 source
 1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0369E24"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 770
 AZ616094/c
 LOCUS
 DEFINITION 27 bp DNA linear GSS 13-DEC-2000
 clone UUGC1M0445E17 R, genomic survey sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0445 row: E column: 17
 Seq primer: CACACAGAAACACGTATGACC
 Class: plasmid ends
 High quality sequence stop: 27.

FEATURES
 source
 1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0445E17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
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 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 771
AZ623186/c
LOCUS
DEFINITION
1M0460D12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0460D12 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ623186 27 bp DNA linear GSS 13-DEC-2000
1M0460D12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0460D12 R, genomic survey sequence.

REFERENCE
AUTHORS

1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0460 row: D column: 12

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 27.

FEATURES
source

1. .27
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0460D12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); Was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 772
AZ627847/c
LOCUS
DEFINITION
1M0474011F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474011 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ627847 27 bp DNA linear GSS 13-DEC-2000
1M0474011F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474011 F, genomic survey sequence.

REFERENCE
AUTHORS

1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0474 row: O column: 11

Seq primer: CGTTGTAAACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 27.

FEATURES
source

1. .27
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474011"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); Was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 773
AZ809295
LOCUS 27 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0073B15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0073B15 F, genomic survey sequence.

ACCESSION AZ809295
VERSION AZ809295.1 GI:12975450
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0073 row: B column: 15

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 27.

Location/Qualifiers

1..27

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0073B15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWB42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 774

CZ917070

LOCUS 27 bp DNA linear GSS 08-AUG-2005

DEFINITION 4021004B03.2EL_Y1 4021 - RescueMu Grid V Zea mays genomic, genomic survey sequence.

ACCESSION CZ917070

VERSION CZ917070.1 GI:71935597

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 27)

AUTHORS Walbot,V.

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished (2001)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4021004 row: B column: 03

Class: transposon-tagged.

Location/Qualifiers

1..27

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A189/B73/K55"

/db_xref="taxon:4577"

/tissue type="leaf"

/dev stage="adult"

/lab_host="DH10B"

/clone_lib="4021 - RescueMu Grid V"

/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27


```

RESULT 775
DX046035
LOCUS
DEFINITION
  DX046035
  KBrB047117R KBrB, Brassica rapa BamHI BAC library Brassica rapa
  subsp. pekinensis genomic clone KBrB047117, genomic survey
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 27)
  Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J.H. and Park,B.S.
  End sequence of Brassica rapa BamHI (KBrB) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  Brassica Genomics Team
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
  KBrB047117
  Seq primer: M13 Reverse
  Class: BAC ends.
  Location/Qualifiers
    1..27
    /organism="Brassica rapa subsp. pekinensis"
    /mol_type="genomic DNA"
    /cultivar="Chilfu"
    /sub_species="pekinensis"
    /db_xref="taxon:51351"
    /clone="KBrB047117"
    /lab_host="E.coli DH10B"
    /notes="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
    pekinensis var. Chilfu BAC library (KBrB BAC) is provided
    by Yong-Pyo Lim (CNU)."
FEATURES
  source
    Query Match
    Best Local Similarity 100.0%; Pred. No. 4.8e+02;
    Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 776
DX056021
LOCUS
DEFINITION
  DX056021
  KBrB060M12F KBrB, Brassica rapa BamHI BAC library Brassica rapa
  subsp. pekinensis genomic clone KBrB060M12, genomic survey
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 27)
  Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J.H. and Park,B.S.
  End sequence of Brassica rapa BamHI (KBrB) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  Brassica Genomics Team
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
  KBrB047117
  Seq primer: M13 Reverse
  Class: BAC ends.
  Location/Qualifiers
    1..27
    /organism="Brassica rapa subsp. pekinensis"
    /mol_type="genomic DNA"
    /cultivar="Chilfu"
    /sub_species="pekinensis"
    /db_xref="taxon:51351"
    /clone="KBrB047117"
    /lab_host="E.coli DH10B"
    /notes="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
    pekinensis var. Chilfu BAC library (KBrB BAC) is provided
    by Yong-Pyo Lim (CNU)."
FEATURES
  source
    Query Match
    Best Local Similarity 100.0%; Pred. No. 4.8e+02;
    Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 777
DX056021
LOCUS
DEFINITION
  DX056021
  KBrB060M12F KBrB, Brassica rapa BamHI BAC library Brassica rapa
  subsp. pekinensis genomic clone KBrB060M12, genomic survey
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
  Sus.
REFERENCE
  1
  Tanaka,M., Suzuki,K., Morozumi,T., Kobayashi,E., Matsumoto,T.,
  Domukai,M., Eguchi-Ogawa,T., Shinkai,H., Awata,I. and Uenishi,H.
  Genomic structure of the distal extended-class II region in swine
  Unpublished
  2 (bases 1 to 27)
  Uenishi,H., Tanaka,M. and Awata,T.
  Direct Submission
  Submitted (25-OCT-2004) Hirohide Uenishi, National Institute of
  Agrological Sciences, Animal Genome Laboratory, Genome Research
  Department, 2 Ikenodai, Tsukuba, Ibaraki, 305-8602, Japan
  (E-mail:huenishi@affrc.go.jp, Tel:81-29-838-8627,
  Fax:81-29-838-8627)
  Correspondence to:
  Hirohide Uenishi
  Animal Genome Laboratory, Genome Research Department, National
  Institute of Agrological Sciences
  2 Ikenodai, Tsukuba, Ibaraki 305-8602, JAPAN
  Tel: +81-29-838-8627
  Fax: +81-29-838-8627
  e-mail: huenishi@affrc.go.jp
  Sequencing was carried out in Animal Genome Research Program

```

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TITLE
JOURNAL
COMMENT
  Hahn,J.H. and Park,B.S.
  End sequence of Brassica rapa BamHI (KBrB) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  Brassica Genomics Team
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
  KBrB060M12
  Seq primer: T7
  Class: BAC ends.
  Location/Qualifiers
    1..27
    /organism="Brassica rapa subsp. pekinensis"
    /mol_type="genomic DNA"
    /cultivar="Chilfu"
    /sub_species="pekinensis"
    /db_xref="taxon:51351"
    /clone="KBrB060M12"
    /lab_host="E.coli DH10B"
    /clone_lib="KBrB, Brassica rapa BamHI BAC library"
    /note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
    pekinensis var. Chilfu BAC library (KBrB BAC) is provided
    by Yong-Pyo Lim (CNU)."
FEATURES
  source
    Query Match
    Best Local Similarity 100.0%; Pred. No. 4.8e+02;
    Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 777
AG829428/c
LOCUS
DEFINITION
  AG829428
  Sus scrofa DNA, BAC clone L243P12, shotgun sequence of subclone
  L243P12S001F01, read with M13Reverse primer, genomic survey
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Sus scrofa (pig)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
  Sus.
REFERENCE
  1
  Tanaka,M., Suzuki,K., Morozumi,T., Kobayashi,E., Matsumoto,T.,
  Domukai,M., Eguchi-Ogawa,T., Shinkai,H., Awata,I. and Uenishi,H.
  Genomic structure of the distal extended-class II region in swine
  Unpublished
  2 (bases 1 to 27)
  Uenishi,H., Tanaka,M. and Awata,T.
  Direct Submission
  Submitted (25-OCT-2004) Hirohide Uenishi, National Institute of
  Agrological Sciences, Animal Genome Laboratory, Genome Research
  Department, 2 Ikenodai, Tsukuba, Ibaraki, 305-8602, Japan
  (E-mail:huenishi@affrc.go.jp, Tel:81-29-838-8627,
  Fax:81-29-838-8627)
  Correspondence to:
  Hirohide Uenishi
  Animal Genome Laboratory, Genome Research Department, National
  Institute of Agrological Sciences
  2 Ikenodai, Tsukuba, Ibaraki 305-8602, JAPAN
  Tel: +81-29-838-8627
  Fax: +81-29-838-8627
  e-mail: huenishi@affrc.go.jp
  Sequencing was carried out in Animal Genome Research Program

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(Japan)
by National Institute of Agrobiological Sciences
and STAFF-Institute.
Subclones of BAC clones were constructed with pUC18 vector.
Basecalling was performed by Phred 0.020425.c.
Vector sequences were eliminated by crossmatch version 0.990319.
Low quality bases were trimmed based on the quality values with the
aid of the trim_alt option of Phred.
FEATURES             source
    Location/Qualifiers
        1..27
            /organism="Sus scrofa"
            /mol_type="genomic DNA"
            /db_xref="taxon:9823"
            /clone="L243P12"
            /sub_clones="L243P12S001F01"
            /clone_lib="Sus scrofa shotgun BAC sequence"
Query Match
Best Local Similarity 100.0%; Score 27; DB 1; Length 27;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 778
TA355B06P          27 bp  DNA  linear  GSS 13-DEC-2000
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 355B06, forward sequence,
genomic survey sequence.
ACCESSION
AL493923
VERSION
AL493923.1 GI:11870552
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 27)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh1@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             source
    Location/Qualifiers
        1..27
            /organism="Trypanosoma brucei"
            /mol_type="genomic DNA"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="355B06"
Query Match
Best Local Similarity 100.0%; Score 27; DB 1; Length 27;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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```

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 779
AL048439          28 bp  mRNA  linear  EST 04-SEP-2003
LOCUS
DEFINITION
DKFZp586i1924.r1.586 (synonym: hutei) Homo sapiens cDNA clone
DKFZp586i1924. mRNA sequence.
ACCESSION
AL048439
VERSION
AL048439.1 GI:4727579
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 28)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Duesterhoeft, et al.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             source
    Location/Qualifiers
        1..28
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKFZp586i1924"
            /tissue_type="uterus"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_lib="586 (synonym: hutei)"
            /note="vector: pSPot1; Site_1: NotI; Site_2: SalI/MluI"
Query Match
Best Local Similarity 100.0%; Score 27; DB 1; Length 28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 780
CF322082/c        28 bp  mRNA  linear  EST 15-AUG-2003
LOCUS
DEFINITION
HD--13-123.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--13-123, mRNA sequence.
ACCESSION
CF322082
VERSION
CF322082.1 GI:33693843
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 28)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             source
    Location/Qualifiers
        1..28

```

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-13-123"
/tissue_type="callus"
/dev_stage="proliferated callus on ZN6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.0%; Score 27; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||
DB 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 781
CF337400 28 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--07-N04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--07-N04, mRNA sequence.
ACCESSION CF337400
VERSION CF337400.1 GI:33823200
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 28)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..28
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-N04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.0%; Score 27; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 2 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28
|||||

RESULT 782
CN545498/c 28 bp mRNA linear EST 30-APR-2004
LOCUS EST 17442 Green Grape Skin Triplex2 Library Vitis vinifera CDNA
DEFINITION clone B3CS00GL005G11 3', mRNA sequence.
CN545498

ACCESSION CN545498.1 GI:46910123
VERSION EST.
KEYWORDS Vitis vinifera
SOURCE Vitis vinifera
ORGANISM Vitis vinifera

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 28)

AUTHORS Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..28
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00GL005G11"
/dev_stage="green stage"
/clone_lib="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 27; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 783
CN546292/c 28 bp mRNA linear EST 30-APR-2004
LOCUS EST 18244 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION CDNA clone B3CS1XGB015D11 3', mRNA sequence.
CN546292

ACCESSION CN546292.1 GI:46910917
VERSION EST.
KEYWORDS Vitis vinifera
SOURCE Vitis vinifera
ORGANISM Vitis vinifera

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 28)

AUTHORS Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages
 Unpublished (2002)
 Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Université de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES

Location/Qualifiers
 1..28
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS1XGB015D11"
 /dev_stage="green stage"
 /clone_lib="Green Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda
 Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 27; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 784

CN546304/c
 LOCUS
 DEFINITION
 EST 18256 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
 cDNA clone B3CS1XGB015E11 3', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 EST.
 CN546304.1 GI:46910929

SOURCE

Vitis vinifera
 Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.

REFERENCE

AUTHORS
 1 (bases 1 to 28)
 Abbal, P., Agasse, A., Agorces, A., Atanasova, R., Barxieu, F.,
 Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
 Hamdi, S., Romieu, C. and Terrier, N.
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages

TITLE

Unpublished (2002)
 Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Université de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France

Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES

Location/Qualifiers
 1..28
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS1XGB015E11"
 /dev_stage="green stage"
 /clone_lib="Green Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda

Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
 Query Match 1.0%; Score 27; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 785

CN988459/c
 LOCUS
 DEFINITION
 EST. 28 bp mRNA linear EST 17-MAY-2005
 ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_C05.abl Bermudagrass line Zebra
 subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone
 ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_C05.abl, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 EST.
 DN988459.1 GI:66248286

SOURCE

Cynodon dactylon (Bermuda grass)
 Cynodon dactylon
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Chloridoidae; Cynodonteae; Cynodon.

REFERENCE

1 (bases 1 to 28)
 Melmaiee, K., Elavarathi, S. and Guenzi, A. C.
 Identification of differentially expressed genes associated with
 cold acclimation using suppression subtraction hybridization (SSH)
 and cDNA microarrays
 Unpublished (2005)

JOURNAL

COMMENT
 Contact: Guenzi AC
 Dep. of Plant and Soil Sciences
 Oklahoma State University
 368 Agriculture Hall, Stillwater, OK 74078-6028, USA
 Tel: 405-744-6028
 Fax: 405-744-6039
 Email: acg@mail.pss.okstate.edu
 PCR Primers
 FORWARD: M13 forward
 BACKWARD: M13 Reverse
 Seq primer: M13 Forward.

FEATURES

Location/Qualifiers
 1..28
 /organism="Cynodon dactylon"
 /mol_type="mRNA"
 /cultivar="Zebra"
 /db_xref="taxon:28909"
 /clone="ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_C05.abl"
 /tissue_type="Crown"
 /lab_host="E. coli"
 /clone_lib="Bermudagrass line Zebra subtracted cold
 acclimated cDNA library"
 /note="vector: Qiagen's pDrive; Messenger RNA was
 extracted from control and cold acclimated bermudagrass
 crown tissue at 2 and 28 days after acclimation and cDNA
 library was constructed following Clontech PCR- select
 cDNA subtraction procedure."

Query Match 1.0%; Score 27; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 786

C2918534/c
 LOCUS
 DEFINITION
 C2918534
 4021009H02.1EL.x1 4021 - RescueMu Grid V Zea mays genomic, genomic
 survey sequence.

ACCESSION C2918534
 VERSION C2918534.1 GI:71938162
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 28)
 REFERENCE Walbot,V.
 AUTHORS Maize genomic sequences found using engineered RescueMu transposon
 TITLE Unpublished (2001)
 JOURNAL
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Very probable ligation site of ends cut by single endonuclease.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 4021009 row: H column: 02
 Class: transposon-tagged.
 Location/Qualifiers
 1..28
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="4021 - RescueMu Grid V"
 /notes="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.0%; Score 27; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 787
 CA853459/c
 LOCUS 32 bp mRNA linear EST 01-AUG-2003
 DEFINITION B08E06.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
 B08E06.5', mRNA sequence.
 ACCESSION CA853459
 VERSION B08E06.5
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 1 (bases 1 to 32)
 REFERENCE Alkharouf,N., Khan,R. and Matthews,B.
 AUTHORS Analysis of expressed sequence tags from roots of resistant soybean
 TITLE Infected by the soybean cyst nematode

JOURNAL PUBMED
 COMMENT Contact: Alkharouf, N.W.
 Soybean Genomics and Improvement Laboratory (SGIL)
 US Department of Agriculture (USDA), ARS, PSI
 Bldg-006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA
 Tel: 301 504 5750
 Fax: 301 504 5728
 Email: alkharouf@ars.usda.gov.
 Location/Qualifiers
 1..32
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Peking"
 /db_xref="taxon:3847"
 /clone="B08E06"
 /tissue_type="Roots"
 /dev_stage="Seedlings"
 /clone_lib="cDNA Peking library 12hr SCN3"
 /note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid."

Query Match 1.0%; Score 27; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 788
 RI6114/c
 LOCUS 32 bp mRNA linear EST 13-APR-1995
 DEFINITION ya51f03.s2 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
 IMAGE:66461.3, similar to gb:M93426 PROTEIN-TYROSINE PHOSPHATASE
 ZETA PRECURSOR (HUMAN);, mRNA sequence.
 ACCESSION RI6114
 VERSION RI6114.1 GI:767923
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 32)
 REFERENCE Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
 AUTHORS The WashU-Merck EST Project
 TITLE Unpublished (1995)
 JOURNAL Contact: Wilson RK
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -21ml3
 High quality sequence stop: 1.
 Location/Qualifiers
 1..32
 /organism="Homo sapiens"


```

ACCESSION      AW332443
VERSION        AW332443.1  GI:6828800
KEYWORDS       EST.
SOURCE         Pneumocystis carinii
ORGANISM       Pneumocystis carinii
               Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
               Pneumocystidaceae; Pneumocystis.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
               Edman,J.C., Kovacs,J. and Cushion,M.
TITLE          Expressed sequence tags from Pneumocystis carinii
JOURNAL        Unpublished (2000)
COMMENT        Contact: Staben C
               School of Biological Sciences
               University of Kentucky
               101 Morgan Building, University of Kentucky, Lexington, KY
               40506-0225, USA
               Tel: 606 257 2161
               Fax: 606 257 1717
               Email: staben@pop.uky.edu.
FEATURES       Location/Qualifiers
               1..28
               /organism="Pneumocystis carinii"
               /mol_type="mRNA"
               /db_xref="taxon:4754"
               /lab_host="E. coli"
               /clone_lib="AGS-1"
               /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
               P. carinii organisms (3x10e9) from a single rat (99-1-6,
               sacrificed on 3/17/99) at Cincinnati VA facilities.
               Trizol extracted RNA. Oligo dT priming, standard
               conditions described by vendor, Stratagene. Further
               details see www.uky.edu/Project/Pneumocystis/"
Query Match    1.0%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
      |||||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 795
CN545659/c
LOCUS          CN545659             28 bp      mRNA      linear      EST 30-APR-2004
DEFINITION    EST 17603 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
               clone B3CS00RL004E11 3', mRNA sequence.
ACCESSION     CN545659
VERSION       CN545659.1  GI:46910284
KEYWORDS      EST.
SOURCE        Vitis vinifera
ORGANISM      Vitis vinifera
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; Vitaceae; Vitis.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
               Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
               Hamdi,S., Romieu,C. and Terrier,N.
TITLE          Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
               or seeds) at Various Developmental Stages
JOURNAL        Unpublished (2002)
COMMENT        Contact: Hamdi S.
               UMR 619 - Equipe Biologie de la Vigne
               Universite de Bordeaux I, Institut National de la Recherche
               Agronomique
               71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
               France
               Tel: 00-33- (0)5-57-12-25-50
               Fax: 00-33- (0)5-57-12-25-48
               Email: s.hamdi@bordeaux.inra.fr
               Seq primer: T7.

```

```

FEATURES       source
               Location/Qualifiers
               1..28
               /organism="Vitis vinifera"
               /mol_type="mRNA"
               /cultivar="Cabernet Sauvignon"
               /db_xref="taxon:29760"
               /clone="B3CS00RL004E11"
               /dev_stage="ripening stage"
               /clone_lib="Ripe Grape Skin Triplex2 Library"
               /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
               SfiI; Site_2: SfiIB; Oriented library"
Query Match    1.0%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
      |||||||
Db 28 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 796
CX001046/c
LOCUS          CX001046             28 bp      mRNA      linear      EST 03-DEC-2004
DEFINITION    t124G08.b7 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,
               mRNA sequence.
ACCESSION     CX001046
VERSION       CX001046.1  GI:56272462
KEYWORDS      EST.
SOURCE        Canis familiaris (dog)
ORGANISM      Canis familiaris
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
               Canis.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE          ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL        Unpublished (2004)
COMMENT        Contact: W. Richard McCombie
               Lita Annenberg Hazen Genome Sequencing Center
               Cold Spring Harbor Laboratory
               PO Box 100, Cold Spring Harbor, NY 11724, USA
               Tel: 516 367 8884
               Fax: 516 367 8874
               Email: mccombie@cshl.org.
FEATURES       source
               Location/Qualifiers
               1..28
               /organism="Canis familiaris"
               /mol_type="mRNA"
               /db_xref="taxon:9615"
               /sex="Unknown"
               /tissue_type="Cardiac muscle"
               /dev_stage="3 month old normal canine"
               /lab_host="XL10 Gold"
               /clone_lib="Left Cardiac Ventricle (DOGEST7)"
               /note="Organ: Heart; Vector: pBluescript II SK; Site 1:
               EcoRI; Site 2: XhoI; Library constructed using pBluescript
               XR kit from Stratagene. Cloned cDNA was size selected
               between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,
               Pathology and Medical Genetics, School of Veterinary
               Medicine, University of Pennsylvania, 3800 Spruce Street,
               Philadelphia, PA 19104-6051"
Query Match    1.0%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
      |||||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 797

```

DR062845
 LOCUS 28 bp mRNA linear EST 06-JUN-2005
 DEFINITION iq22809.g1 Cytas ovule (NYBG) Cytas rumphii cDNA 3', mRNA sequence.
 ACCESSION DR062845
 VERSION DR062845.1 GI:66986411
 KEYWORDS EST.
 SOURCE Cytas rumphii
 ORGANISM Cytas rumphii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Cycadophyta; Cycadales; Cycadaceae; Cytas.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.
 TITLE Expressed tag sequences from Cytas ovules (NYBG)
 JOURNAL Unpublished (2005)
 COMMENT Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Seq primer: -21M13UnivRev.

FEATURES
 source
 1..28
 Location/Qualifiers

/organism="Cytas rumphii"
 /mol_type="mRNA"
 /db_xref="taxon:58031"
 /sex="Female"
 /clone_lib="Cytas ovule (NYBG)"
 /notes="Organ: Ovules; Vector: pBK-CMV; Site 1: XhoI;
 Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
 The library was size-fractionated to enrich for large
 inserts."

Query Match 1.0%; Score 26.4; DB 1; Length 28;
 Best Local Similarity 96.4%; Pred. No. 5.3e+02;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
 |
 Db 1 AATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 798
 AZ514352/c
 LOCUS 28 bp DNA linear GSS 05-OCT-2000
 DEFINITION 1M0360F06R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGIM0360F06 R, genomic survey sequence.

ACCESSION AZ514352
 VERSION AZ514352.1 GI:10695668
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 28)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0360 row: F column: 06
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.

FEATURES
 Location/Qualifiers

source

1..28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGIM0360F06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF125072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.0%; Score 26.4; DB 1; Length 28;
 Best Local Similarity 96.4%; Pred. No. 5.3e+02;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
 |
 Db 28 AAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 799
 AZ824574/c
 LOCUS 28 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0099D17F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCG2M0099D17 F, genomic survey sequence.

ACCESSION AZ824574
 VERSION AZ824574.1 GI:12994482
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 28)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0039 row: D column: 17
 Seq primer: CGTTGTAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 28.

FEATURES

source

```
1. .28
Location/Qualifiers
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC2M0099D17"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UGC1M library"
  /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
  (http://www.jax.org/resources/documents/dnares/). The DNA
  was hydrodynamically sheared by repeated passage through a
  0.005 inch orifice at constant velocity. The sheared DNA
  was blunt end-repaired with T4 DNA polymerase and T4
  polynucleotide kinase. Adaptor oligonucleotides were
  ligated to the blunt ends in high molar excess. The
  adaptor DNA was purified and size-selected for a 9.5 to
  10.5 kb range using preparative agarose gel
  electrophoresis. Vector DNA was prepared from a derivative
  of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
  inducible derivative of plasmid R1. The vector was ligated
  with adaptors complementary to the insert adaptors and
  purified. The sheared, adaptor mouse DNA was annealed to
  adaptor vector DNA, and transformed into
  chemically-competent E. coli XL10-Gold (Stratagene) cells
  and selected for ampicillin resistance."
```

```
Query Match 1.0%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db 28 AAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA 1
```

RESULT 800

CZ916890

LOCUS

```
DEFINITION CZ916890 28 bp DNA linear GSS 08-AUG-2005
survey sequence.
```

ACCESSION

CZ916890

VERSION

CZ916890.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 28)

Walbot V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4021003 row: D column: 05

Class: transposon-tagged.

FEATURES

source

```
1. .28
Location/Qualifiers
  /organism="Zea mays"
  /mol_type="genomic DNA"
  /cultivar="mixed background W23/A188/B73/K55"
  /db_xref="taxon:4577"
  /tissue_type="leaf"
  /dev_stage="adult"
  /lab_host="DH10B"
  /clone_lib="4021 - RescueMu Grid V"
  /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
```

```
Query Match 1.0%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28
```

RESULT 801

TA29A09P/C

LOCUS

DEFINITION

T. brucei sheared genomic DNA clone 29A09, forward sequence, genomic survey sequence.

ACCESSION

AL453073

VERSION

AL453073.1

KEYWORDS

GSS.

SOURCE

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

1 (bases 1 to 28)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajadream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000)

Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers

1. .28

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="29A09"

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Query Match          1.0%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
      |||||
Db  28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 802
CF328476
LOCUS
DEFINITION
NACL--03-G12.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--03-G12, mRNA
sequence.
ACCESSION
CF328476
VERSION
CF328476.1 GI:33805199
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 29)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
UNPUBLISHED (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..29
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-03-G12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          1.0%; Score 26.4; DB 1; Length 29;
Best Local Similarity 96.4%; Pred. No. 5.4e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
      |||||
Db  1 AAAAAAAAAAAAAAAAAAAAAAAAAAAACCAA 28

RESULT 803
AU268044
LOCUS
DEFINITION
AU268044 VS Dictyostelium discoideum cDNA clone VSH836 5', mRNA
sequence.
ACCESSION
AU268044
VERSION
AU268044.1 GI:20526842
KEYWORDS
EST.
SOURCE
Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE
1 (bases 1 to 31)
AUTHORS
Urushihara,H., Morio,T., Saito,T., Kohara,Y., Koriki,E., Ochiai,H.,
Maeda,M., Williams,J.G., Takeuchi,I. and Tanaka,Y.

```

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TITLE
Analyses of cDNAs from growth and slug stages of Dictyostelium
discoideum
JOURNAL
Nucleic Acids Res. 32 (5), 1647-1653 (2004)
PUBMED
15010511
COMMENT
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

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/db_xref="taxon:44689"
/clone="VSH836"
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Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 804
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CF297930
31 bp mRNA linear EST 15-AUG-2003
7LEAF--01-B17.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--01-B17, mRNA
sequence.
ACCESSION
CF297930
VERSION
CF297930.1 GI:33669691
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 31)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
UNPUBLISHED (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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TITLE Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
JOURNAL Microarray analysis identifies genes preferentially expressed in
COMMENT the lung schistosomulum of Schistosoma mansoni
 Unpublished (2005)
CONTACT: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.
FEATURES
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DEFINITION mansoni cDNA clone SmlC18f01.q1k, mRNA sequence.
ACCESSION AM045820
VERSION AM045820.1 GI:75969112
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE
AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
 Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE Microarray analysis identifies genes preferentially expressed in
JOURNAL the lung schistosomulum of Schistosoma mansoni
COMMENT Unpublished (2005)
CONTACT: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.
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DEFINITION mansoni cDNA clone SmlC23c06.q1k, mRNA sequence.

ACCESSION AM046959
VERSION AM046959.1 GI:72292765
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE
AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
 Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE Microarray analysis identifies genes preferentially expressed in
JOURNAL the lung schistosomulum of Schistosoma mansoni
COMMENT Unpublished (2005)
CONTACT: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.
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Db 1 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26
RESULT 810
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LOCUS AM047208 Schistosoma mansoni lung schistosomulum Schistosoma
DEFINITION mansoni cDNA clone SmlC12e04.q1k, mRNA sequence.
ACCESSION AM047208
VERSION AM047208.1 GI:72293264
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE
AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
 Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE Microarray analysis identifies genes preferentially expressed in
JOURNAL the lung schistosomulum of Schistosoma mansoni
COMMENT Unpublished (2005)
CONTACT: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.
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Db      26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
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LOCUS   26 bp mRNA linear EST 14-AUG-2003
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-D22,
mRNA sequence.
ACCESSION
CF278359
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 26)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
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RESULT 813
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LOCUS   26 bp mRNA linear EST 14-AUG-2003
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--07-L18, mRNA
sequence.
ACCESSION
CF297087
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 26)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
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RESULT 812
CF282426
LOCUS   26 bp mRNA linear EST 14-AUG-2003
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-P01,
mRNA sequence.
ACCESSION
CF282426
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 26)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
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RESULT 812
CF282426
LOCUS   26 bp mRNA linear EST 14-AUG-2003
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-P01,
mRNA sequence.
ACCESSION
CF282426
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 26)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
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JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
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/clone_lib="Rice etiolated leaf plasmid cDNA library
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with oligoribonucleotides and then used as templates for
RT-PCR."
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 813
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LOCUS   26 bp mRNA linear EST 14-AUG-2003
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--07-L18, mRNA
sequence.
ACCESSION
CF297087
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 26)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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CONTACT: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
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DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-P01,
mRNA sequence.
ACCESSION
CF282426
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 26)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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CONTACT: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
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Query Match      0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 814
CF299701/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-N03, mRNA
sequence.
ACCESSION
CF299701
VERSION
CF299701.1 GI:33671462
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 816
CF311369/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1..26
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="7LEAF--03-N03"
/tissue_type="leaf"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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CF302874/c
LOCUS
DEFINITION
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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/tissue_type="leaf"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 816
CF311369/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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CONTACT: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/tissue_type="leaf"
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with oligoribonucleotides and then used as templates for
RT-PCR."

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/note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
    |||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 817
CF331439/c
LOCUS      26 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--07-J02.b1 Rice callus plasmid cDNA library (NACL) Oryza
           sativa (japonica cultivar-group) cDNA clone NACL--07-J02, mRNA
           sequence.
ACCESSION  CF331439.1 GI:33811097
VERSION     CF331439
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzoae; Oryza.
REFERENCE   1 (bases 1 to 26)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Gyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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            /db_xref="taxon:39947"
            /clone="NACL-07-J02"
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            /clone_lib="Rice callus plasmid cDNA library (NACL)"
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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
    |||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 818
AW327613/c
LOCUS      26 bp mRNA linear EST 28-JAN-2000
DEFINITION dq01b09.y1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846536 3', mRNA
           sequence.
ACCESSION  AW327613

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VERSION      AW327613.1 GI:6798108
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE    1 (bases 1 to 26)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Edge BioSystems
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Plate: L1CM0028 row: C Column: 17
            Seq primer: M13Rpl reverse primer (ABI).
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                /note="Organ: Blood; Vector: pOTB7a; Library prepared by
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Query Match      0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
    |||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 819
CN545213/c
LOCUS      26 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17157 Green Grape Skin Triplex2 Library Vitis vinifera CDNA
           clone B3CS00GL004E11 3', mRNA sequence.
ACCESSION  CN545213
VERSION     CN545213.1 GI:46909668
KEYWORDS    EST.
SOURCE       Vitis vinifera
ORGANISM     Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; Vitaceae; Vitis.
REFERENCE    1 (bases 1 to 26)
AUTHORS      Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Gramplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
            Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
            Unpublished (2002)
            Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Université de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.

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FEATURES
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        /notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
        SfiIA; Site_2: SfiIB; Oriented library"

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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
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Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 820
CN545225/c
LOCUS
  DEFINITION
    EST 17169 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
  ACCESSION
    CN545225
  VERSION
    CN545225.1 GI:46909680
  KEYWORDS
    EST
  SOURCE
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  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; Vitaceae; Vitis.
  AUTHORS
    Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
    Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
    Hamdi,S., Romieu,C. and Terrier,N.
  TITLE
    Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
    or seeds) at Various Developmental Stages
  JOURNAL
    Unpublished (2002)
  COMMENT
    Contact: Hamdi S.
    UMR 619 - Equipe Biologie de la Vigne
    Universite de Bordeaux I, Institut National de la Recherche
    Agronomique
    71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
    France
    Tel: 00-33-(0)5-57-12-25-50
    Fax: 00-33-(0)5-57-12-25-48
    Email: s.hamdi@bordeaux.inra.fr
    Seq primer: T7.

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        SfiIA; Site_2: SfiIB; Oriented library"

Query Match
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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
    |||||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 822
CN545888/c
LOCUS
  DEFINITION
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  ACCESSION
    CN545888
  VERSION
    CN545888.1 GI:46910513
  KEYWORDS
    EST
  SOURCE
    Vitis vinifera
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; Vitaceae; Vitis.
  AUTHORS
    Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
    Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
    Hamdi,S., Romieu,C. and Terrier,N.
  TITLE
    Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
    or seeds) at Various Developmental Stages
  JOURNAL
    Unpublished (2002)
  COMMENT
    Contact: Hamdi S.
    UMR 619 - Equipe Biologie de la Vigne
    Universite de Bordeaux I, Institut National de la Recherche
    Agronomique
    71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
    France
    Tel: 00-33-(0)5-57-12-25-50
    Fax: 00-33-(0)5-57-12-25-48
    Email: s.hamdi@bordeaux.inra.fr
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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
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Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 821

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CN545546/c
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    CN545546
  VERSION
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  KEYWORDS
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  SOURCE
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  ORGANISM
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    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; Vitaceae; Vitis.
  AUTHORS
    Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
    Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
    Hamdi,S., Romieu,C. and Terrier,N.
  TITLE
    Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
    or seeds) at Various Developmental Stages
  JOURNAL
    Unpublished (2002)
  COMMENT
    Contact: Hamdi S.
    UMR 619 - Equipe Biologie de la Vigne
    Universite de Bordeaux I, Institut National de la Recherche
    Agronomique
    71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
    France
    Tel: 00-33-(0)5-57-12-25-50
    Fax: 00-33-(0)5-57-12-25-48
    Email: s.hamdi@bordeaux.inra.fr
    Seq primer: T7.

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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
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Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 822
CN545888/c
LOCUS
  DEFINITION
    EST 17832 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
  ACCESSION
    CN545888
  VERSION
    CN545888.1 GI:46910513
  KEYWORDS
    EST
  SOURCE
    Vitis vinifera
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; Vitaceae; Vitis.
  AUTHORS
    Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
    Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
    Hamdi,S., Romieu,C. and Terrier,N.
  TITLE
    Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
    or seeds) at Various Developmental Stages
  JOURNAL
    Unpublished (2002)
  COMMENT
    Contact: Hamdi S.
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    71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
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    Tel: 00-33-(0)5-57-12-25-50
    Fax: 00-33-(0)5-57-12-25-48
    Email: s.hamdi@bordeaux.inra.fr
    Seq primer: T7.

FEATURES
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
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Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 822
CN545888/c
LOCUS
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  ACCESSION
    CN545888
  VERSION
    CN545888.1 GI:46910513
  KEYWORDS
    EST
  SOURCE
    Vitis vinifera
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; Vitaceae; Vitis.
  AUTHORS
    Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
    Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
    Hamdi,S., Romieu,C. and Terrier,N.
  TITLE
    Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
    or seeds) at Various Developmental Stages
  JOURNAL
    Unpublished (2002)
  COMMENT
    Contact: Hamdi S.
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    Tel: 00-33-(0)5-57-12-25-50
    Fax: 00-33-(0)5-57-12-25-48
    Email: s.hamdi@bordeaux.inra.fr
    Seq primer: T7.

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Query Match
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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
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Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 821

```

Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES

Location/Qualifiers

1..26
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/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006A07"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 26; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 5.4e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 823

CN546608/c

LOCUS

DEFINITION EST 18752 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera

ACCESSION CN546608

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

REFERENCE

AUTHORS

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

Unpublished (2002)

CONTACT: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,

France

Tel: 00-33- (0)5-57-12-25-50

Fax: 00-33- (0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

FEATURES

Location/Qualifiers

1..26
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58RB008H03"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 824

CN546649/c

LOCUS

DEFINITION

EST 18420 Turning Grape Berry Lambda Triplex2 Library Vitis

vinifera cDNA clone B3CS37TB007C08 3', mRNA sequence.

ACCESSION CN546649

VERSION

KEYWORDS

SOURCE

ORGANISM

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

REFERENCE

AUTHORS

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

Unpublished (2002)

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France

Tel: 00-33- (0)5-57-12-25-50

Fax: 00-33- (0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..26

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS37TB007C08"

/dev_stage="version stage"

/clone_lib="Turning Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 825

CN546649/c

LOCUS

DEFINITION

EST 18420 Turning Grape Berry Lambda Triplex2 Library Vitis

vinifera cDNA clone B3CS37TB007C08 3', mRNA sequence.

ACCESSION CN546649

VERSION

KEYWORDS

SOURCE

ORGANISM

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

REFERENCE

AUTHORS

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

Unpublished (2002)

CONTACT: Hamdi S.

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Fax: 00-33- (0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..26

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS37TB007C08"

/dev_stage="version stage"

/clone_lib="Turning Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Mismatches 0; Indels 0; Gaps 0;

TITLE Expressed tag sequences from Gnetum female cone (NYBG)
JOURNAL Unpublished (2003)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES

source
1. .26
Location/Qualifiers
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
/note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site.1: XhoI; Site.2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 826

DN955188 26 bp mRNA linear EST 04-MAY-2005
LOCUS it83d08.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
DEFINITION sequence.

ACCESSION DN955188
VERSION DN955188.1 GI:63027326
KEYWORDS EST.
SOURCE Gnetum gnemon

ORGANISM

Gnetum gnemon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 26)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballia,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

Unpublished (2003)

Expressed tag sequences from Gnetum female cone (NYBG)

Unpublished (2003)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.

Location/Qualifiers

1. .26

/organism="Gnetum gnemon"

/mol_type="mRNA"

/db_xref="taxon:3382"

/sex="female"

/clone_lib="Gnetum female cone (NYBG)"

/note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site.1: XhoI; Site.2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 827

DN955188 26 bp mRNA linear EST 08-JUN-2005
LOCUS ik86f11.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
DEFINITION sequence.

ACCESSION DN955188
VERSION DN955188.1 GI:67050976
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)

ORGANISM

Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoales; Ginkgoales; Ginkgoales; Ginkgo.
1 (bases 1 to 26)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballia,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

Unpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.

Location/Qualifiers

1. .26

/organism="Ginkgo biloba"

/mol_type="mRNA"

/db_xref="taxon:3311"

/sex="female"

/clone_lib="Ginkgo female leaf (NYBG)"

/note="Organ: leaf; Vector: pBK-CMV; Site.1: XhoI;
Site.2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 828

DN955188 26 bp DNA linear GSS 02-OCT-2000
LOCUS AZ359871
DEFINITION 1M0102H23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0102H23 R, genomic survey sequence.

ACCESSION AZ359871
VERSION AZ359871.1 GI:10473571
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Muridae; Muridae;
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausearn, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0102 row: H column: 23
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES
SOURCE

1. 26
location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0102H23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Query Match      0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734
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Dp      2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 26
        10000000000000000000000000000000

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RESULT	829
AZ376664	
LOCUS	AZ376664
DEFINITION	mouse 10kb plasmid UGSCIM library Mus musculus genomic clone UGSCIM013E08 R. genomic survey sequence.
	26 bp DNA linear GSS 02-OCT-2000

AZ376664
 AZ376664.1
 GI:10490364

VERSION
 KEYWORDS
 GSS.
 Mus musculus (house mouse)
 SOURCE
 A23/0004:1 GI:10430304

SOURCE	MUS MUSCULUS	MUS MUSCULUS (HOUSE MOUSE)	ORGANISM
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus

REFERENCE

1 (bases 1 to 26)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Peilley, M., Rose, M., Rose, R., Strokes, R., Tingey, A. von

Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Place: 0130 row: E column: 08
 Seq primer: CACACGAGNACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES
source

1. .26

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/organism="Mus musculus"  
/mol_type="genomic DNA"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone="UUGC1M0130E08"  
/sex="Male"  
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 [gi|4732114|gb|AF129072.1|], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."
```

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Query Match      0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2734
|||||

D_b 1 AAAAAAAAAAAAAAAAAAAAAA 26
|||||

[illegible]

ACCESSION AZ389765
VERSION AZ389765.1 GI:10503473

KEYWORDS
GSS.
Mus musculus (house mouse)
SOURCE

Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 26)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

TITLE
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: D column: 13
Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES
source
1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0150D13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 831
AZ414673
LOCUS
AZ414673 26 bp DNA linear GSS 03-OCT-2000
DEFINITION
1M0189M07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0189M07 F, genomic survey sequence.
ACCESSION
AZ414673
VERSION
AZ414673.1 GI:10538686
KEYWORDS
GSS.
SOURCE
Mus musculus
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0189 row: M column: 07
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES
source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0189M07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 832
AZ593300
LOCUS
AZ593300 26 bp DNA linear GSS 13-DEC-2000
DEFINITION
1M0404E16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0404E16 R, genomic survey sequence.
ACCESSION
AZ593300
VERSION
AZ593300.1 GI:11715490
KEYWORDS
GSS.
SOURCE
Mus musculus
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE
JOURNAL
COMMENT

Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0404 row: E column: 16
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers
 1. .26
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0404E16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
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 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
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Query Match 0.9%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
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 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 833
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AZ612722 26 bp DNA linear GSS 13-DEC-2000
 IM0439B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0439B17 R, genomic survey sequence.
 AZ612722
 AZ612722.1 GI:11734912
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

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 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0439 row: E column: 17
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
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 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0439E17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
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 /clone="UUGC1M0439E17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
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 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
 |||||
 Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 834
AZ624441/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AZ624441 26 bp DNA linear GSS 13-DEC-2000
 IM0463G07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0463G07 F, genomic survey sequence.
 AZ624441
 AZ624441.1 GI:11746631
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0463 row: G column: 07
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0463G07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 835
AZ627846/c
LOCUS
DEFINITION
1M0474H08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474H08 F, genomic survey sequence.

ACCESSION
AZ627846
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
SOURCE
ORGANISM

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: H column: 08
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source
1. .26
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0474H08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 836
AZ652515
LOCUS
DEFINITION
1M0525H15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0525H15 R, genomic survey sequence.

ACCESSION
AZ652515
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
SOURCE
ORGANISM

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0525 row: H column: 15
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0525H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 837
AZ800453/c
LOCUS
DEFINITION
2M0058023F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0058023 F, genomic survey sequence.

ACCESSION
AZ800453
VERSION
AZ800453.1 GI:12952583
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0058 row: O column: 23
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0058O23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
DB 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 838
AZ963974/c
LOCUS
DEFINITION
2M0233N01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0233N01 F, genomic survey sequence.

ACCESSION
AZ963974
VERSION
AZ963974.1 GI:13835201
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: N column: 01
Seq primer: CGTTGTAACAGCAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source

1..26
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0233N01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 839
CZ490199/c
LOCUS
DEFINITION
CZ490199 26 bp DNA linear GSS 29-APR-2005
f07397-3prime Exelixis piggyBac WH insertions Drosophila
melanogaster genomic sequence recovered from 3' end of piggyBac,
genomic survey sequence.
CZ490199
CZ490199.1 GI:62987637
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 26)
REFERENCE
Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,

TITLE
JOURNAL
PUBMED
COMMENT

Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
piggyBac element.
The piggyBac insertion position is unspecified in the 26 bases.
This insertion position refers to the first base of the 4 base TTAA
target recognition sequence.
Class: transposon insertion site.

FEATURES

source

1..26
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac WH insertions"
/notes="Vector: piggyBac WH (GenBank accession number
AY151148); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the WH element using the
constitutive alpha-1 tubulin-piggyBac transposase source.
We remobilized the WH element from a single ammunition
element on the Binsncy balancer chromosome in dysgenic
females. We outcrossed dysgenic virgin females in vials to
the isogenic w- strain and selected new hops in the
following generation. All lines were mapped to a
chromosome by standard genetic methods, examined for
homologous viability, and used for recovery of flanking
genomic sequence by inverse PCR."

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 840
CZ910095
LOCUS
DEFINITION
CZ910095 26 bp DNA linear GSS 08-AUG-2005
4012001C02.2EL.y1 4012 - RescueMu Grid BB Zea mays genomic, genomic
survey sequence.
CZ910095
CZ910095.1 GI:719223489
GSS.
SOURCE
Ze mays
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 26)
REFERENCE
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
JOURNAL
COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University

855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: wabot@stanford.edu

Reverse ligation site of ends cut by 2 different endonucleases.
Possible complemented post-ligation sequence from source sequence.
Plate: 4012001 row: C column: 02
Class: transposon-tagged.

FEATURES

Location/Qualifiers
1..26

source

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4012 - RescueMu Grid BB"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid BB was grown at UC Berkeley in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match

Best Local Similarity 0.9%; Score 26; DB 1; Length 26;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2734

Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 841

DU832827/c

LOCUS

DEFINITION
DU832827 26 bp DNA linear GSS 22-DEC-2005
KBRs010P08F KBRs, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBRs010P08, genomic survey
sequence.

ACCESSION

VERSION
DU832827.1 GI:83869423

KEYWORDS

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS

1 (bases 1 to 26)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.

TITLE

JOURNAL

COMMENT

End sequence of Brassica rapa Sau3AI (KBRs) BAC clone

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone

KBRs010P08

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..26

source

/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clones="KBRs010P08"
/lab_host="E. coli DH10B"
/clone_lib="KBRs, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBRs BAC) is
available at NIAB."

Query Match

Best Local Similarity 0.9%; Score 26; DB 1; Length 26;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2734

Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 842

DU835360/c

LOCUS

DEFINITION
DU835360 26 bp DNA linear GSS 22-DEC-2005
KBRs016105R KBRs, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBRs016105, genomic survey
sequence.

ACCESSION

VERSION
DU835360.1 GI:83871956

KEYWORDS

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS

1 (bases 1 to 26)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.

TITLE

JOURNAL

COMMENT

End sequence of Brassica rapa Sau3AI (KBRs) BAC clone

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone

KBRs016105

Seq primer: M13 Reverse

Class: BAC ends.

Location/Qualifiers

1..26

source

/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clones="KBRs016105"
/lab_host="E. coli DH10B"
/clone_lib="KBRs, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBRs BAC) is
available at NIAB."

Query Match

Best Local Similarity 0.9%; Score 26; DB 1; Length 26;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2734

Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

FEATURES

Location/Qualifiers

1..26

source

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RESULT 843
DX034224
LOCUS
DEFINITION
    DX034224 26 bp DNA linear GSS 10-JAN-2006
    KBrB031P17R KBrB, Brassica rapa BamHI BAC library Brassica rapa
    subsp. pekinensis genomic clone KBrB031P17, genomic survey
    sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Brassica rapa subsp. pekinensis
    Brassica rapa subsp. pekinensis
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
    1 (bases 1 to 26)
    Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
    Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
    Hahn, J.H. and Park, B.S.
    End sequence of Brassica rapa BamHI (KBrB) BAC clone
    Unpublished (2005)
    Contact: Beom-Seok Park
    Brassica Genomics Team
    National Institute of Agricultural Biotechnology
    225 Seodun-Dong, Suwon, 441-707, Korea
    Tel: +82-31-299-1670
    Fax: +82-31-299-1672
    Email: pbeom@da.go.kr
    BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
    KBrB031P17
    Seq primer: M13 Reverse
    Class: BAC ends.
FEATURES
    source
    Location/Qualifiers
    1..26
        /organism="Brassica rapa subsp. pekinensis"
        /mol_type="genomic DNA"
        /cultivar="Chifu"
        /sub_species="pekinensis"
        /db_xref="taxon:51351"
        /clone="KBrB031P17"
        /lab_host="E.coli DH10B"
        /clone_lib="KBrB, Brassica rapa BamHI BAC library"
        /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
        pekinensis var. Chifu BAC library (KBrB BAC) is provided
        by Yong-Pyo Lim (CNU)."
```

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Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 844
TA324D07P
LOCUS
DEFINITION
    T. brucei sheared genomic DNA clone 324D07, forward sequence,
    genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Trypanosoma brucei
    Trypanosoma brucei
    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
    Trypanosoma.
REFERENCE
    1 (bases 1 to 26)
    Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
    Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
    Melville, S.E., Rajandream, M.A. and Barrell, B.G.
    Direct Submission
```

```

JOURNAL
    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
    project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
    Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
    nh1@sanger.ac.uk
    Constructed at the Institute for Genomic Research (TIGR),
    Rockville, MD. Genomic DNA isolated from a cloned population of
    Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
    to give a tight size distribution (
    4 kb). The v + i method used for the library construction is
    described in detail in Smith, H. and Venter, J.C. (Making small
    insert libraries for whole genome shotgun sequencing projects. In
    Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
    Barrell, Oxford University Press, 1999).
    Email: nelsayed@tigr.org
    Details of T. brucei sequencing at the Sanger Centre are available
    at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
    source
    Location/Qualifiers
    1..26
        /organism="Trypanosoma brucei"
        /mol_type="genomic DNA"
        /strain="TREU927"
        /db_xref="taxon:5691"
        /clone="324D07"

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 845
CN545777/c
LOCUS
DEFINITION
    CN545777 27 bp mRNA linear EST 30-APR-2004
    EST 17721 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
    clone B3CS00RL005G11 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Vitis vinifera
    Vitis vinifera
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; Vitaceae; Vitis.
REFERENCE
    1 (bases 1 to 27)
    Abbal, P., Agasse, A., Agasse, A., Agasse, A., Agasse, A., Agasse, A.,
    Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
    Hamdi, S., Romieu, C. and Terrier, N.
    Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
    or seeds) at Various Developmental Stages
    Unpublished (2002)
    Contact: Hamdi S.
    UMR 619 - Equipe Biologie de la Vigne
    Université de Bordeaux I, Institut National de la Recherche
    Agronomique
    71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
    France
    Tel: 00-33-(0)5-57-12-25-50
    Fax: 00-33-(0)5-57-12-25-48
    Email: s.hamdi@bordeaux.inra.fr
    Seq primer: T7.
FEATURES
    source
    Location/Qualifiers
    1..27
        /organism="Vitis vinifera"
        /mol_type="mRNA"
        /cultivar="Cabernet Sauvignon"
        /db_xref="taxon:29760"
        /clone="B3CS00RL005G11"
        /dev_stage="ripening stage"
        /clone_lib="Ripe Grape Skin Triplex2 Library"
        /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:"
```


to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsaved@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
1. .27
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="257b07"
Query Match 0.9%; Score 26; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 5.5e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 849

AJ658314
LOCUS AJ658314 KN277 Sus scrofa cDNA clone C0005212_K01, mRNA EST 28-JUN-2004
DEFINITION AJ658314
ACCESSION AJ658314
VERSION AJ658314.1 GI:49342393
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 29)

REFERENCE Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
AUTHORS Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
TITLE Unpublished (2004)
JOURNAL Genomics and Bioinformatics
COMMENT Contact: Anderson SI
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector: pBlueScriptII(SK+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pooled early embryos, from 8- cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

Location/Qualifiers
1. .29
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005212_K01"
/tissue_type="embryo"
/clone_lib="KN277"
/notes="Vector: pBlueScriptII(SK+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."
Query Match 0.9%; Score 26; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 850

AZ819924
LOCUS AZ819924
DEFINITION 29 bp DNA linear GSS 20-FEB-2001
clone UUGC2M0091A19 R, genomic survey sequence.

ACCESSION

AZ819924
VERSION AZ819924.1 GI:12989832

KEYWORDS

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS 1 (bases 1 to 29)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

FEATURES

Location/Qualifiers
1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0091A19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWB42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
High quality sequence stop: 29.

FEATURES

Location/Qualifiers
1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0091A19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWB42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match 0.9%; Score 26; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734

```

Db      1  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26
|||||
|||||

CN545889      30 bp  mRNA  linear  EST 30-APR-2004
EST 17833 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
Clone B3CS00RL006A08 3', mRNA sequence.
CN545889
CN545889.1  GI:46910514
EST.
CN545889
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE
1  (bases 1 to 30)
Abbal, P., Agase, A., Agorces, A., Atanasova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Komieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 77.
FEATURES
source
1. .30
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006A08"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/clone_org="Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"
Query Match 0.9%; Score 26; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
|||||
|||||
Db 26 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
|||||
|||||

RESULT 852
A2962183
LOCUS 2M0230124R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0230124 R, genomic survey sequence.
ACCESSION A2962183
VERSION A2962183.1 GI:13833410
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1  (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
REFERENCE
AUTHORS

Db      1  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26
|||||
|||||

CN545889      30 bp  mRNA  linear  EST 30-APR-2004
EST 17833 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
Clone B3CS00RL006A08 3', mRNA sequence.
CN545889
CN545889.1  GI:46910514
EST.
CN545889
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE
1  (bases 1 to 30)
Abbal, P., Agase, A., Agorces, A., Atanasova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Komieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 77.
FEATURES
source
1. .30
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006A08"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/clone_org="Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"
Query Match 0.9%; Score 26; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
|||||
|||||
Db 26 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
|||||
|||||

RESULT 851
CN545889/c
LOCUS 2M0230124R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0230124 R, genomic survey sequence.
ACCESSION A2962183
VERSION A2962183.1 GI:13833410
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1  (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
REFERENCE
AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0230 row: I column: 24
Seq primer: CACACAGAGAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 30.
FEATURES
Location/Qualifiers
1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0230124"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.9%; Score 26; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26
|||||
|||||

RESULT 853
AM044314
LOCUS AM044314 Schistosoma mansoni lung schistosomulum Schistosoma
DEFINITION mansoni cDNA clone SmlC21b09.q1k, mRNA sequence.
ACCESSION AM044314
VERSION AM044314.1 GI:75966407
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigoida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1  (bases 1 to 31)
Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.,
Nikolaïdou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
JOURNAL

```

COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
source 1. .31
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC21b09.qik"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="Country: Puerto Rico"

Query Match 0.9%; Score 26; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 854
CD577496
LOCUS
DEFINITION 47(2)W-20_20_F06_048 ESTs from wild-caught Anopheles funestus EST 15-JUN-2004
populations Anopheles funestus cDNA 5', mRNA sequence.

ACCESSION CD577496
VERSION CD577496
KEYWORDS EST.
SOURCE CD577496.1 GI:48718511
ORGANISM Anopheles funestus
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
REFERENCE 1 (bases 1 to 32)
AUTHORS Besansky,N.J., Serazin,A.C. and Dana,A.
TITLE Towards the transcriptome of Anopheles funestus: a molecular snapshot
JOURNAL Unpublished (2003)
COMMENT Contact: Andrew Serazin
Collins/Besansky Lab
Center for Tropical Disease Research and Training, University of
Notre Dame
317 Galvin Life Science, Notre Dame, IN 46556, USA
Tel: 5746319321
Email: nbesansk@nd.edu
These sequences may be of either nuclear or mitochondrial origin.

FEATURES
source 1. .32
/organism="Anopheles funestus"
/mol_type="mRNA"
/strain="West African"
/db_xref="taxon:62324"
/sex="male and female"
/dev_stage="embryo, larvae, pupae, and adult"
/clone_lib="ESTs from wild-caught Anopheles funestus populations"
/note="Vector: LambdaTriplex2"

Query Match 0.9%; Score 26; DB 1; Length 32;
Best Local Similarity 96.3%; Pred. No. 5.9e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||
Db 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 855
BQ583967/c
LOCUS
DEFINITION EST 06-DEC-2002
clone BQ583967.1 GI:26113544
EST.
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 29)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 29 Std Error: 0.00
Plate: 4 row: B column: 01
Seq primer: T7; GTAATACGACTCACTATAGGC.
Location/Qualifiers
1. .29
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:182728"
/db_xref="taxon:161934"
/clone="024-004-B01"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.9%; Score 25.8; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 5.8e+02;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 29 AAAAAAAAAACACAAAAAAAAAAAAAAAAACAAA 1

RESULT 856
CN545957/c
LOCUS
DEFINITION EST 30-APR-2004
clone B3CS00RL006G11 3', mRNA sequence.

ACCESSION CN545957
VERSION CN545957.1 GI:46910582
KEYWORDS EST.
SOURCE CN545957.1
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 29)

DEFINITION S013297-024-004-B01-T7 MPiZ-ADIS-024-inflorescence Beta vulgaris
cDNA clone 024-004-B01 3-PRIME, mRNA sequence.

ACCESSION BQ583967
VERSION BQ583967.1 GI:26113544
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 29)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 29 Std Error: 0.00
Plate: 4 row: B column: 01
Seq primer: T7; GTAATACGACTCACTATAGGC.
Location/Qualifiers
1. .29
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:182728"
/db_xref="taxon:161934"
/clone="024-004-B01"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.9%; Score 25.8; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 5.8e+02;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 29 AAAAAAAAAACACAAAAAAAAAAAAAAAAACAAA 1

RESULT 856
CN545957/c
LOCUS
DEFINITION EST 30-APR-2004
clone B3CS00RL006G11 3', mRNA sequence.

ACCESSION CN545957
VERSION CN545957.1 GI:46910582
KEYWORDS EST.
SOURCE CN545957.1
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 29)

AUTHORS Abbal,P., Agase,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romeu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES Location/Qualifiers
source
1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006G11"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 25.8; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 5.8e+02;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||||
Db 29 AAAAAAAAAAGCAAAAAAAAAAAAAAAAAA 1

RESULT 857
R59306/c 32 bp mRNA linear EST 24-MAY-1995
LOCUS Yh16c10.s1 Soares infant brain INIB Homo sapiens cDNA clone
DEFINITION IMAGE:37903 3' similar to gb:M29064 HETEROGENEOUS NUCLEAR
RIBONUCLEOPROTEINS A2/B1 (HUMAN);, mRNA sequence.

ACCESSION R59306.1 GI:830001
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarctontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 32)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marta,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: SP6
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source
1..32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:410444"
/db_xref="taxon:9606"
/clone="IMAGE:37903"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain INIB"
/note="Organ: whole brain; Vector: Lfamid BA; Site_1: Not
I; Site_2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5',
ACTGGGAAGATTCCGCCGCGCAGGATTTTITTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lfamid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 0.9%; Score 25.6; DB 1; Length 32;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2705 TACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 32 TTCTAAGGGAAGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 858
AZ326012 32 bp DNA linear GSS 29-SEP-2000
LOCUS IM0048A19R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0048A19 R, genomic survey sequence.

ACCESSION AZ326012
VERSION AZ326012.1 GI:10383271
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarctontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 32)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0048 row: A column: 19
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.

FEATURES Location/Qualifiers
source
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0048A19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"


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Db      1 AAAAAAAAAAAAAAAAAAAAAAGGAGAGAAAA 32
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RESULT 861
AZ434285      27 bp  DNA  linear  GSS 03-OCT-2000
LOCUS      1M0220808R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION  clone UUGC1M0220808 R, genomic survey sequence.
ACCESSION  AZ434285
VERSION    AZ434285.1 GI:10558298
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0220 row: B column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
FEATURES             source
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0220808"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.9%; Score 25.4; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 5.9e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAGGAGAGAAAA 2735

```

```

Db      1 AAAAAAAAAAAAAAAAAAAAAATAAAAAAA 27
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RESULT 862
AZ458228      27 bp  DNA  linear  GSS 04-OCT-2000
LOCUS      1M0262C12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION  clone UUGC1M0262C12 F, genomic survey sequence.
ACCESSION  AZ458228
VERSION    AZ458228.1 GI:10616353
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0262 row: C column: 12
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
FEATURES             source
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0262C12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.9%; Score 25.4; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 5.9e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAATAAAAAAA 2735

```

```

Db      1  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 863
AZ941721/c
LOCUS   AZ941721
DEFINITION 27021004R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0201004 R, genomic survey sequence.
ACCESSION AZ941721
VERSION   AZ941721.1 GI:13804440
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus

REFERENCE
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0201 row: 0 column: 04
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 27.
FEATURES
          Location/Qualifiers
            1..27
              /organism="Mus musculus"
              /mol_type="genomic DNA"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUGC2M0201004"
              /sex="Female"
              /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUGC2M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (female) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to
              adapted vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
          Query Match      0.9%; Score 25.4; DB 1; Length 27;
          Best Local Similarity 96.3%; Pred. No. 5.9e+02;
          Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735

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Db      27  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 864
AZ970621/c
LOCUS   AZ970621
DEFINITION 2M0243N14R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0243N14 R, genomic survey sequence.
ACCESSION AZ970621
VERSION   AZ970621.1 GI:13841848
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus

REFERENCE
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0243 row: N column: 14
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 27.
FEATURES
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            1..27
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              /mol_type="genomic DNA"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUGC2M0243N14"
              /sex="Female"
              /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUGC2M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (female) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to
              adapted vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
          Query Match      0.9%; Score 25.4; DB 1; Length 27;
          Best Local Similarity 96.3%; Pred. No. 5.9e+02;
          Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735

```


and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 8889549
 COMMENT
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -21ml3
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .28
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:494737"
 /db_xref="taxon:9606"
 /clone="IMAGE:73072"
 /tissue_type="fetal spleen"
 /dev_stage="fetal"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Stratagene fetal spleen (#937205)"
 /note="Organ: spleen; Vector: Bluescript SK-; Site_1:
 EcoRI, Site_2: XhoI; Cloned unidirectionally.
 Oligo dt. Pooled spleens. Average insert size: 1.0 Kb;
 Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGG
 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

FEATURES source

Query Match 0.9%; Score 25.4; DB 1; Length 28;
 Best Local Similarity 92.9%; Pred. No. 6e+02; 2; Indels 0; Gaps 0;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
 |||||
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAATNAAA 1

RESULT 868
 AZ836072/c
 LOCUS
 DEFINITION
 2M0130K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0130K08 R, genomic survey sequence.
 AZ836072
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 28)
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 TITLE
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0130 row: K column: 08
 Seq primer: CACACAGAAACAGCTGACCC
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
 1. .28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0130K08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES source

Query Match 0.9%; Score 25.4; DB 1; Length 28;
 Best Local Similarity 96.3%; Pred. No. 6e+02; 1; Indels 0; Gaps 0;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 28 AAAAAAAAAAAAAAAAAAGAAAAAAAAA 2

RESULT 869
 CF299716/c
 LOCUS
 DEFINITION
 7LEAF--03-N11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--03-N11, mRNA
 sequence.
 CF299716
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE
 1 (bases 1 to 30)
 AUTHORS
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE
 JOURNAL
 COMMENT
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1. .30
 /organism="Oryza sativa (japonica cultivar-group)"

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/mol_type="mrna"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-N11"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 0.9%; Score 25.2; DB 1; Length 30;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
DB 30 AAAAGAGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 870
CZ919253
LOCUS 4021012D11.2EL x1 4021 - RescueMu Grid V Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION CZ919253
VERSION CZ919253.1 GI:71939587
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 30)
Walbot.V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021012 row: D column: 11
Class: transposon-tagged.
FEATURES
    source
        1..30
            Location/Qualifiers
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /cultivar="mixed background W23/A188/B73/K55"
                /db_xref="taxon:4577"
                /tissue_type="leaf"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="4021 - RescueMu Grid V"
                /note="Organ: leaf; Vector: RescueMu (engineered from
                pBluescript backbone); Site 1: BamHI; Site 2: BglII;
                RescueMu is a 4.9 kb, modified maize Mu transposon
                designed to allow plasmid rescue from total genomic DNA.
                Mu elements insert preferentially into transcription
                unite. For more information on RescueMu, go to the web
                site 'http://www.mutransposon.org/project/RescueMu/'. Grid
                V was grown at University of Arizona in 2003. DNA was
                extracted from leaf strips, double digested using BamHI
                and BglII, and ligated to form circular plasmids. DH10B
                cells were transformed and then screened on LB plates with
                ampicillin."

Query Match
0.9%; Score 25.2; DB 1; Length 30;

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Best Local Similarity 90.0%; Pred. No. 6.4e+02;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGAAA 30

RESULT 871
DX082113
LOCUS 30 bp DNA linear GSS 10-JAN-2006
DEFINITION KBrB095E11R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB095E11, genomic survey
sequence.
ACCESSION DX082113
VERSION DX082113.1 GI:84776409
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 30)
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa spp. pekinensis BamHI BAC clone
KBrB095E11
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
    source
        1..30
            Location/Qualifiers
                /organism="Brassica rapa subsp. pekinensis"
                /mol_type="genomic DNA"
                /cultivar="Chifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBrB095E11"
                /lab_host="E.coli DH10B"
                /clone_lib="KBrB, Brassica rapa BamHI BAC library"
                /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
                pekinensis var. Chifu BAC library (KBrB BAC) is provided
                by Yong-Pyo Lim (CNU)."

Query Match
0.9%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 6.4e+02;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2701 TTTGTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2730
DB 1 TTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 872
CZ918715/c
LOCUS 4021010E09.2EL x1 4021 - RescueMu Grid V Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION CZ918715
VERSION CZ918715.1 GI:71938523
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 31)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021010 row: E column: 09
Class: transposon-tagged.

FEATURES
source

1..31
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

Query Match 0.9%; Score 25.2; DB 1; Length 31;
Best Local Similarity 90.0%; Pred. No. 6.5e+02;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
||||| ||||||| ||||||| ||||||| |||
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAATA 2

RESULT 873
CF291048/c
LOCUS

DEFINITION
14ROOT--01-F05.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--01-F05, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF291048
CF291048.1 GI:33660081

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS

1 (bases 1 to 25)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE
JOURNAL
COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

FEATURES
source

Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-F05"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match

Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
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Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 874
CF291646/c

LOCUS
DEFINITION
14ROOT--02-C14.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-C14, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF291646
CF291646.1 GI:33660679

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS

1 (bases 1 to 25)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE
JOURNAL
COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

FEATURES
source

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..25

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="14ROOT--02-C14"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match

Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
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Db      25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 875
CF299288
LOCUS   25 bp mRNA linear EST 15-AUG-2003
DEFINITION
sativa (japonica cultivar-group) cDNA clone 7LEAF--03-E01, mRNA
sequence.
ACCESSION CF299288
VERSION   1 GI:33671049
KEYWORDS EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="7LEAF--04-L02"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAA 25

RESULT 876
CF300333/c
LOCUS   25 bp mRNA linear EST 15-AUG-2003
DEFINITION
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-L02, mRNA
sequence.
ACCESSION CF300333
VERSION   1 GI:33672094
KEYWORDS EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-E01"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAA 25

RESULT 877
CF316323/c
LOCUS   25 bp mRNA linear EST 15-AUG-2003
DEFINITION
HD--05-J05.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-J05, mRNA sequence.
ACCESSION CF316323
VERSION   1 GI:33688084
KEYWORDS EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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Location/Qualifiers
1..25
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="HD--05-J05"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="7LEAF--04-L02"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db      25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 877
CF316323/c
LOCUS   25 bp mRNA linear EST 15-AUG-2003
DEFINITION
HD--05-J05.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-J05, mRNA sequence.
ACCESSION CF316323
VERSION   1 GI:33688084
KEYWORDS EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
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/clone="HD--05-J05"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match          0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 878
CF317714/c
LOCUS
DEFINITION
HD--07-103.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
CF317714
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..25
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match          0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 879
CF319073/c
LOCUS
DEFINITION
HD--09-H05.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
CF319073
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
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cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match          0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 880
CF330786/c
LOCUS
DEFINITION
NAC1--06-K11.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--06-K11, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

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/cultivar="Nackdong"
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 /lab_host="E.coli DH10B"
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 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
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Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
 |||||||
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 881
 CN545505/c
 LOCUS
 DEFINITION EST 17449 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
 clone B3CS00GL005H06 3', mRNA sequence.
 CN545505
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

25 bp mRNA linear EST 30-APR-2004
 clone B3CS00GL005H06 3', mRNA sequence.
 CN545505.1 GI:46910130
 EST.
 Vitis vinifera
 Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Abbal,P., Agasse,A., Agorces,A., Atanassova,R., Barrieu,F.,
 Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
 Hamdi,S., Romieu,C. and Terrier,N.
 Title Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 JOURNAL Unpublished (2002)
 COMMENT

UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.
 Location/Qualifiers
 1..25
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
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 /dev_stage="green grape"
 /clone_lib="Green Grape Skin Triplex2 Library"
 /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
 SfiIA; Site_2: SfiIB; Oriented library"

FEATURES
 source

Query Match 0.9%; Score 25; DB 1; Length 25;
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 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
 |||||||
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 882
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LOCUS
 DEFINITION EST 17993 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
 clone B3CS00RL007G10 3', mRNA sequence.
 CN546041
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

25 bp mRNA linear EST 30-APR-2004
 clone B3CS00RL007G10 3', mRNA sequence.
 CN546041.1 GI:46910666
 EST.
 Vitis vinifera
 Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
 Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
 Hamdi,S., Romieu,C. and Terrier,N.
 Title Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 JOURNAL Unpublished (2002)
 COMMENT

Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.
 Location/Qualifiers
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 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
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 /clone="B3CS00RL007G10"
 /dev_stage="ripening stage"
 /clone_lib="Ripe Grape Skin Triplex2 Library"
 /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
 SfiIA; Site_2: SfiIB; Oriented library"

FEATURES
 source

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
 |||||||
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 883
 CN546397/c
 LOCUS
 DEFINITION EST 18350 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
 cDNA clone B3CS1XGB016E10 3', mRNA sequence.
 CN546397
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

25 bp mRNA linear EST 30-APR-2004
 cDNA clone B3CS1XGB016E10 3', mRNA sequence.
 CN546397.1 GI:46911022
 EST.
 Vitis vinifera
 Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
 Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
 Hamdi,S., Romieu,C. and Terrier,N.
 Title Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 JOURNAL Unpublished (2002)
 COMMENT

Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche
 Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES

source
 Location/Qualifiers

1..25
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
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 /dev_stage="green stage"
 /clone_lib="Green Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733

Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 884

CN546477/c

LOCUS

DEFINITION EST 18621 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CN546477 25 bp mRNA linear EST 30-APR-2004
 EST 18621 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
 cDNA clone B3CS7RB007D09 3', mRNA sequence.

CN546477
 EST.
 Vitis vinifera
 Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.

1 (bases 1 to 25)
 Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
 Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
 Hamdi,S., Romieu,C. and Terrier,N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages

Unpublished (2002)
 Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche
 Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France

Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

FEATURES

source
 Location/Qualifiers

1..25
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS7RB007D09"
 /dev_stage="ripe stage"
 /clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733

Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 885

CN546728/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CN546728 25 bp mRNA linear EST 30-APR-2004
 EST 18499 Turning Grape Berry Lambda Triplex2 Library Vitis
 vinifera cDNA clone B3CS8TB008B03 3', mRNA sequence.

CN546728
 EST.
 Vitis vinifera
 Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.

1 (bases 1 to 25)
 Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
 Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
 Hamdi,S., Romieu,C. and Terrier,N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages

Unpublished (2002)
 Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche
 Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France

Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

FEATURES

source
 Location/Qualifiers

1..25
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS8TB008B03"
 /dev_stage="veraison stage"
 /clone_lib="Turning Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733

Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 886

CV999835/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

CV999835 25 bp mRNA linear EST 03-DEC-2004
 iv53d12.b1 Right Cardiac Ventricle (DOGEST6) Canis familiaris cDNA,
 mRNA sequence.

CV999835
 EST.
 Canis familiaris (dog)
 Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.

1 (bases 1 to 25)
 Balija,V.S., Nascimento,L.U. and McCombie,W.R.
 ESTs from Canis familiaris right cardiac ventricle (dog)
 Unpublished (2004)

COMMENT

Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org

FEATURES

source

1. .25
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /db_xref="taxon:9615"
 /sex="Unknown"
 /tissue_type="Cardiac muscle"
 /dev_stages="3 month old normal canine"
 /lab_host="XL10 Gold"
 /clone_lib="Right Cardiac Ventricle (DOGEST6)"
 /note="Organ: Heart; Vector: pBluescript II SK; Site 1:
 EcoRI; Site 2: XhoI; Library constructed using pBluescript
 XR kit from Stratagene. Cloned cDNA was size selected
 between 1-3 Kb. Tissue supplied by Mark Haskins VMD, PhD,
 Pathology and Medical Genetics, School of Veterinary
 Medicine, University of Pennsylvania, 3800 Spruce Street,
 Philadelphia, PA 19104-6051"

Query Match

Best Local Similarity 0.9%; Score 25; DB 1; Length 25;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733

Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 887

LOCUS

DR073093 25 bp mRNA linear EST 08-JUN-2005
 ik8sh08.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA

DEFINITION

sequence.

ACCESSION

DR073093

VERSION

DR073093.1

KEYWORDS

EST.

SOURCE

Ginkgo biloba

ORGANISM

Eukaryota;

Viridiplantae;

Streptophyta;

Embryophyta;

Tracheophyta;

Spermatophyta;

Ginkgoales;

Ginkgoaceae;

Ginkgo.

REFERENCE

AUTHORS

1 (bases 1 to 25)

Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,

O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,

Benfey,P., Coruzzi,G. and Stevenson,D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

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Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.

FEATURES

source

1. .25
 /organism="Ginkgo biloba"
 /mol_type="mRNA"
 /db_xref="taxon:3311"
 /sex="female"
 /clone_lib="Ginkgo female leaf (NYBG)"
 /note="Organ: leaf; Vector: :pBK-CMV; Site 1: XhoI;
 Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
 The library was size-fractionated to enrich for large
 inserts."

Query Match

0.9%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 25

RESULT 888

LOCUS

DR073104/c 25 bp mRNA linear EST 08-JUN-2005
 ik86c01.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA

DEFINITION

sequence.

ACCESSION

DR073104

VERSION

DR073104.1

KEYWORDS

EST.

SOURCE

Ginkgo biloba

ORGANISM

Eukaryota;

Viridiplantae;

Streptophyta;

Embryophyta;

Tracheophyta;

Spermatophyta;

Ginkgoales;

Ginkgoaceae;

Ginkgo.

REFERENCE

AUTHORS

1 (bases 1 to 25)

Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,

O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,

Benfey,P., Coruzzi,G. and Stevenson,D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.

FEATURES

source

1. .25

/organism="Ginkgo biloba"

/mol_type="mRNA"

/db_xref="taxon:3311"

/sex="female"

/clone_lib="Ginkgo female leaf (NYBG)"

/note="Organ: leaf; Vector: :pBK-CMV; Site 1: XhoI;
 Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
 The library was size-fractionated to enrich for large
 inserts."

Query Match

0.9%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733

Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 889

LOCUS

DR073105/c 25 bp mRNA linear EST 08-JUN-2005
 ik86c07.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA

DEFINITION

sequence.

ACCESSION

DR073105

VERSION

DR073105.1

KEYWORDS

EST.

SOURCE

Ginkgo biloba

ORGANISM

Eukaryota;

Viridiplantae;

Streptophyta;

Embryophyta;

Tracheophyta;

Spermatophyta;

Ginkgoales;

Ginkgoaceae;

Ginkgo.

REFERENCE

AUTHORS

1 (bases 1 to 25)

Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,

O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,

Benfey,P., Coruzzi,G. and Stevenson,D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.

Qy 2709 AAAAAAAAAAAAAAAAAA 2733

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0078 row: I column: 24
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

source

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1. .25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0078124"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 25
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RESULT 893
 AZ350777/c
 LOCUS
 DEFINITION
 1M0088A04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0088A04 R, genomic survey sequence.
 ACCESSION
 AZ350777.1 GI:10430014
 VERSION
 GSS.
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 25)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0088 row: A column: 04
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

source

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1. .25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0088A04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
      |||||||
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1
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RESULT 894
 AZ389458
 LOCUS
 DEFINITION
 1M0150B06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0150B06 F, genomic survey sequence.
 ACCESSION
 AZ389458
 VERSION
 AZ389458.1 GI:10503166
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 25)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0150 row: B column: 06
 Seq primer: CGTTGTAACAGCAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

1. .25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0150B06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 25

RESULT 895
 AZ609234/c
 LOCUS 25 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0433H19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0433H19 R, genomic survey sequence.

ACCESSION AZ609234
 VERSION AZ609234.1 GI:11731424
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 25)
 DUNN, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0433 row: H column: 19
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

1. .25
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0433H19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
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 Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 896
 AZ623157/c

LOCUS 25 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0460L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0460L02 R, genomic survey sequence.

ACCESSION AZ623157
 VERSION AZ623157.1 GI:11745347
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 25)
 DUNN, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0460 row: L column: 02
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0460L02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
 Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 897

AZ788646/c
 LOCUS AZ788646 25 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M00351L19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M00351L9 R, genomic survey sequence.

ACCESSION AZ788646
 VERSION AZ788646.1 GI:12928656
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 25)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss
 University of Utah Genome Center

RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0035 row: L column: 19
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES

Location/Qualifiers
 1..25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0035L19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
 Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 898

AZ949287
 LOCUS AZ949287 25 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0212008R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0212008 R, genomic survey sequence.

ACCESSION AZ949287
 VERSION AZ949287.1 GI:13820514
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 25)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss
 University of Utah Genome Center

RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0212 row: 0 column: 08
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

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 /clone="UUGC2M0212008"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
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Query Match 0.98; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
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RESULT 899
 AZ980407/c
 LOCUS
 DEFINITION
 2M0257M19F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0257M19 F, Genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
 JOURNAL
 COMMENT
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
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 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

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 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
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 Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 900
 CZ914066
 LOCUS
 DEFINITION
 4013005D04.2EL_Y1 4013 - RescueMu Grid 0 Zea mays genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Zea mays
 Zea mays

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 25)
 Walbot,V.
 Unpublished (2001)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 4013005 row: D column: 04
 Class: transposon-tagged.

FEATURES
source

Location/Qualifiers
1..25
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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site.1: BamHI; Site.2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 901
LOCUS

DEFINITION CZ918479.1 25 bp DNA linear GSS 08-AUG-2005
4021009F02.2EL x1 4021 - RescueMu Grid v Zea mays genomic, genomic survey sequence.

ACCESSION CZ918479
VERSION CZ918479.1 GI:71938052
KEYWORDS GSS.

SOURCE

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 25)

REFERENCE Walbot.V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)

JOURNAL

COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221

Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021009 row: F column: 02
Class: transposon-tagged.

FEATURES

source

Location/Qualifiers
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/dev_stage="adult"
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/clone_lib="4021 - RescueMu Grid V"

/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site.1: BamHI; Site.2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
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Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 902
LOCUS

DEFINITION DUB29648/c 25 bp DNA linear GSS 22-DEC-2005
KBR5005E24F KBRs, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBR5005E24, genomic survey sequence.

ACCESSION DUB29648
VERSION DUB29648.1 GI:83866244

KEYWORDS

SOURCE GSS.

ORGANISM

Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 (bases 1 to 25)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seo, Y.J., Park, D.S., Hahn, J. H. and Park, B.S.

TITLE

End sequence of Brassica rapa Sau3AI (KBRs) BAC clone

JOURNAL

COMMENT Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa subsp. pekinensis Sau3AI BAC clone KBR5005E24
Seq primer: T7
Class: BAC ends.

FEATURES

source

Location/Qualifiers

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/clone="KBR5005E24"
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/note="Vector: pCUGIBAC1; Site.1: Sau3AI; Brassica rapa subsp pekinensis var. Chiifu BAC library (KBRs BAC) is available at NIAB."

Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
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Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 903
DUE832111/c
LOCUS
DEFINITION
  KBRs009K01R KBrS, Brassica rapa Sau3AI BAC library GSS 22-DEC-2005
  subsp. pekinensis genomic clone KBrS009K01, genomic survey
  sequence.
ACCESSION
  DUE832111
VERSION
  DUE832111.1 GI:83868707
KEYWORDS
  GSS.
SOURCE
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 25)
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J. H. and Park,B.S.
  End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
  KBrS009K01
  Seq primer: M13 Reverse
  Class: BAC ends.
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    available at NIAB."
  Query Match 0.9%; Score 25; DB 1; Length 25;
  Best Local Similarity 100.0%; Pred. No. 6e+02;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 904
DUE834405/c
LOCUS
DEFINITION
  KBRs014D09F KBrS, Brassica rapa Sau3AI BAC library GSS 22-DEC-2005
  subsp. pekinensis genomic clone KBrS014D09, genomic survey
  sequence.
ACCESSION
  DUE834405
VERSION
  DUE834405.1 GI:83871001
KEYWORDS
  GSS.
SOURCE
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
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  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 25)
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J. H. and Park,B.S.
  End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
  KBrS014D09
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  Best Local Similarity 100.0%; Pred. No. 6e+02;
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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 905
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LOCUS
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ACCESSION
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VERSION
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KEYWORDS
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SOURCE
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  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
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  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J. H. and Park,B.S.
  End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
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JOURNAL
COMMENT
  Unpublished (2005)
  Contact: Beom-Seok Park
  Brassica Genomics Team
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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    /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
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    available at NIAB."
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Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

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  Best Local Similarity 100.0%; Pred. No. 6e+02;
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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 905
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DEFINITION
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  subsp. pekinensis genomic clone KBrS014E03, genomic survey
  sequence.
ACCESSION
  DUE834424
VERSION
  DUE834424.1 GI:83871020
KEYWORDS
  GSS.
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  Brassica rapa subsp. pekinensis
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  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 25)
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J. H. and Park,B.S.
  End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  Brassica Genomics Team
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
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  Seq primer: M13 Reverse
  Class: BAC ends.
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ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NTAB."

Query Match      0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
    |||||||
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 906
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LOCUS      KBrS014K15F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
DEFINITION      subsp. pekinensis genomic clone KBrS014K15, genomic survey
sequence.
ACCESSION      DU834577
VERSION      DU834577.1 GI:83871173
KEYWORDS      GSS.
SOURCE      Brassica rapa subsp. pekinensis
ORGANISM      Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 25)
AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE      End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS014K15
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
    1..25
    /organism="Brassica rapa subsp. pekinensis"
    /mol_type="genomic DNA"
    /cultivar="Chiifu"
    /sub_species="pekinensis"
    /db_xref="taxon:51351"
    /clone="KBrS014K15"
    /lab_host="E. coli DH10B"
    /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
    /notes="Vector: pCUGIBAC1; Site.1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NTAB."

Query Match      0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
    |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 907
DX075967/c      25 bp      DNA      linear      GSS 10-JAN-2006
LOCUS      KBrS087B17F KBrS, Brassica rapa BamHI BAC library Brassica rapa
DEFINITION      subsp. pekinensis genomic clone KBrS087B17, genomic survey
sequence.
ACCESSION      DX075967
VERSION      DX075967.1 GI:84770263
KEYWORDS      GSS.
SOURCE      Brassica rapa subsp. pekinensis
ORGANISM      Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 25)
AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE      End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrS087B17
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
    1..25
    /organism="Brassica rapa subsp. pekinensis"
    /mol_type="genomic DNA"
    /cultivar="Chiifu"
    /sub_species="pekinensis"
    /db_xref="taxon:51351"
    /clone="KBrS087B17"
    /lab_host="E. coli DH10B"
    /clone_lib="KBrS, Brassica rapa BamHI BAC library"
    /notes="Vector: pCUGIBAC1; Site.1: BamHI; Brassica rapa ssp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match      0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
    |||||||
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 908
TA324E10P/c      25 bp      DNA      linear      GSS 13-DEC-2000
LOCUS      T. brucei sheared genomic DNA clone 324e10, forward sequence,
genomic survey sequence.
ACCESSION      AL493396
VERSION      AL493396.1 GI:11867761
KEYWORDS      GSS.
SOURCE      Trypanosoma brucei
ORGANISM      Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE      1 (bases 1 to 25)
AUTHORS      Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT      Constructed at the Institute for Genomic Research (TIGR),

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/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmiC2B02.q1k"
/dev_stages="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match      0.9%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db 1 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 912
CF296851/c
LOCUS
DEFINITION
30DGS--07-G13.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--07-G13, mRNA
sequence.
ACCESSION
CF296851
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..26
source
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--07-G13"
/tissue_type="leaf"
/dev_stages="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db 26 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 913
CN545723/c
LOCUS
DEFINITION
CN545723
EST 17667 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL005C03 3', mRNA sequence.
ACCESSION
CN545723

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CN545723.1 GI:46910348
EST
SOURCE
Vitis vinifera
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 26)
AUTHORS
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
FEATURES
Location/Qualifiers
1..26
source
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL005C03"
/dev_stages="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiI; Site_2: SfiI; Oriented library"

Query Match      0.9%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 914
AJ789548
LOCUS
DEFINITION
AJ789548 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018.2.03.c14, mRNA sequence.
ACCESSION
AJ789548
KEYWORDS
VERSION
AJ789548.1 GI:51058064
SOURCE
Antirrhinum majus (snapdragon)
ORGANISM
Antirrhinum majus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Lamiales; Plantaginaceae; Antirrhineae;
Antirrhinum.
1 (bases 1 to 27)
AUTHORS
Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
TITLE
Characterization of Antirrhinum Petal Development and
Identification of target Genes of the Class B MADS Box Gene
DEFICIENS
JOURNAL
Plant Cell 16 (12), 3197-3215 (2004)
COMMENT
15539471
Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
Location/Qualifiers
1..27
source

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/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_2_03_c14"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

Query Match      0.9%; Score 25; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
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Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 25

RESULT 915
TA244G08P/c
LOCUS TA244G08P/c 31 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 244g08, forward sequence,
genomic survey sequence.
ACCESSION AL483539
VERSION AL483539.1 GI:11849040
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 31)
Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R.,
Chillingworth C., Ormond B., Harris B., El-Sayed N., Hou L.,
Melville S.B., Rajandream M.A. and Barrell B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nleaved@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
1..31
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="244g08"

Query Match      0.9%; Score 25; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
    |||||||
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 916
CZ469056/c
LOCUS CZ469056/c 28 bp DNA linear GSS 29-APR-2005
DEFINITION c04188-Sprime Exelixis piggyBac PB insertions Drosophila
melanogaster genomic sequence recovered from 5' end of piggyBac,
genomic survey sequence.
ACCESSION CZ469056

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KEYWORDS
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
AUTHORS Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 26)
TITLE Dillon,G.P., Fellwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
1. .26
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmiC25d11.q1k"
/dev_stages="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match 0.9%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 918
CR546444
LOCUS DKFZp459P0513_r1 459 (synonym: pcorl) Pongo pygmaeus CDNA clone
DEFINITION DKFZp459P0513 5', mRNA sequence.
ACCESSION CR546444
VERSION CR546444.1 GI:49898669
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Pongo.
REFERENCE 1 (bases 1 to 26)
AUTHORS Ansoerge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
Pongo pygmaeus mRNA (Ansoerge,W., Krieger,S., Regiert,T., et al.)
Unpublished (2004)
Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European
Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp459P0513) is available at the RZPD in Berlin. Please contact
the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
1. .26
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp459P0513"
/tissue_type="cortex"

FEATURES
source
1. .26
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="459 (synonym: pcorl)"
/note="vector: pSPori_Sfi; Site_1: SfiI; Site_2: SfiIb"

Query Match 0.9%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 919
AZ355083
LOCUS 1M0094D14R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0094D14 R, genomic survey sequence.
ACCESSION AZ355083
VERSION AZ355083.1 GI:10467134
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0094 row: D column: 14
Seq primer: CACACAGGAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0094D14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and 14
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

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purified. The sheared, adapted mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 920
AZ623156/c
LOCUS
DEFINITION
A2623156 26 bp DNA linear GSS 13-DEC-2000
1M0460L01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0460L01 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
A2623156.1 GI:11745346
GSS.
Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: L column: 01
Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES
source
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0460L01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 921
AZ635695/c
LOCUS
DEFINITION
A2635695 26 bp DNA linear GSS 13-DEC-2000
1M0493G18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0493G18 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
A2635695.1 GI:11757885
GSS.
Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0493 row: G column: 18
Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES
source
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0493G18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

	Query Match	0.98;	Score 24.4;	DB 1;	Length 26;
	Best Local Similarity	96.2%;	Pred.No. 6.7e+02;		
	Matches	25;	Conservative	0; Mismatches	1; Indels
	Gaps	0;			
Qy	2709	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2734		
Dd	26	AAAAAAAAAGAAAAAAAAAAAAAAAAAAA	1		

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	Walbot V.	Maize genomic sequences found using engineered RescueMu transposon	Unpublished (2001)	
	Contact: Walbot V			
	Department of Biological Sciences			
	Stanford University			
	855 California Ave, Palo Alto, CA 94304, USA			
	Tel: 650 723 2227			
	Fax: 650 725 8221			
	Email: walbot@stanford.edu			
	Possible ligation site of ends cut by 2 different endonucleases.			
	Reverse complemented post-ligation sequence from source sequence.			
	Plate: 4021006	row: D	column: 12	
	Class: transposon-tagged.			

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FEATURES
source
Location/Qualifiers
1. 26
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A186/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. G
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

```

Query Match	0.9%	Score 24.4;	DB 1;	Length 26;
Best Local Similarity	96.2%;	Pred. No. 6.7e+03;		
Matches 25;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	2709	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2734	
Dd	26	AGAAAAAAAAAAAAAAAAAAAAAAAAAAA	1	

RESULT 923	CZ919575	26 bp	DNA	linear	GSS 08-AUG-2005
LOCUS	CZ919575/c				
DEFINITION	4021013G11.2EL.Y1 4021 - RescueMu Grid V Zea mays genomic, genomic survey sequence.				
ACCESSION	CZ919575				
VERSION	CZ919575.1	GI:71940233			
KEYWORDS	GSS.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
REFERENCE	1 (bases 1 to 26)				
AUTHORS	Walbot,V.				
TITLE	Maize genomic sequences found using engineered RescueMu transposon				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Walbot V				
	Department of Biological Sciences				
	Stanford University				
	855 California Ave, Palo Alto, CA 94304, USA				
	Tel: 650 723 2227				
	Fax: 650 725 8221				
	Email: walbot@stanford.edu				
	Possible ligation site of ends cut by 2 different endonucleases.				
	Reverse complemented post-ligation sequence from source sequence.				
	Plate: 4021013 row: G column: 11				

FEATURES

1. .26
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/Al98/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid v"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site '<http://www.mutransposon.org/project/RescueMu/>'. Grid v was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with

Query Match	0.9%	Score 24.4;	DB 1;	Length 26;
Best Local Similarity	96.2%	Pred. No. 6.7e+02;		
Matches 25: Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

2709 AAAAAAAAAAAAAAAAAAAAAA 2734

Db 26 AACAAAAAAAAAAAAAAAAAAAAA 1

RESULT	924
AG201580/c	
LOCUS	
DEFINITION	AG201580 Pan troglodytes DNA, clone: RP43-084C22.T7, Genomic survey sequence.
ACCESSION	AG201580
VERSION	AG201580.1 GI:45233755
KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes
Eukaryota; Metazoa;	
Mammalia; Eutheria;	
Euarchontoglires; Primates; Catarrhini;	
Vertebrata; Craniata; Chordata;	
Euteleostomi;	

```

REFERENCE
AUTHORS      Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
              Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
TITLE        BAC end sequences of Library RP-43
JOURNAL      Unpublished
REFERENCE
AUTHORS      Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
              Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
TITLE        Direct Submission
JOURNAL      Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
              Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
              52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
              (E-mail:redstone@mail.krrib.re.kr, URL:http://pbs.grc.krrib.re.kr/,
              Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT      Clones are derived from the chimpanzee BAC library RP-43 This BAC
              end was generated during the R&D process and may have higher chance
              of PRIMER tracking errors.
SEQUENCING: T7
LIBRARY
Vector       : pBACe3.6
R.Site 1     : EcoRI
R.Site 2     : EcoRI
FEATURES
source      Location/Qualifiers
              1..26
                /organism="Pan troglodytes"
                /mol_type="genomic DNA"
                /db_xref="taxon:9598"
                /clone="RP43-084C22.T7"
                /sex="male"
                /cell_type="lymphocytes"
                /clone_lib="RP-43 Chimpanzee Male BAC Library"
Query Match      0.9%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
Db 26 AAAAAAAAAAAGAAAAAAAAAAAAAAAAA 1

RESULT 925
LOCUS      DT471186
DEFINITION DT471186 BR_N05 PT-GT-FL-A-3 Populus trichocarpa cDNA clone
ACCESSION  DT471186
VERSION     DT471186.1 GI:73868448
KEYWORDS   EST.
SOURCE      Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
ORGANISM    Populus trichocarpa
REFERENCE
AUTHORS      Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,
              Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,
              Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,
              Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
              Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
              Bohlmann,J.
TITLE        The poplar transcriptome: Analysis of expressed sequence tags from
              multiple cDNA libraries
JOURNAL      Unpublished (2004)
COMMENT      Contact: Joerg Bohlmann
              Genome BC Forest Genomics program
              University of British Columbia
              Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
              Vancouver, British Columbia, Canada, V6T 1Z3
              Tel: 1-604-822-0282
              Fax: 1-604-822-2114

Hominidae; Pan.
1 Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
  Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
BAC end sequences of Library RP-43
2 (bases 1 to 26)
Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.krrib.re.kr, URL:http://pbs.grc.krrib.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of PRIMER tracking errors.
Sequencing: T7
LIBRARY
Vector       : pBACe3.6
R.Site 1     : EcoRI
R.Site 2     : EcoRI
FEATURES
source      Location/Qualifiers
              1..27
                /organism="Populus trichocarpa"
                /mol_type="mRNA"
                /cultivar="383-2499 (Nisqually-1)"
                /db_xref="taxon:3694"
                /clone="WS01212_N05"
                /sex="Female"
                /lab_host="E. coli DH10B T1 phage resistant cells"
                /clone_lib="PT-GT-FL-A-3"
                /notes="Vector: pBluescript II SK (+) XR; Site 1: SstI (5'
                end of cDNA); Site 2: XhoI (3' end of cDNA); Young and
                mature leaves, along with green stems, from 8 year old
                trees harvested within the Boise Cascade region of
                Washington state on May 15th, 2001. mRNA was isolated from
                each tissue source independently and equal quantities of
                mRNA from each tissue were then pooled. cDNA was prepared
                from 20 micrograms of mRNA according to the full-length
                cDNA library construction method described by Carninci P.
                et al. (2000), Genome Research 10(10):1617-1630 and
                directionally ligated into the pBluescript II SK (+) XR
                vector digested with SstI (5' end) and XhoI (3'). Plasmid
                DNA was then transformed by electroporation into DH10B
                cells (Invitrogen) for propagation."
Query Match      0.9%; Score 24.4; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 6.8e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2702 TTGTACTATAAAAAAAAAAAAAAAAAA 2728
Db 1 TTTTACNAAAAAAAAAAAAAAAAA 27

RESULT 926
LOCUS      N52529/c
DEFINITION N52529 27 bp mRNA linear EST 15-FEB-1996
              YV35a12.s1 Soares fetal liver spleen INFUS Homo sapiens cDNA clone
              IMAGE:244702 3' similar to gb:X68242 PUTATIVE HIV-1 INDUCED PROTEIN
              HIN-1 (HUMAN); mRNA sequence.
ACCESSION  N52529
VERSION     N52529.1 GI:1193695
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE
AUTHORS      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini,
              Homnidae; Homo.
              1 (bases 1 to 27)
              Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
              Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
              Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,P.,
              Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
              Wilson,R.
TITLE        The WashU-Merck EST Project
JOURNAL      Unpublished (1995)
COMMENT      Contact: Wilson RK
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              This clone is available royalty-free through LLNL; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              Trace considered overall poor quality
              Seq primer: m13 -40 forward
              High quality sequence stop: 1.
              Location/Qualifiers
              1..27

```

```

Query Match      0.9%; Score 24.4; DB 1; Length 28;
Best Local Similarity 96.2%; Pred. No. 6.9e+03;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 929
 T52836/c

LOCUS 28 bp mRNA linear EST 06-FEB-1995
 DEFINITION Y881809.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone
 IMAGE:68057 3' similar to gb:X53463 GLUTATHIONE
 PROXIDASE-GASTROINTESTINAL (HUMAN), mRNA sequence.

ACCESSION T52836

VERSION T52836.1 GI:654696

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 28)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
 Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
 Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
 Trevasakis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
 and Marra, M.

AUTHORS

1 (bases 1 to 28)

Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 8889549
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Insert Size: 51

TITLE

JOURNAL

PUBMED

COMMENT

High quality sequence starts: 1 High quality sequence stops: 1

Source: IMAGE Consortium, LLNL This clone is available royalty-free
 through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
 for further information. Trace considered overall poor quality
 Insert Length: 51 Std Error: 0.00
 Seq primer: -21ml3
 High quality sequence stop: 1.

FEATURES

source

1. .28

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:504314"

/db_xref="taxon:9606"

/clone="IMAGE:68057"

/sex="female"

/dev_stage="49 year old"

/lab_host="SOLR cells (kanamycin resistant)"

/clone_lib="Stratagene ovary (#937217)"

/notes="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI;
 Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt.
 Total ovary tissue, normal, caucasian. Average insert
 size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
 GAATTCGGCAGCG 3' -3' adaptor sequence: 5'
 CTCGAGTTTTTTTTTTTTTTTTTTT 3'."

Query Match

Best Local Similarity 0.9%; Score 24.4; DB 1; Length 28;

Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 930

AZ481286/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1. .28

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0303L24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source

1. .28

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0303L24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match

Best Local Similarity 0.9%; Score 24.4; DB 1; Length 28;

Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 931

CF299155/c

AZ481286 28 bp DNA linear GSS 04-OCT-2000
 IM0303L24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0303L24 F, genomic survey sequence.

ACCESSION AZ481286

VERSION AZ481286.1 GI:10642351

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 28)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 5606
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0303 row: 1 column: 24
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 28.

FEATURES

source

1. .28

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0303L24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."


```

RESULT 934
TA378G07P/c
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 378g07, forward sequence,
genomic survey sequence.
ACCESSION
AL497621
VERSION
AL497621.1 GI:11873343
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
1 (bases 1 to 29)
AUTHORS
Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R.,
Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,
Melville S.E., Rajandream M.A. and Barrell B.G.
DIRECT SUBMISSION
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhi@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kbp). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
1..29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/db_xref="TREU927"
/sb_xref="taxon:5691"
/clone="378g07"

Query Match 0.9%; Score 24.2; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 7.2e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2702 TTGTACTAAAAA 2730
|||
29 TTTTAAAAA 1

RESULT 935
AJ921827
LOCUS
DEFINITION
AJ921827 Theileria annulata piroplasm Theileria annulata CDNA clone
TAC20g08_pika, mRNA sequence.
ACCESSION
AJ921827
VERSION
AJ921827.1 GI:67492152
KEYWORDS
EST.
SOURCE
Theileria annulata
ORGANISM
Theileria annulata
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
Theileria.
REFERENCE
1 (bases 1 to 24)
AUTHORS
Pain A., Renaud H., Berriman M., Murphy L., Yeats C.A., Weir W.,
Kerhornou A., Aslett M., Bishop R., Bouchier C., Cochet M.,
Coulson R.M.R., Cronin A., de Villiers E., Fraser A., Fosker N.,
Gardner M., Goble A., Griffiths-Jones S., Harris D.E., Katzer F.,
Larke N., Lord A., Maser P., McKellar S., Mooney P., Morton F.,
Nene V., O'Neill S., Price C., Quail M.A., Rabinowitsch E.,
Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T.,
Squares R., Squares S., Tivey A., Walker A.R., Woodward J.,
Dobbelare D.A.E., Langsley G., Rajandream M.-A., McKeever D.,
Shiels B., Tait A., Barrell B. and Hall N.

The genome of the host-cell transforming parasite Theileria
annulata and a comparison with T. parva
Unpublished (2005)
Contact: Pain A
The Pathogen Sequencing Unit
The Wellcome Trust Sanger Institute
Genome Campus, CB10 1SA, UNITED KINGDOM
Piroplasm cDNA library: Frank Katzer and Brian Shiels, Division of
Veterinary Infection and Immunity, ICM, University of Glasgow, UK.
FEATURES
Location/Qualifiers
1..24
/organism="Theileria annulata"
/mol_type="mRNA"
/isolate="Ankara (clone D7)"
/db_xref="taxon:5874"
/clone="TAC20g08_pika"
/dev_stage="piroplasm"
/lab_host="Bos taurus (cow)"
/clone_lib="Theileria annulata piroplasm"
/note="country: Turkey; Ankara"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAA 2732
|||
1 AAAAAA 24

RESULT 936
AM043978
LOCUS
DEFINITION
AM043978 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC20c02.q1k, mRNA sequence.
ACCESSION
AM043978
VERSION
AM043978.1 GI:72292377
KEYWORDS
EST.
SOURCE
Schistosoma mansoni
ORGANISM
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 24)
AUTHORS
Dillon G.P., Feltwell T., Skelton J.P., Ashton P.D., Coulson P.S.,
Nikolaïdou-Katsaridou N., Quail M.A., Wilson R.A. and Ivens A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
1..24
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC20c02.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAA 2732
|||
1 AAAAAA 24

RESULT 937
AM045511

```


LOCUS AM045511 24 bp mRNA linear EST 20-SEP-2005
 DEFINITION AM045511 Schistosoma mansoni lung schistosomulum Schistosoma
 mansoni cDNA clone SmlC18g01.q1k, mRNA sequence.

ACCESSION AM045511
 VERSION AM045511.1 GI:75968795
 KEYWORDS EST.

SOURCE Schistosoma mansoni
 ORGANISM Schistosoma mansoni

REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 1 (bases 1 to 24)

AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
 Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
 TITLE Microarray analysis identifies genes preferentially expressed in
 the lung schistosomulum of Schistosoma mansoni

JOURNAL Unpublished (2005)

COMMENT Pathogen Microarrays Group
 Contact: Ivens AC
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
 source 1..24
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmlC18g01.q1k"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /note="country: Puerto Rico"

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 938

AM046329

LOCUS AM046329 24 bp mRNA linear EST 20-SEP-2005
 DEFINITION AM046329 Schistosoma mansoni lung schistosomulum Schistosoma
 mansoni cDNA clone SmlC20a08.q1k, mRNA sequence.

ACCESSION AM046329
 VERSION AM046329.1 GI:75970408
 KEYWORDS EST.

SOURCE Schistosoma mansoni
 ORGANISM Schistosoma mansoni

REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 1 (bases 1 to 24)

AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
 Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
 TITLE Microarray analysis identifies genes preferentially expressed in
 the lung schistosomulum of Schistosoma mansoni

JOURNAL Unpublished (2005)

COMMENT Pathogen Microarrays Group
 Contact: Ivens AC
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
 source 1..24
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmlC20a08.q1k"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /note="country: Puerto Rico"

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 939

AM048042/c

LOCUS AM048042 24 bp mRNA linear EST 20-SEP-2005
 DEFINITION AM048042 Schistosoma mansoni lung schistosomulum Schistosoma
 mansoni cDNA clone SmlC18f02.q1k, mRNA sequence.

ACCESSION AM048042
 VERSION AM048042.1 GI:75967816
 KEYWORDS EST.

SOURCE Schistosoma mansoni
 ORGANISM Schistosoma mansoni

REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 1 (bases 1 to 24)

AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
 Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
 TITLE Microarray analysis identifies genes preferentially expressed in
 the lung schistosomulum of Schistosoma mansoni

JOURNAL Unpublished (2005)

COMMENT Pathogen Microarrays Group
 Contact: Ivens AC
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
 source 1..24
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmlC18f02.q1k"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /note="country: Puerto Rico"

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
 Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 940

BG670391

LOCUS BG670391 24 bp mRNA linear EST 30-APR-2001
 DEFINITION DRNBAF06 Rat DRG Library Rattus norvegicus CDNA clone DRNBAF06 5',
 mRNA sequence.

ACCESSION BG670391
 VERSION BG670391.1 GI:13892490
 KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

AUTHORS Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,
 Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
 Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.

TITLE Identification of gene expression profile of dorsal root ganglion
 in the rat peripheral axotomy model of neuropathic pain

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)

PubMed 12060780

COMMENT Contact: Zhang Xu
 Laboratory of Sensory System
 Institute of Neuroscience
 320 Yue Yang Road, Shanghai 200031, P.R. China

Tel: 86-21-64748700-121
Fax: 86-21-64713446

Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong New Area, P.R.China. Please contact with Zhang Xu (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)

PCR Primers
FORWARD: T3
BACKWARD: T7

Seq primer: T3

POLYA=No.

FEATURES
source Location/Qualifiers
1. .24

/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRNBAP06"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732

Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 941

BX554611/c

LOCUS

DEFINITION BX554611 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse16d06_pic, mRNA sequence.

ACCESSION BX554611

VERSION BX554611.1

KEYWORDS BX554611.1 GI:33378684

SOURCE EST.

ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Hippoboscoidae; Glossiniidae; Glossina.

REFERENCE 1 (bases 1 to 24)

AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,

Hamilton, J., Soares, M.B., Bonaldo, W.F., Lehane, S. and Hall, N.

Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune

response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)

PUBMED 14519198

COMMENT

Contact: Hall N

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J.Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from

the 3' end.

FEATURES

source

1. .24 Location/Qualifiers

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clone="Tse16d06_pic"

/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/notes="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732

Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 942

CF276855

LOCUS

DEFINITION CF276855 24 bp mRNA linear EST 14-AUG-2003
Oryza sativa Japonica cultivar-group) cDNA clone 14ETL--02-C19,
mRNA sequence.

ACCESSION CF276855

VERSION CF276855.1

KEYWORDS GI:33654241

SOURCE EST.

ORGANISM Oryza sativa Japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzoae; Oryza.

REFERENCE 1 (bases 1 to 24)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .24 Location/Qualifiers

/organism="Oryza sativa Japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ETL--02-C19"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice etiolated leaf plasmid cDNA library

(14ETL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.9%; Score 24; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732

Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 943

CF301561/c

LOCUS

DEFINITION CF301561

7LEAF--06-H15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa Japonica cultivar-group) cDNA clone 7LEAF--06-H15, mRNA

sequence.

ACCESSION CF301561

VERSION

Best Local Similarity 100.0%; Pred. No. 6.8e+02; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 949
CN546689/c
LOCUS
DEFINITION EST 18460 Turning Grape Berry Lambda Triplex2 Library Vitis
vinifera cDNA clone B3C537B007F12 3', mRNA sequence.

ACCESSION CN546689.1 GI:46911314
VERSION
KEYWORDS
SOURCE

ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

REFERENCE
AUTHORS 1 (bases 1 to 24)

TITLE
JOURNAL
COMMENT Abbal P., Agasse A., Agorces A., Atanassova R., Barrieu F.,
Couture C., Dedaldecamp F., Delrot S., Glissant D., Grimplet J.,
Haudry S., Romieu C. and Terrier N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages

UNPUBLISHED (2002)
CONTACT: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France

Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..24
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:23760"
/clone="B3C537B007F12"
/dev_stage="veraison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 950
DR073080/c
LOCUS
DEFINITION ik85902.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.

ACCESSION DR073080.1 GI:67050929
VERSION
KEYWORDS
SOURCE

ORGANISM
Ginkgo biloba (maidenhair tree)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

REFERENCE
AUTHORS 1 (bases 1 to 24)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,

O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)

CONTACT: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES
source
1..24
Location/Qualifiers

/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 951
DR074082/c

LOCUS
DEFINITION ik95a04.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.

ACCESSION DR074082.1 GI:67052028
VERSION
KEYWORDS
SOURCE

ORGANISM
Ginkgo biloba (maidenhair tree)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

REFERENCE
AUTHORS 1 (bases 1 to 24)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Ginkgo male leaf (NYBG)
Unpublished (2005)

CONTACT: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES
source
1..24
Location/Qualifiers

/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="male"
/clone_lib="Ginkgo male leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI; Site_2:
Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large
inserts."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 |||||
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 952
 AZ328848
 LOCUS
 DEFINITION 24 bp DNA linear GSS 29-SEP-2000
 clone UUGC1M0052M17 R, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS

1 (bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0052 row: M column: 17
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES
 source
 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0052M17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 953
 AZ363562
 LOCUS
 DEFINITION 24 bp DNA linear GSS 02-OCT-2000
 1M0109G10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0109G10 F, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS

1 (bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0109 row: G column: 10
 Seq primer: CGTTGTAAACGACGCCGACGT
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES
 source
 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0109G10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 954
AZ386491 24 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0145D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0145D02 R, genomic survey sequence.
ACCESSION AZ386491
VERSION AZ386491.1 GI:10500191
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: D column: 02
Seq primer: CACACGAGNACGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0145D02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [GI|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
Source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0145D02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [GI|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 955
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LOCUS 1M0152H07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0152H07 F, genomic survey sequence.
ACCESSION AZ390642
VERSION AZ390642.1 GI:10505685
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0152 row: H column: 07
Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
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/clone="UUGC1M0152H07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [GI|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
Source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0152H07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [GI|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
      |||||
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 956
AZ459280/c
LOCUS
DEFINITION
  AZ459280 24 bp DNA linear GSS 04-OCT-2000
  clone UUGC1M0264A05 F, genomic survey sequence.
ACCESSION
  AZ459280
VERSION
  AZ459280.1 GI:10617405
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 24)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
JOURNAL
  Contact: Robert B. Weiss
COMMENT
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0264 row: A column: 05
  Seq primer: CGTGTAAACAGCGCCAGT
  Class: plasmid ends
  High quality sequence stop: 24.

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    /clone="UUGC1M0264A05"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /notes="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
      |||||
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 957
AZ644621/c
LOCUS
DEFINITION
  AZ644621 24 bp DNA linear GSS 14-DEC-2000
  clone UUGC1M0508F12 R, genomic survey sequence.
ACCESSION
  AZ644621
VERSION
  AZ644621.1 GI:11773331
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 24)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
JOURNAL
  Contact: Robert B. Weiss
COMMENT
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0508 row: F column: 12
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 24.

FEATURES
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    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0508F12"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /notes="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2732

Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 958
A2834990
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

A2834990 24 bp DNA linear GSS 20-FEB-2001
2M0129A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0129A05 F, genomic survey sequence.

A2834990
A2834990.1 GI:13004898
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: A column: 05
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [GI|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source
1. .24
/organism="Mus musculus"
/mol_type="Genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0243J02"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [GI|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2732

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 959
A2970038
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

A2970038 24 bp DNA linear GSS 27-APR-2001
2M0243J02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0243J02 F, genomic survey sequence.

A2970038
A2970038.1 GI:13841265
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0243 row: J column: 02
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
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(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
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electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [GI|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 960
 AZ984490
 LOCUS
 DEFINITION 24 bp DNA linear GSS 27-APR-2001
 clone UUGC2M0266H05 F, genomic survey sequence.
 ACCESSION AZ984490
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 24)

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0266 row: H column: 05
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES
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 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
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 /clone="UUGC2M0266H05"
 /sex="Female"
 /lab_hosts="E. coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
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 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 961
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 LOCUS
 DEFINITION 24 bp DNA linear GSS 27-APR-2001
 clone UUGC2M0278019 F, genomic survey sequence.
 ACCESSION AZ993423
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 24)

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0278 row: O column: 19
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES
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 /db_xref="taxon:10090"
 /clone="UUGC2M0278019"
 /sex="Female"
 /lab_hosts="E. coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 962
DU829467/c
LOCUS
DEFINITION
subsp. pekinensis genomic clone KBrS004P08, genomic survey
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis Sau3AI BAC clone
KBrS004P08
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
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1..24
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/clone="KBrS004P08"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 964
DX047568/c
LOCUS
DEFINITION
subsp. pekinensis genomic clone KBrS049J13, genomic survey
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrS049J13
Seq primer: T7
Class: BAC ends.

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 963
DU830197/c
LOCUS
DEFINITION
subsp. pekinensis genomic clone KBrS006E20, genomic survey
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS006E20
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
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/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 964
DX047568/c
LOCUS
DEFINITION
subsp. pekinensis genomic clone KBrS049J13, genomic survey
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrS049J13
Seq primer: T7
Class: BAC ends.

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FEATURES
  source
    Location/Qualifiers
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        /lab_host="E.coli DH10B"
        /clone_lib="KBrB, Brassica rapa BamHI BAC library"
        /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
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        by Yong-Pyo Lim (CNU)."

Query Match      0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 965
DX049347/C
LOCUS
DEFINITION
  KBrB051P01F KBrB, Brassica rapa BamHI BAC library Brassica rapa
  subsp. pekinensis genomic clone KBrB051P01, genomic survey
  sequence.
ACCESSION
  DX049347
KEYWORDS
  GSS.
SOURCE
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 24)
  Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J.H. and Park,B.S.
  End sequence of Brassica rapa BamHI (KBrB) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  Brassica Genomics Team
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa spp. pekinensis BamHI BAC clone
  KBrB051P01
  Seq primer: T7
  Class: BAC ends.
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      /sub_species="pekinensis"
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      /clone="KBrB051P01"
      /lab_host="E.coli DH10B"
      /clone_lib="KBrB, Brassica rapa BamHI BAC library"
      /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
      pekinensis var. Chiifu BAC library (KBrB BAC) is provided
      by Yong-Pyo Lim (CNU)."

Query Match      0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732

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Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 966
DX053980/C
LOCUS
DEFINITION
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  subsp. pekinensis genomic clone KBrB058A21, genomic survey
  sequence.
ACCESSION
  DX053980
KEYWORDS
  GSS.
SOURCE
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 24)
  Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J.H. and Park,B.S.
  End sequence of Brassica rapa BamHI (KBrB) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  Brassica Genomics Team
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa spp. pekinensis BamHI BAC clone
  KBrB058A21
  Seq primer: M13 Reverse
  Class: BAC ends.
  Location/Qualifiers
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      /sub_species="pekinensis"
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      /clone="KBrB058A21"
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      /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
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      by Yong-Pyo Lim (CNU)."

Query Match      0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 967
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LOCUS
DEFINITION
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  subsp. pekinensis genomic clone KBrB081P14, genomic survey
  sequence.
ACCESSION
  DX072040
KEYWORDS
  GSS.
SOURCE
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 24)

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AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
              Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
              Hahn,J.H. and Park,B.S.
TITLE        End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
              Brassica Genomics Team
              National Institute of Agricultural Biotechnology
              225 Seodun-Dong, Suwon, 441-707, Korea
              Tel: +82-31-299-1670
              Fax: +82-31-299-1672
              Email: pbeom@da.go.kr
              BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
              KBrB081p14
Seq primer:  T7
Class:  BAC ends.
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                /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
                pekinensis var. Chiifu BAC library (KBrB BAC) is provided
                by Yong-Pyo Lim (CNU)."
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Query Match      0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 969
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LOCUS
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                  KBrB095116F KBrB, Brassica rapa BamHI BAC library Brassica rapa
                  subsp. pekinensis genomic clone KBrB095116, genomic survey
                  sequence.
ACCESSION      DX082296
VERSION        DX082296.1 GI:84776592
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
                  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
                  Hahn,J.H. and Park,B.S.
TITLE          End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL        Unpublished (2005)
COMMENT        Contact: Beom-Seok Park
                  Brassica Genomics Team
                  National Institute of Agricultural Biotechnology
                  225 Seodun-Dong, Suwon, 441-707, Korea
                  Tel: +82-31-299-1670
                  Fax: +82-31-299-1672
                  Email: pbeom@da.go.kr
                  BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                  KBrB095116
Seq primer:  T7
Class:  BAC ends.
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                /clone="KBrB095116"
                /lab_host="E.coli DH10B"
                /clone_lib="KBrB, Brassica rapa BamHI BAC library"
                /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
                pekinensis var. Chiifu BAC library (KBrB BAC) is provided
                by Yong-Pyo Lim (CNU)."
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Query Match      0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 968
DX080492
LOCUS
DEFINITION      DX080492 24 bp DNA linear GSS 10-JAN-2006
                  KBrB093A19R KBrB, Brassica rapa BamHI BAC library Brassica rapa
                  subsp. pekinensis genomic clone KBrB093A19, genomic survey
                  sequence.
ACCESSION      DX080492
VERSION        DX080492.1 GI:84774788
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
                  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
                  Hahn,J.H. and Park,B.S.
TITLE          End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL        Unpublished (2005)
COMMENT        Contact: Beom-Seok Park
                  Brassica Genomics Team
                  National Institute of Agricultural Biotechnology
                  225 Seodun-Dong, Suwon, 441-707, Korea
                  Tel: +82-31-299-1670
                  Fax: +82-31-299-1672
                  Email: pbeom@da.go.kr
                  BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
                  KBrB093A19
Seq primer:  M13 Reverse
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                1. .24
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RESULT 970
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LOCUS
DEFINITION
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genomic survey sequence.
ACCESSION
AL478922
VERSION
AL478922.1 GI:11840452
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma
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/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="169d12"
REFERENCE
AUTHORS
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE
Direct Submission
JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
1..24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="169d12"
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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 971
TA27B08Q
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 27b08, reverse sequence,
genomic survey sequence.
ACCESSION
AL453584
VERSION
AL453584.1 GI:11850982
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma
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/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="169d12"
REFERENCE
AUTHORS
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE
Direct Submission
JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),

```

Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

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1..24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
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Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732

Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 972

TA354C06P

LOCUS

DEFINITION

T. brucei sheared genomic DNA clone 354c06, forward sequence,

genomic survey sequence.

ACCESSION

AL494439

VERSION

AL494439.1 GI:11870896

KEYWORDS

GSS.

SOURCE

Trypanosoma brucei

ORGANISM

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma

1 (bases 1 to 24)

REFERENCE

AUTHORS

Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajandream,M.A. and Barrell,B.G.

TITLE

Direct Submission

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nhl@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

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1..24
/organism="Trypanosoma brucei"
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="354c06"

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 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 973
TA371F1LP 24 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 371f11, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL495622
VERSION AL495622.1 GI:11871906
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..24
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/strain="TREU927"
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/clone="371f11"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 975
AL587648/c
LOCUS AL587648 BP Chicken Brain Library Gallus gallus cdna clone
DEFINITION ROS060C07, mRNA sequence.
ACCESSION AL587648
VERSION AL587648.1 GI:13192682
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archoeauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 25)
AUTHORS Murray,F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
(*6854-

Seq primer: M13F.
Location/Qualifiers
1..25
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS060C07"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_hosts="DH10B"
/clone_lib="BP Chicken Brain Library"
/notes="vector: pSPORil; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 974
TA95B08P 24 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 95b08, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL459003
VERSION AL459003.1 GI:11861374
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

```

```

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..24
/organism="Trypanosoma brucei"
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/db_xref="taxon:5691"
/clone="95b08"

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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 975
AL587648/c
LOCUS AL587648 BP Chicken Brain Library Gallus gallus cdna clone
DEFINITION ROS060C07, mRNA sequence.
ACCESSION AL587648
VERSION AL587648.1 GI:13192682
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archoeauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 25)
AUTHORS Murray,F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
(*6854-

Seq primer: M13F.
Location/Qualifiers
1..25
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS060C07"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_hosts="DH10B"
/clone_lib="BP Chicken Brain Library"
/notes="vector: pSPORil; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from

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Clonetechn (*6854-1)

Query Match      0.9%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 976
CF317007/c
LOCUS
DEFINITION
HD-06-114.g1 OsHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD-06-114, mRNA sequence.
CF317007
CF317007.1 GI:33688768
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzoideae; Oryza.
1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-06-114"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.9%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2731
Db 24 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 977
CF638767
LOCUS
DEFINITION
D06.G05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
sequence.
CF638767
CF638767.1 GI:37402758
EST.
Ustilago maydis

Clonetechn (*6854-1)

Query Match      0.9%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 976
CF317007/c
LOCUS
DEFINITION
HD-06-114.g1 OsHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD-06-114, mRNA sequence.
CF317007
CF317007.1 GI:33688768
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzoideae; Oryza.
1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.9%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2731
Db 24 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 977
CF638767
LOCUS
DEFINITION
D06.G05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
sequence.
CF638767
CF638767.1 GI:37402758
EST.
Ustilago maydis

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This clone is available royalty-free through LNLN ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: ml3 -40 forward
High quality sequence stop: 1.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:270480"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2NbHM"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCACTCTGAGTCGAGCGCGCGACTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaído. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

Query Match 0.9%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e+07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732

DB 25 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 979

AZ381039
LOCUS 25 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0137N18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0137N18 F, genomic survey sequence.
ACCESSION AZ381039
VERSION AZ381039.1 GI:10494739
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Place: 0137 row: N column: 18
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1. .25
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0137N18"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMP42 [GI4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732

DB 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 980

CF639306
LOCUS 26 bp mRNA linear EST 02-OCT-2003
DEFINITION D14_A02 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA sequence.
ACCESSION CF639306
VERSION CF639306.1 GI:37403783
KEYWORDS EST.
SOURCE Ustilago maydis
ORGANISM Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE 1 (bases 1 to 26)
AUTHORS Nugent,K.G., Choffe,K. and Saville,B.J.
TITLE Gene expression during Ustilago maydis diploid filamentous growth: EST library creation and analyses
JOURNAL Fungal Genet. Biol. 41 (3), 349-360 (2004)
PUBMED 14761795
COMMENT Contact: Barry J. Saville
Saville Lab
University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utoronto.ca
Plate: UTM-UM-D126/7-014-UTM row: 02 column: A
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')
High quality sequence stop: 26.
Location/Qualifiers
1. .26
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="FBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"

FEATURES

source
Location/Qualifiers
1. .26
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/strain="FBD12"
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/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"

Query Match 0.9%; Score 24; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
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 Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 983
 CF299084/c
 LOCUS
 DEFINITION HD--08-B07.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-P02, mRNA sequence.

ACCESSION CF299084 GI:33670845
 VERSION
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1 (bases 1 to 27)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..27
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--02-P02"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 23.8; DB 1; Length 27;
 Best Local Similarity 92.6%; Pred. No. 7.4e+02;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 27 AAACCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 984
 CF318113
 LOCUS
 DEFINITION HD--08-B07.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--08-B07, mRNA sequence.

ACCESSION CF318113 GI:33689874
 VERSION
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE
 AUTHORS
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..27
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--08-B07"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.9%; Score 23.8; DB 1; Length 27;
 Best Local Similarity 92.6%; Pred. No. 7.4e+02;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 1 AAAAAAAAAACCAAAAAAAAAAAAAA 27

RESULT 985
 R59382/c
 LOCUS
 DEFINITION YH17e07.g1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:37726 3' similar to gb:M65131 METHYLMALONYL-COA MUTASE PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION R59382 GI:830077
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 27)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality

Possible reversed clone: polyT not found

Seq primer: SP6

High quality sequence stop: 1.

FEATURES

source

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1. .27
  /location="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="GDB:410267"
  /db_xref="taxon:9606"
  /clone="IMAGE:37726"
  /sex="female"
  /dev_stage="73 days post natal"
  /lab_host="DH10B (ampicillin resistant)"
  /clone_lib="Soares infant brain INIB"
  /notes="Organ: whole brain; Vector: Lfamid BA; Site 1: Not
  I; Site 2: Hind III; 1st strand cDNA was primed with a Not
  I - oligo(dT) primer [5',
  AACTGGAAGATTGCGGCGCGAGGATTTTCTTTTCTTTT 3'];
  double-stranded cDNA was ligated to Hind III adaptors
  (Pharmacia), digested with Not I and directionally cloned
  into the Not I and Hind III sites of the Lfamid BA vector.
  Library went through one round of normalization. Library
  constructed by Bento Soares and M.Fatima Bonaldo."
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Query Match 0.9%; Score 23.8; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 7.4e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2707 CTAAGAAAAA 28 bp DNA linear GSS 08-AUG-2005

LOCUS 4013005F10.2EL_x1 4013 - RescueMu Grid O Zea mays genomic, genomic

DEFINITION survey sequence.

ACCESSION CZ914142

VERSION CZ914142.1 GI:71930586

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 28)
AUTHORS Walbot,V.
TITLE Possible ligations site of ends cut by 2 different endonucleases.
JOURNAL Possible ligation site of ends cut by 2 different endonucleases.
COMMENT Reverse complemented post-ligation sequence from source sequence.
Plate: 4013005 row: F column: 10
Class: transposon-tagged.

FEATURES
source
1. .28
/location="Homo sapiens"
/mol_type="genomic DNA"
/cultivar="mixed background w23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII;

FEATURES

source

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1. .28
  /organism="Zea mays"
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  /cultivar="mixed background w23/A188/B73/K55"
  /db_xref="taxon:4577"
  /tissue_type="leaf"
  /dev_stage="adult"
  /lab_host="DH10B"
  /clone_lib="4013 - RescueMu Grid O"
  /note="Organ: leaf; Vector: RescueMu (engineered from
  pBluescript backbone); Site_1: BamHI; Site_2: BglII;

```

RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.9%; Score 23.8; DB 1; Length 28;
Best Local Similarity 92.8%; Pred. No. 7.5e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 28 bp DNA linear GSS 10-JAN-2006

LOCUS KBR081124F KBrB, Brassica rapa BamHI BAC library Brassica rapa

DEFINITION subsp. pekinensis genomic clone KBR081124, genomic survey

ACCESSION DX071727

VERSION DX071727.1 GI:84766023

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis

REFERENCE 1 (bases 1 to 28)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBR081124
Seq primer: T7
Class: BAC ends.

FEATURES
source
1. .28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBR081124"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.9%; Score 23.8; DB 1; Length 28;
Best Local Similarity 92.6%; Pred. No. 7.5e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 28 bp DNA linear GSS 10-JAN-2006

LOCUS KBR081124F KBrB, Brassica rapa BamHI BAC library Brassica rapa

DEFINITION subsp. pekinensis genomic clone KBR081124, genomic survey

ACCESSION DX071727

VERSION DX071727.1 GI:84766023

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis

REFERENCE 1 (bases 1 to 28)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBR081124
Seq primer: T7
Class: BAC ends.

FEATURES
source
1. .28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBR081124"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.9%; Score 23.8; DB 1; Length 28;
Best Local Similarity 92.6%; Pred. No. 7.5e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 28 bp DNA linear GSS 10-JAN-2006

LOCUS KBR081124F KBrB, Brassica rapa BamHI BAC library Brassica rapa

DEFINITION subsp. pekinensis genomic clone KBR081124, genomic survey

ACCESSION DX071727

VERSION DX071727.1 GI:84766023

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis

REFERENCE 1 (bases 1 to 28)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBR081124
Seq primer: T7
Class: BAC ends.

FEATURES
source
1. .28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBR081124"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.9%; Score 23.8; DB 1; Length 28;
Best Local Similarity 92.6%; Pred. No. 7.5e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 28 bp DNA linear GSS 10-JAN-2006

LOCUS KBR081124F KBrB, Brassica rapa BamHI BAC library Brassica rapa

DEFINITION subsp. pekinensis genomic clone KBR081124, genomic survey

ACCESSION DX071727

VERSION DX071727.1 GI:84766023

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis

REFERENCE 1 (bases 1 to 28)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBR081124
Seq primer: T7
Class: BAC ends.

FEATURES
source
1. .28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBR081124"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.9%; Score 23.8; DB 1; Length 28;
Best Local Similarity 92.6%; Pred. No. 7.5e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 28 bp DNA linear GSS 10-JAN-2006

LOCUS KBR081124F KBrB, Brassica rapa BamHI BAC library Brassica rapa

DEFINITION subsp. pekinensis genomic clone KBR081124, genomic survey

ACCESSION DX071727

VERSION DX071727.1 GI:84766023

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis

REFERENCE 1 (bases 1 to 28)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBR081124
Seq primer: T7
Class: BAC ends.

FEATURES
source
1. .28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBR081124"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.9%; Score 23.8; DB 1; Length 28;
Best Local Similarity 92.6%; Pred. No. 7.5e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 28 bp DNA linear GSS 10-JAN-2006

LOCUS KBR081124F KBrB, Brassica rapa BamHI BAC library Brassica rapa

DEFINITION subsp. pekinensis genomic clone KBR081124, genomic survey

ACCESSION DX071727

VERSION DX071727.1 GI:84766023

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis

REFERENCE 1 (bases 1 to 28)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBR081124
Seq primer: T7
Class: BAC ends.

FEATURES
source
1. .28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBR081124"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

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RESULT 988
AZ404078
LOCUS
DEFINITION
  AZ404078F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0172J07 F, genomic survey sequence.
ACCESSION
  AZ404078.1 GI:10528091
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 25)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Bescorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0172 row: J column: 07
  Seq primer: CGTTGTAAACACGCGCCAGT
  Class: plasmid ends
  High quality sequence stop: 25.
FEATURES
  source
    1..25
    Location/Qualifiers
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0172J07"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnates/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adaptor DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
      inducible derivative of plasmid R1. The vector was ligated
      with adaptors complementary to the insert adaptors and
      purified. The sheared, adaptor mouse DNA was annealed to
      adaptor vector DNA, and transformed into
      chemically-competent E. coli XL10-Gold (Stratagene) cells
      and selected for ampicillin resistance."

```

```

Query Match      0.9%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 7.5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
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Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 25

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RESULT 989
DU833936/C
LOCUS
DEFINITION
  DU833936F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
  subsp. pekinensis genomic clone KBrS013B15, genomic survey
  sequence.
ACCESSION
  DU833936
VERSION
  DU833936.1 GI:83870532
KEYWORDS
  GSS.
SOURCE
  Brassica rapa subsp. pekinensis
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 25)
AUTHORS
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seo,I.Y.J., Park,D.S.,
  Hahn,J. H. and Park,B.S.
TITLE
  End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL
  Unpublished (2005)
COMMENT
  Contact: Beom-Seok Park
  Brassica Genomics Team
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@daum.net
  BAC end sequence of Brassica rapa subsp. pekinensis Sau3AI BAC clone
  KBrS013B15
  Seq primer: T7
  Class: BAC ends.
FEATURES
  source
    1..25
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      /mol_type="genomic DNA"
      /cultivar="Chiifu"
      /sub_species="pekinensis"
      /db_xref="taxon:51351"
      /clone="KBrS013B15"
      /lab_host="E. coli DH10B"
      /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
      /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
      subsp. pekinensis var. Chiifu BAC library (KBrS BAC) is
      available at NIAB."
Query Match      0.9%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 7.5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
      ||||||||||||||||||||||||||||
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 990
DU834323
LOCUS
DEFINITION
  DU834323F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
  subsp. pekinensis genomic clone KBrS013P19, genomic survey
  sequence.
ACCESSION
  DU834323
VERSION
  DU834323.1 GI:83870919
KEYWORDS
  GSS.
SOURCE
  Brassica rapa subsp. pekinensis
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 25)
AUTHORS
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seo,I.Y.J., Park,D.S.,
  Hahn,J. H. and Park,B.S.

```



```

TITLE
JOURNAL
COMMENT
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa esp. pekinensis Sau3AI BAC clone
KBrS013P19
Seq primer: T7
Class: BAC ends
Location/Qualifiers
1. .25
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS013P19"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: PCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chifu BAC library (KBrS BAC) is
available at NIAB."

Query Match
Best Local Similarity 0.9%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
||||| AAAAAAAAAAAAAAAAAAAAAA 25
Db 1 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 991
CF299646/c
LOCUS
DEFINITION
26 bp mRNA linear EST 15-AUG-2003
7LEAF--03-L24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L24, mRNA
sequence.
CF299646
CF299646.1 GI:33671407
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BIP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nam,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nam B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .26
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-L24"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

FEATURES
source

```

```

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 0.9%; Score 23.4; DB 1; Length 26;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAA 2730
||||| AAAAAAAAAAAAAAAAAAAAAA 1
Db 25 ATTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 992
AZ316353
LOCUS
DEFINITION
26 bp DNA linear GSS 29-SEP-2000
1M0034D09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0034D09 F, genomic survey sequence.
AZ316353
AZ316353.1 GI:10364094
GSS.
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: D column: 09
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0034D09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWP42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to

```

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match      0.9%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 7.6e+00;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 1 AAAAAAAAAAAATAAAAAAAAAAAAAAAAA 25

```

RESULT 993	AL587582/C	28 bp	linear	EST 02-MAR-2001
LOCUS	AL587582	28 bp	linear	EST 02-MAR-2001
DEFINITION	BP Chicken Brain Library Gallus gallus clone ROS059D03. mRNA sequence.	28 bp	linear	EST 02-MAR-2001

ACCESSION NUMBER	VERSION	KEYWORDS	SOURCE	ORGANISM
AL587582	AL587582.1	GI:13192616	Gallus gallus (chicken)	
EST.			Gallus gallus	
			Gallus gallus	
			Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
			Phasianidae; Galliformes; Phasianinae; Gallus.	
			Phasianinae; Gallus.	

REFERENCE
Murray, F.
AUTHORS
BP Chicken Brain Library
TITLE
Unpublished (2001)
JOURNAL
Contact: Frazer Murray
COMMENT
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGCGCGCTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13F.

```

seq primer: 5181.
Location/Qualifiers
1. .28
  /organism="Gallus gallus"
  /mol_type="mRNA"
  /db_xref="taxon:9031"
  /clone="ROS059D03"
  /tissue_type="Brain"
  /dev_stage="Unknown"
  /lab_host="DH10B"
  /clone_lib="BP Chicken Brain Library"
  /note="Vector: pSPORT1; Site 1: Not1; Site 2: Sal1; Cloned
  unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
  5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
  GCGCCGCGCTTTTTTTTTTTTTTTT 3' poly A RNA purchased from
  Clontech (*6854-1)"

```

```

Query Match      0.9%; Score 23.4; DB 1; Length 28;
Best Local Similarity 92.3%; Pred. No. 7.9e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2707 CTAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2732
    | | | | | | | | | | | | | | | | | |
Db 27 CCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAA 2
    | | | | | | | | | | | | | | | | | |

```

RESULT 994	AU257468	28 bp	linear	EST 25-APR-2002
LOCUS	AU257468	3'-directed mouse cDNA library	Mus musculus	
DEFINITION	BD0010669	3', mRNA sequence.		
ACCESSION	AU257468			
VERSION	AU257468.1	GI:20322117		
KEYWORDS	EST.			

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 28)
TITLE	Kato,K. and Matoba,R.
JOURNAL	Generation of expressed sequence tags from mouse brain
COMMENT	Unpublished (2002) Contact: Kikuya Kato Graduate School of Biological Sciences Nara Institute of Science and Technology 8916-5 Takayama, Ikoma, Nara 630-0101, Japan Tel: 81-743-72-5581 Fax: 81-743-72-5589 Email: k.kato@bs.nara.ac.jp, URL: http://love2.aist-nara.ac.jp/BED/index.html . Location/Qualifiers
FEATURES	

```

1. .28
source
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0010669"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"

Query Match      0.9%; Score 23.4; DB 1; Length 28;
Best Local Similarity 92.3%; Pred. No. 7.9e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
      |||||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3
      |||||||

```

RESULT	995				
DR064440					
LOCUS	DR064440	29 bp	mRNA	linear	EST 06-JUN-2005
DEFINITION	ip65c01.g1	Ginkgo megasporophyll	(NYBG)	Ginkgo biloba	cDNA 3', mRNA sequence.

ACCESSION	DR064440	GI:69888008	
VERSION	DR064440.1		
KEYWORDS	EST.		
SOURCE	Ginkgo biloba (maidenhair tree)		
ORGANISM	Ginkgo biloba		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo. 1 (bases 1 to 29)		
AUTHORS	Brenner E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.		
TITLE	Expressed tag sequences from Ginkgo megasporophyll (NYBG)		
JOURNAL	Unpublished (2005)		

CONTACT: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Original 3 prime EST has been reverse completed to be in 5 prime
 direction
 Seq primer: -21M13UnivRev.
 Location/Qualifiers
 source 1. .29

```

/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="Female"
/clone_lib="Ginkgo megasporophyll (NYBG)"
/notes="Organ: megasporophyll; Vector: pBK-CMV; Site: 1: xhoI; Site 2: Eco RI; Stragene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich

```

T67079					
ACCESSION	T67079.1	GI:676519			
VERSION	EST.				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa;				
	Mammalia; Eutheria;				
	Primates; Catarrhini;				
	Hominoidea; Homo.				
REFERENCE	1 (bases 1 to 29)				

AUTHORS	TITLE	JOURNAL	COMMENT
...

```

Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
Seq primer: M13 Forward.

FEATURES             source
    source
        Location/Qualifiers
            1..28
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="NHTCael6e07"
                /sex="Female"
                /tissue_type="Bone"
                /cell_type="Trabecular Bone Cells"
                /lab_host="SURE"
                /clone_lib="Normal Human Trabecular Bone Cells"
                /note="Organ: Hip; Vector: pBluescript; Site 1: EcoRI;
                Library constructed by Dr. Marian Young and Dr. Pamela
                Gehron Robey (NIDCR)"

Query Match          0.8%;   Score 23.2;   DB 1;   Length 28;
Best Local Similarity 89.3%;   Pred. No. 8.1e+02;
Matches 25;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

Qy  2704  GTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2731
      ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  28  GCACGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 999
CF314795/c
LOCUS
DEFINITION
HD--03-H09.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--03-H09, mRNA sequence.
CF314795
CF314795.1 GI:33686556
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryote: viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Gyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
    1..29
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:39947"
        /clone="HD--03-H09"
        /tissue_type="callus"
        /dev_stage="proliferated callus on 2N6 media for 2 weeks"
        /lab_host="E.coli DH10B"
        /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
        cDNA library (HD)"
        /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
        treated with ABA(20um) for 1hr. Oligo-capped mRNA was
        reverse transcribed and then used for PCR. mRNA was
        derived from rice Histone Deacetylase overexpression
        line."

Query Match          0.8%;   Score 23.2;   DB 1;   Length 29;

```

Reilly, M., Rose, M., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: F column: 17
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
source
1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0103F17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.8%; Score 23.2; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 8.2e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
||||| ||||||| ||||||| ||||||| |||||||
Db 29 AAAAAAAAAAAAAAAAAACACACAAAAAAAAA 2

RESULT 1002
LOCUS C2171125 29 bp DNA linear GSS 31-JAN-2005
DEFINITION M1AA-SK22b.b1 Meloidogyne incognita BAC end sequence library
(M1AAGSS 001) Meloidogyne incognita genomic, genomic survey
sequence.
ACCESSION C2171125
VERSION C2171125.1 GI:58339418
KEYWORDS GSS.
SOURCE Meloidogyne incognita (southern root-knot nematode)
ORGANISM Meloidogyne incognita
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.
1 (bases 1 to 29)
REFERENCE Mitreva, M., McCarter, J.P., Pape, D., Martin, J., Wylie, T.,
Clifton, S., Budiman, A., Lakey, N., Opperman, C. and Bird, D. Mck.

Genome Survey sequences from the parasitic nematode Meloidogyne
incognita
Unpublished (2005)
Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: nematode@watson.wustl.edu
BAC ends sequenced by Washington University Genome Sequencing
Center
Class: BAC ends.
Location/Qualifiers
source
1. .29
/organism="Meloidogyne incognita"
/mol_type="genomic DNA"
/strain="Race 1"
/db_xref="taxon:6306"
/dev_stage="L2"
/clone_lib="Meloidogyne incognita BAC end sequence library
(M1AAGSS 001)"
/note="Vector: pCUGI; Site 1: HindIII; Site 2: HindIII;
BAC library constructed by Arief Budiman and Nathan Lakey
at Orion Genomics, and David Bird and Charles Opperman at
Center for the Biology of Nematode Parasitism at NCSU."

Query Match 0.8%; Score 23.2; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 8.2e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2707 CTTAAAAA 2734
||||| ||||||| ||||||| ||||||| |||||||
Db 2 CCAACACAGAAAAA 29

RESULT 1003
LOCUS AJ695799/c 23 bp mRNA linear EST 29-JUN-2004
DEFINITION AJ695799 KN261 Bos taurus cDNA clone KN261-055_007, mRNA sequence.
ACCESSION AJ695799
VERSION AJ695799.1 GI:49429218
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 23)
REFERENCE Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
AUTHORS Development of cDNA and EST resources for studying reproduction and
TITLE embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minsore 20
and -minmatch 12 options. Vector: pBlueScriptII(SK+) R. Stiel: EcoRI
R. Stiel: SmaI 5', Seq Primer T3 Normalised library constructed from
bovine ovary. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
source
1. .23
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-055_007"
/tissue_type="ovary"
/clone_lib="KN261"
/note="Vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2:

SmaI; Single pass sequencing. Normalised library constructed from bovine ovary."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1004

AJ747297 23 bp mRNA linear EST 07-JUL-2004
LOCUS AJ747297 reverse - unstimulated minus stimulated macrophage Sus
DEFINITION scrofa cDNA clone R_1_D05, mRNA sequence.

ACCESSION AJ747297

VERSION AJ747297.1 GI:49917514

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 23)
Hopwood,P.A., Zhang,F., Lowden,S., Talbot,R., Burt,D., Archibald,A.
and Dixon,L.

TITLE Development of a porcine cDNA microarray

JOURNAL Unpublished (2004)

COMMENT Contact: Hopwood PA

Dept. of Preclinical Veterinary Sciences

Royal School for Veterinary Studies

Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM

Sequencing was performed by ARK genomics. This clone is available

from ARK- Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS,

UK. See www.ark-genomics.org or contact info@arkgenomics.org.

FEATURES

Location/Qualifiers

1..23

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="R_1_D05"

/tissue_type="lung"

/cell_type="macrophage"

/clone_lib="reverse - unstimulated minus stimulated

macrophage"

Query Match 0.8%; Score 23; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1005

AM044732 23 bp mRNA linear EST 20-SEP-2005
LOCUS AM044732 Schistosoma mansoni lung schistosomulum Schistosoma
DEFINITION mansoni cDNA clone SmlC30h01.q1k, mRNA sequence.

ACCESSION AM044732

VERSION AM044732.1 GI:75967222

KEYWORDS EST.

SOURCE Schistosoma mansoni

ORGANISM Schistosoma mansoni

REFERENCE 1 (bases 1 to 23)

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

Microarray analysis identifies genes preferentially expressed in

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,

Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.

Microarray analysis identifies genes preferentially expressed in

the lung schistosomulum of Schistosoma mansoni

Unpublished (2005)

Contact: Ivens AC

Pathogen Microarrays Group

Wellcome Trust Sanger Institute

Hinxton, CB10 1SA, UNITED KINGDOM.

JOURNAL

COMMENT

Pathogen Microarrays Group

Wellcome Trust Sanger Institute

Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES

Location/Qualifiers

1..23

/organism="Schistosoma mansoni"

/mol_type="mRNA"

/db_xref="taxon:6183"

/clone="SmlC30h01.q1k"

/dev_stage="lung schistosomulum"

/clone_lib="Schistosoma mansoni lung schistosomulum"

/note="Country: Puerto Rico"

Query Match 0.8%; Score 23; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1006

AM047142 23 bp mRNA linear EST 11-AUG-2005
LOCUS AM047142 Schistosoma mansoni lung schistosomulum Schistosoma
DEFINITION mansoni cDNA clone SmlC26b06.q1k, mRNA sequence.

ACCESSION AM047142

VERSION AM047142.1 GI:72293133

KEYWORDS EST.

SOURCE Schistosoma mansoni

ORGANISM Schistosoma mansoni

REFERENCE 1 (bases 1 to 23)

Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,

Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.

Microarray analysis identifies genes preferentially expressed in

the lung schistosomulum of Schistosoma mansoni

Unpublished (2005)

Contact: Ivens AC

Pathogen Microarrays Group

Wellcome Trust Sanger Institute

Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES

Location/Qualifiers

1..23

/organism="Schistosoma mansoni"

/mol_type="mRNA"

/db_xref="taxon:6183"

/clone="SmlC26b06.q1k"

/dev_stage="lung schistosomulum"

/clone_lib="Schistosoma mansoni lung schistosomulum"

/note="Country: Puerto Rico"

Query Match 0.8%; Score 23; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 7.6e+02;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731

Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1007

CF279238/c 23 bp mRNA linear EST 14-AUG-2003
LOCUS CF279238/c 14ETL--05-H12.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-H12,
mRNA sequence.

ACCESSION CF279238

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CF297943.1 GI:33656624
EST.
ORYZA SATIVA (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14ETL--05-H12"
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/clone_lib="Rice leaf plasmid cDNA library"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library"
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14ETL--05-H12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library"
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library"
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library"
(14ETL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
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/clone_lib="Rice leaf plasmid cDNA library"
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/organism="Oryza sativa (japonica cultivar-group)"
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/clone_lib="Rice leaf plasmid cDNA library"
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2
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```

RESULT 1010
CF319212/c
LOCUS
DEFINITION
HD--09-K06.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-K06, mRNA sequence.
ACCESSION
CF319212
VERSION
CF319212.1 GI:33690973
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
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/db_xref="taxon:39947"
/clone="HD--09-K06"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
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cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1011
CF322953
LOCUS
DEFINITION
HDN--02-109.g1 OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA
clone HDN--02-109, mRNA sequence.
ACCESSION
CF322953
VERSION
CF322953.1 GI:33794126
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)

```

```

COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone_lib="OSHDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1012
CF329042
LOCUS
DEFINITION
NACL--04-D14.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-D14, mRNA
sequence.
ACCESSION
CF329042
VERSION
CF329042.1 GI:33806320
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for

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SOURCE	ORGANISM
Vitis vinifera	Vitis vinifera
Vitis vinifera	Vitis vinifera

FEATURES
source

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/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
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/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex; Site_1: SfIA; Site_2: SfIB; Oriented library"

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1016
COS577495/c
LOCUS TVEST077D06 TV30236_PT cDNA Library Trichomonas vaginalis cDNA 5',
DEFINITION mRNA sequence.
ACCESSION COS577495 23 bp mRNA linear EST 20-JUL-2004
VERSION COS577495 GI:50407891
KEYWORDS EST.
SOURCE Trichomonas vaginalis
ORGANISM Trichomonas vaginalis; Trichomonadida;
Eukaryota; Parabasalides; Trichomonada; Trichomonadida;
Trichomonadidae; Trichomonadinae; Trichomonas.
REFERENCE 1 (bases 1 to 23)
AUTHORS Zhou,Y., Shu,W.M., Huang,S.C.C., Huang,K.Y. and Tang,P.
TITLE Analysis of Gene Expression Profile in Trichomonas vaginalis by EST
Sequencing
JOURNAL Unpublished (2003)
COMMENT Contact: Tang, P.
Molecular Regulation and Bioinformatics Laboratory, College of
Medicine
Chang Gung University
259 Wenhsa 1st. Road, Kweishan, Taoyuan 333, Taiwan
Tel: +886 3 3283016 EXT5136
Fax: +886 3 3283031
Email: petang@mail.cgu.edu.tw
PCR Primers
FORWARD: T7
BACKWARD: T3
Seq primer: T3.
FEATURES
source
Location/Qualifiers
1..23
/mol_type="mRNA"
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/lab_host="XLI Blue-MRP"
/clone_lib="TV30236 PT cDNA Library"
/note="Vector: Lambda ZAP-Express (Stratagene); Site_1:
ECORI; Site_2: XhoI"

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1017
CX004980/c
LOCUS t122h08.b7 Brain - Cerebellum Library (DOGEST8) Canis familiaris
DEFINITION
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cDNA, mRNA sequence.
ACCESSION CX004980
VERSION CX004980.1 GI:56276396
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 23)
AUTHORS Baliya,V., Nascimento,L.U. and McCombie,W.R.
TITLE ESTs from Canis familiaris cerebellum (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombe@cshl.org.
FEATURES
source
Location/Qualifiers
1..23
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cerebellum"
/dev_stage="3 month old normal canine"
/lab_host="XLI0 Gold"
/clone_lib="Brain - Cerebellum Library (DOGEST8)"
/note="Organ: Brain; Vector: pBluescript II SK; Site_1:
ECORI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1018
DR063413
LOCUS ip65a09.g1 Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA
DEFINITION sequence.
ACCESSION DR063413 23 bp mRNA linear EST 06-JUN-2005
VERSION DR063413 GI:66986981
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
REFERENCE 1 (bases 1 to 23)
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE Expresed tag sequences from Ginkgo megasporophyll (NYBG)
JOURNAL Unpublished (2005)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombe@cshl.org
Seq primer: -21M13UnivRev.
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FEATURES
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    Location/Qualifiers
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        /organism="Ginkgo biloba"
        /mol_type="mRNA"
        /db_xref="taxon:3311"
        /sex="Female"
        /clone_lib="Ginkgo megasporophyll (NYBG)"
        /notes="Organ: megasporophyll; Vector: pBK-CMV; Site 1:
        XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA
        Synthesis Kit. The library was size-fractionated to enrich
        for large inserts."

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2731
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1019
DR072928
LOCUS DR072928 23 bp mRNA linear EST 08-JUN-2005
DEFINITION ik79h04.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
ACCESSION DR072928
VERSION DR072928
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
REFERENCE 1 (bases 1 to 23)
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
Bentley,P., Coruzzi,G., Ballig,V., Martienssen,R.A., McCombie,R.W.,
O'Shaughnessy,A.L.,
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -2M13UnivRev.

FEATURES
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        /mol_type="mRNA"
        /db_xref="taxon:3311"
        /sex="female"
        /clone_lib="Ginkgo female leaf (NYBG)"
        /notes="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
        Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
        The library was size-fractionated to enrich for large
        inserts."

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2731
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1020
DR073135
LOCUS DR073135 23 bp mRNA linear EST 08-JUN-2005
DEFINITION ik86h10.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.

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ACCESSION	DR073135				
VERSION	DR073135.1	GI:67050986			
KEYWORDS	EST.				
SOURCE	Ginkgo biloba (maidenhair tree)				
ORGANISM	Ginkgo biloba				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Ginkgoales; Ginkgoaceae; Ginkgo.				
AUTHORS	Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo. 1 (bases 1 to 23) Brenner E.D., Twigg R.W., Runko S.J., Katari M.S., Dedhia N.N., O'Shaughnessy A.L., Baliya V., Martienssen R.A., McCombie R.W., Benfey P., Coruzzi G. and Stevenson D.				
TITLE	Expressed tag sequences from Ginkgo female leaf (NYBG)				
JOURNAL	Unpublished (2005)				
COMMENT	Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mcombie@cshl.org Seq primer: -21M13UnivRev.				
FEATURES	Location/Qualifiers				
source	1..23				
	/organism="Ginkgo biloba"				
	/mol_type="mRNA"				
	/db_xref="taxon:3311"				
	/sex="female"				
	/clone_lib="Ginkgo female leaf (NYBG)"				
	/note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Stragene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."				
Query Match	0.8%	Score 23;	DB 1:	Length 23;	
Best Local Similarity	100.0%;	Pred. No. 7.6e+02;	Mismatches	0;	Gaps 0;
Matches	23;	Conservative	0;	Mismatches	0;
<hr/>					
QY	2709	AAAAAAAAAAAAAAAAAAAAA	2731		
Db	1	AAAAAAAAAAAAAAAAAAAAA	23		
<hr/>					
RESULT 1021					
DR074008/c					
LOCUS	ik92a08.g1	Ginkgo male leaf (NYBG)	Ginkgo biloba cDNA 3'	mRNA	EST 08-JUN-2005
DEFINITION	sequence.				
ACCESSION	DR074008				
VERSION	DR074008.1	GI:67051937			
KEYWORDS	EST.				
SOURCE	Ginkgo biloba (maidenhair tree)				
ORGANISM	Ginkgo biloba				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.				
AUTHORS	1 (bases 1 to 23) Brenner E.D., Twigg R.W., Runko S.J., Katari M.S., Dedhia N.N., O'Shaughnessy A.L., Baliya V., Martienssen R.A., McCombie R.W., Benfey P., Coruzzi G. and Stevenson D.				
TITLE	Expressed tag sequences from Ginkgo male leaf (NYBG)				
JOURNAL	Unpublished (2005)				
COMMENT	Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mcombie@cshl.org Seq primer: -21M13UnivRev.				
FEATURES	Location/Qualifiers				
source	1..23				
	/organism="Ginkgo biloba"				
	/mol_type="mRNA"				
	/db_xref="taxon:3311"				

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/sex="male"
/clone.lib="Ginkgo male leaf (NVBC)"
/notes="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI; Site_2:
Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large
inserts."

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Query Match          0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
      |||||||
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 1022
AZ309219/c
LOCUS          AZ309219          23 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION    1M0013G08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0013G08 F, genomic survey sequence.
ACCESSION     AZ309219
VERSION       AZ309219.1 GI:10349986
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus

```

```

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts

```

```

TITLE
JOURNAL
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0013 row: 08 column: 08
              Seq primer: CGTTGTAAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 23.

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FEATURES
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    /mol_type="genomic DNA"
    /strain="C57BL/6J"
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    /clone="UUGC1M0013G08"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

```

```

inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

```

Query Match          0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
      |||||||
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 1023
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LOCUS          AZ309851          23 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION    1M0017L12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0017L12 F, genomic survey sequence.
ACCESSION     AZ309851
VERSION       AZ309851.1 GI:10351256
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus

```

```

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts

```

```

TITLE
JOURNAL
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0017 row: L column: 12
              Seq primer: CGTTGTAAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 23.

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FEATURES
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    /clone="UUGC1M0017L12"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1024
AZ312314/c
LOCUS AZ312314 23 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0028006F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0028006 F, genomic survey sequence.

ACCESSION AZ312314
VERSION AZ312314.1 GI:10356138
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0028 row: 0 column: 06
Seq primer: CGTTGTAACGACGGCCACT
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
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/strain="C57BL/6J"
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/clone="UUGC1M0028006"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1025
AZ313922/c
LOCUS AZ313922 23 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0030A02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0030A02 R, genomic survey sequence.

ACCESSION AZ313922
VERSION AZ313922.1 GI:10359299
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0030 row: A column: 02
Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
source
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0030A02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match          0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
      |||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 1026
AZ351354
LOCUS          AZ351354          23 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION    clone UGCI1M0089D19 F, genomic survey sequence.
ACCESSION     AZ351354
VERSION       AZ351354.1   GI:10430591
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 23)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000   Std Error: 0.00
              Plate: 0089   row: D   column: 19
              Seq primer: CGTTGTAAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 23.
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                  /organism="Mus musculus"
                  /mol_type="genomic DNA"
                  /strain="C57BL/6J"
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                  /clone="UGCI1M0089D19"
                  /sex="Male"
                  /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                  /clone_lib="Mouse 10kb plasmid UGCI1M library"
                  /note="Vector: PWD42nv; Purified genomic DNA from M.
                  musculus C57BL/6J (male) was obtained from the Jackson
                  Laboratory Mouse DNA Resource
                  (http://www.jax.org/resources/documents/dnares/). The DNA
                  was hydrodynamically sheared by repeated passage through a
                  0.005 inch orifice at constant velocity. The sheared DNA
                  was blunt end-repaired with T4 DNA polymerase and T4
                  polynucleotide kinase. Adaptor oligonucleotides were
                  ligated to the blunt ends in high molar excess. The
                  adapted DNA was purified and size-selected for a 9.5 to
                  10.5 kb range using preparative agarose gel
                  electrophoresis. Vector DNA was prepared from a derivative
                  of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match          0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
      |||||
Db 1  AAAAAAAAAAAAAAAAAAAAAA 23

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RESULT 1027
AZ357645
LOCUS          AZ357645          23 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION    clone UGCI1M0095C23 F, genomic survey sequence.
ACCESSION     AZ357645
VERSION       AZ357645.1   GI:10471345
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 23)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000   Std Error: 0.00
              Plate: 0099   row: C   column: 23
              Seq primer: CGTTGTAAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 23.
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                  /mol_type="genomic DNA"
                  /strain="C57BL/6J"
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                  /clone="UGCI1M0095C23"
                  /sex="Male"
                  /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                  /clone_lib="Mouse 10kb plasmid UGCI1M library"
                  /note="Vector: PWD42nv; Purified genomic DNA from M.
                  musculus C57BL/6J (male) was obtained from the Jackson
                  Laboratory Mouse DNA Resource
                  (http://www.jax.org/resources/documents/dnares/). The DNA
                  was hydrodynamically sheared by repeated passage through a
                  0.005 inch orifice at constant velocity. The sheared DNA
                  was blunt end-repaired with T4 DNA polymerase and T4
                  polynucleotide kinase. Adaptor oligonucleotides were
                  ligated to the blunt ends in high molar excess. The
                  adapted DNA was purified and size-selected for a 9.5 to
                  10.5 kb range using preparative agarose gel
                  electrophoresis. Vector DNA was prepared from a derivative
                  of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

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FEATURES
      source
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          /db_xref="taxon:10090"
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          /sex="Male"
          /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
          /clone_lib="Mouse 10kb plasmid UGCI1M library"
          /note="Vector: PWD42nv; Purified genomic DNA from M.
          musculus C57BL/6J (male) was obtained from the Jackson
          Laboratory Mouse DNA Resource
          (http://www.jax.org/resources/documents/dnares/). The DNA
          was hydrodynamically sheared by repeated passage through a
          0.005 inch orifice at constant velocity. The sheared DNA
          was blunt end-repaired with T4 DNA polymerase and T4
          polynucleotide kinase. Adaptor oligonucleotides were
          ligated to the blunt ends in high molar excess. The
          adapted DNA was purified and size-selected for a 9.5 to
          10.5 kb range using preparative agarose gel
          electrophoresis. Vector DNA was prepared from a derivative
          of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

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FEATURES
      source
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          /organism="Mus musculus"
          /mol_type="genomic DNA"
          /strain="C57BL/6J"
          /db_xref="taxon:10090"
          /clone="UGCI1M0095C23"
          /sex="Male"
          /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
          /clone_lib="Mouse 10kb plasmid UGCI1M library"
          /note="Vector: PWD42nv; Purified genomic DNA from M.
          musculus C57BL/6J (male) was obtained from the Jackson
          Laboratory Mouse DNA Resource
          (http://www.jax.org/resources/documents/dnares/). The DNA
          was hydrodynamically sheared by repeated passage through a
          0.005 inch orifice at constant velocity. The sheared DNA
          was blunt end-repaired with T4 DNA polymerase and T4
          polynucleotide kinase. Adaptor oligonucleotides were
          ligated to the blunt ends in high molar excess. The
          adapted DNA was purified and size-selected for a 9.5 to
          10.5 kb range using preparative agarose gel
          electrophoresis. Vector DNA was prepared from a derivative
          of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

```


inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match          0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
      |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

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RESULT 1030
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LOCUS
DEFINITION
  1M0275K12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0275K12 F, genomic survey sequence.
ACCESSION
  AZ465327
VERSION
  AZ465327.1 GI:106233452
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 23)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0275 row: K column: 12
  Seq primer: CGTTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 23.

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      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adapted DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match          0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
      |||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 1031
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LOCUS
DEFINITION
  1M0306E11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0306E11 F, genomic survey sequence.
ACCESSION
  AZ481702
VERSION
  AZ481702.1 GI:10642767
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 23)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0306 row: E column: 11
  Seq primer: CGTTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 23.

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      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adapted DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XLI0-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
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 Pb 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1033					
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LOCUS	AZ593540	23 bp	DNA	linear	GSS 13-DEC-2000
DEFINITION	IM0405C07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0405C07 F. genomic survery sequence.				

AZ593540
 AZ593540.1
 GSS.
 Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kbp

Journal Comment

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT
84112 USA

Tel.: 801 595 5606
 Fax: 801 595 7177
 Email: ddm@genetics.utah.edu
 Insert Length 10000 Std Error: 0.00
 Plate: 0400 Row: C Column: 07
 Seq primer: CGTCTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stron. 23

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="JUGC1M0405C07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|47321114|gb|AF129072.1), a contig-number

```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1034

AZ610785
LOCUS AZ610785 23 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0436N07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0436N07 F, genomic survey sequence.

ACCESSION AZ610785
VERSION AZ610785.1 GI:11732975
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0436 row: N column: 07
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 23.

FEATURES

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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
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DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1035

AZ647637/c
LOCUS AZ647637 23 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0514E09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0514E09 F, genomic survey sequence.

ACCESSION AZ647637
VERSION AZ647637.1 GI:11779301
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0514 row: E column: 09
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 23.

FEATURES

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Location/Qualifiers
/organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="UUGC1M0514E09"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1036
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LOCUS
DEFINITION
AZ654903
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 23)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: D column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

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/db_xref="taxon:10090"
/clone="UUGC1M0529D03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWB42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (G1|4732114|gb|AF129072.1), a copy-number

FEATURES
source

source

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1037
AZ778751
LOCUS
DEFINITION
AZ778751
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 23)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0014 row: 0 column: 08
Seq primer: CGTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0014C08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWB42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (G1|4732114|gb|AF129072.1), a copy-number

FEATURES
Location/Qualifiers

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match          0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
      |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

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RESULT 1038
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LOCUS          AZ787184          23 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION    2M0033C07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
              clone UUGC2M0033C07 F, genomic survey sequence.
ACCESSION     AZ787184
VERSION       AZ787184.1 GI:12925692
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 23)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0033 row: C column: 07
              Seq primer: CGTTGTAAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 23.

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FEATURES             Location/Qualifiers
     1..23
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         /mol_type="genomic DNA"
         /strain="C57BL/6J"
         /db_xref="taxon:10090"
         /clone="UUGC2M0033C07"
         /sex="Male"
         /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
         /clone_lib="Mouse 10kb plasmid UUGC1M library"
         /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match          0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
      |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

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RESULT 1039
AZ792751/c
LOCUS          AZ792751          23 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION    2M0045K24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
              clone UUGC2M0045K24 F, genomic survey sequence.
ACCESSION     AZ792751
VERSION       AZ792751.1 GI:12937005
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muroidea; Muridae; Murinae; Mus.
              1 (bases 1 to 23)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Iellam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0045 row: K column: 24
              Seq primer: CGTTGTAAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 23.

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FEATURES             Location/Qualifiers
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         /mol_type="genomic DNA"
         /strain="C57BL/6J"
         /db_xref="taxon:10090"
         /clone="UUGC2M0045K24"
         /sex="Male"
         /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
         /clone_lib="Mouse 10kb plasmid UUGC1M library"
         /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptorised mouse DNA was annealed to adaptorised vector DNA, and transformed into chemically-competent *E. coli* X10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match          0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT	1041				
AZ939608					
LOCUS	AZ939608	23 bp	DNA	linear	GSS 26-APR-2001
DEFINITION	2M0198107R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0198107 R, genomic survey sequence.				

VERSION AZ939608.1 GI:13800390
KEYWORDS GSS.

SOURCE	ORGANISM
Mus musculus (house mouse)	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.	

**REFERENCE
AUTHORS**

1. (bases 1 to 23)

Cyprinodontidae, Poeciliidae, Mollusca, Murinae, Mus.
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL OF PLASMA INERTS UNPUBLISHED (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0198 row: I column: 07
Seq primer: CACACAGGAAACAGCTATGACC

Seq primer: CACACAG
Class: plasmid ends

High quality sequence stop: 23.

FEATURES	Location/Qualifiers
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/organism="Mus musculus"  
/mol_type="genomic DNA"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone="YUCC2M0198107"  
/sex="Female"]
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/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/clon_lib="Mouse 10kb plasmid UUC2M library"  
/note="Vector: PWD42hv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource"
```

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g147321211.qb.af129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2709	AAAAAAAAAAAAAAAAAAAA	27311
Db	23	AAAAAAAAAAAAAAAAAAAA	1

RESULT	1043
DU830086/c	
LOCUS	
DEFINITION	DU830086 23 bp DNA linear GSS 23-DEC-2005 KBR5006B23F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS006B23, genomic survey sequence.

ACCESSION	DU830086
VERSION	DU830086.1
KEYWORDS	GSS.
SOURCE	Brassica rapa subsp. pe
ORGANISM	Brassica rapa subsp. pe

ORGANISM

rosids; eurosids I

REFERENCE
AUTHORS

1 (bases 1 to 23)
Yang, T. J., Kwon, S. J., Kim, J. A., Kim, J. S., Lim, K. B., Jin, M.,
Park, J. Y., Lim, H. J., Kim, H. I., Choi, B. S., Seol, Y. J., Park, D. S.,
Hahn, J. H. and Park, B. S.

TITLE
End sequence of Brassica rapa Sau3AI (KBrs) BAC clone

COMMENTS

Contract: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel : +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr

BAC end sequence of *Brassica rapa* ssp. *pekinensis* sau3AI BAC clone KB1S006B23
Seq primer: T7
Class: BAC ends.

source
/organizational

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Query Match          0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e-02;
Matches 23: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/sub_species="pekinensis"
/db_xref="taxon:51351"
/clonetype="KBR5006B23"
/lab_host="E. coli DH10B"
/clonetype="KBR5" Brassica rapa Sau3AI BAC library"
/notes=vector: PCUGIBAC1; Site: Sau3AI; Brassica rapa
ssp pekinensis var. Chilifu BAC library (KBS BAC) is
available at NIAB."

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Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1044		
DU834017/c		
LOCUS	DU834017	DNA
	23 bp	linear
		GSS 22-DEC-2005

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DEFINITION   KBrS013E12R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
              subsp. pekinensis genomic clone KBrS013E12, genomic survey
              sequence.
ACCESSION    DU834017
VERSION      DU834017.1 GI:83870613
KEYWORDS     GSS.
SOURCE       Brassica rapa subsp. pekinensis
ORGANISM     Brassica rapa subsp. pekinensis
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
              Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
              Hahn,J.H. and Park,B.S.
TITLE        End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
              Brassica Genomics Team
              National Institute of Agricultural Biotechnology
              225 Seodun-Dong, Suwon, 441-707, Korea
              Tel: +82-31-299-1670
              Fax: +82-31-299-1672
              Email: pheom@da.go.kr
              BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
              KBrS013E12
              Seq primer: M13 Reverse
              Class: BAC ends.
FEATURES     source
              Location/Qualifiers
                1..23
                /organism="Brassica rapa subsp. pekinensis"
                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBrS013E12"
                /lab_host="E. coli DH10B"
                /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                /notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
                available at NIAB."
Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db  23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1045
LOCUS    DX071679/c
DEFINITION   KBrS081H24F KBrB, Brassica rapa BamHI BAC library Brassica rapa
              subsp. pekinensis genomic clone KBrS081H24, genomic survey
              sequence.
ACCESSION    DX071679
VERSION      DX071679.1 GI:84765975
KEYWORDS     GSS.
SOURCE       Brassica rapa subsp. pekinensis
ORGANISM     Brassica rapa subsp. pekinensis
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
              Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
              Hahn,J.H. and Park,B.S.
TITLE        End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
              Brassica Genomics Team

```

```

National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pheom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrS081H24
Seq primer: T7
Class: BAC ends.
FEATURES     source
              Location/Qualifiers
                1..23
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                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBrS081H24"
                /lab_host="E. coli DH10B"
                /clone_lib="KBrB, Brassica rapa BamHI BAC library"
                /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
                pekinensis var. Chiifu BAC library (KBrB BAC) is provided
                by Yong-Pyo Lim (CNU)."
Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db  23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1046
LOCUS    TA151C02Q
DEFINITION   T. brucei sheared genomic DNA clone 151c02, reverse sequence,
              genomic survey sequence.
ACCESSION    AL473028
VERSION      AL473028.1 GI:11838301
KEYWORDS     GSS.
SOURCE       Trypanosoma brucei
ORGANISM     Trypanosoma brucei
              Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
              Trypanosoma.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
              Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
              Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE        Direct Submission
JOURNAL      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
              project, Sanger Centre, The Wellcome Trust Genome Campus,
              Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
              nh@sanger.ac.uk
COMMENT      Constructed at the Institute for Genomic Research (TIGR),
              Rockville, MD. Genomic DNA isolated from a cloned population of
              Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
              to give a tight size distribution (
              4 kb). The v + i method used for the library construction is
              described in detail in Smith, H. and Venter, J.C. (Making small
              insert libraries for whole genome shotgun sequencing projects. In
              Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
              Barrell, Oxford University Press, 1999).
              Email: nelsayed@tigr.org
              Details of T. brucei sequencing at the Sanger Centre are available
              at http://www.sanger.ac.uk/Projects/T_brucei/.
              Location/Qualifiers
                1..23
                /organism="Trypanosoma brucei"
                /mol_type="genomic DNA"
                /strain="TREU927"
                /db_xref="taxon:5691"
                /clone="151c02"

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0031H11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.8%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 24 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1051
AZ386891
LOCUS
DEFINITION
IM0146A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0146A08 F, genomic survey sequence.
ACCESSION
AZ386891
VERSION
AZ386891.1 GI:10500591
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0146 row: A column: 08
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0146A08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0031H11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.8%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 24 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1050
CF301712/c
LOCUS
DEFINITION
7LEAF--06-K21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-K21, mRNA
sequence.
ACCESSION
CF301712
VERSION
CF301712.1 GI:33673473
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhna@ggbio.com, bhna@bio.myongji.ac.kr.
Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--06-K21"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

Query Match      0.8%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 24 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1051
AZ386891
LOCUS
DEFINITION
IM0146A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0146A08 F, genomic survey sequence.
ACCESSION
AZ386891
VERSION
AZ386891.1 GI:10500591
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0146 row: A column: 08
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0146A08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1052

AZ832800/c

LOCUS AZ832800 25 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0113M21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0113M21 F, genomic survey sequence.

ACCESSION AZ832800
VERSION
KEYWORDS

SOURCE GI:13002708
Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Becorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0113 row: M column: 21
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.

FEATURES

source

1..25
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0113M21"
/sex="Male"
/lab_host="S. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1053

BQ583199/c

LOCUS BQ583199 26 bp mRNA linear EST 06-DEC-2002
DEFINITION E012097-024-006-E10-SP6 MP1Z-ADIS-024-Inflorance Beta vulgaris cDNA clone 024-006-E10 5-PRIME, mRNA sequence.

ACCESSION BQ583199
VERSION
KEYWORDS

SOURCE GI:26112776
Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 26)
AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 26 Std Error: 0.00
Plate: 6 row: E column: 10
Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES

source

1..26
Location/Qualifiers
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:181502"
/db_xref="taxon:161934"
/clone="024-006-E10"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-Inflorance"
/note="Vector: PCWVSP076; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatgut AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI. Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.8%; Score 23; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAAAAAA 2729
|||||
DB 23 CTAATAAAAAAAAAAAAAAAAAA 1

```

RESULT 1054
R26779/c
LOCUS
DEFINITION
  R26779          26 bp      mRNA          linear      EST 24-APR-1995
  IMAGE:132611.3' similar to gb:M5164 SERUM RESPONSE FACTOR
  ACCESSORY PROTEIN 1A (HUMAN);, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Homo sapiens (human)

REFERENCE
AUTHORS
  Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
  Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
  Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
  Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
  Wilson,R.
  1 (bases 1 to 26)

TITLE
  The WashU-Merck EST Project
JOURNAL
COMMENT
  Contact: Wilson RK
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  High quality sequence starts: 1
  High quality sequence stops: 1
  Source: IMAGE Consortium, LLNL
  This clone is available royalty-free through LLNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Trace considered overall poor quality
  Insert length: 1384 Std Error: 0.00
  Seq primer: Promega -21m13
  High quality sequence stop: 1.
  Location/Qualifiers
    1..26
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="GDB:538233"
      /db_xref="taxon:9606"
      /clone="IMAGE:132611"
      /sex="Female"
      /dev_stage="placenta obtained at birth (full term)"
      /lab_host="DH10B (ampicillin resistant)"
      /clone_lib="Soares placenta NB2HP"
      /notes="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
      modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
      strand cDNA was primed with a Not I - oligo(dT) primer [5'
      AATGGAAGATTCCGGCGCAGGAATTTTTTTTTTTTTTTT 3'],
      double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Not I and cloned into the Not I
      and Eco RI sites of the modified pT7T3 vector. Library
      went through one round of normalization. Library
      constructed by Bento Soares and M.Fatima Bonaldo."

Query Match          0.8%; Score 23; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2730
Db 23 TAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1055
N29432/c
LOCUS
DEFINITION
  N29432          27 bp      mRNA          linear      EST 05-JAN-1996
  IMAGE:271114.3' similar to gb:D00174 ALPHA-2-ANTIPLASMIN PRECURSOR
  (HUMAN);, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Homo sapiens (human)

```

```

DEFINITION
  yw86h10.s1 Soares_placenta.8to9weeks.2NbHP8to9W Homo sapiens cDNA
  (HUMAN);, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Homo sapiens (human)

REFERENCE
AUTHORS
  Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
  Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
  Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
  Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
  Wilson,R.
  1 (bases 1 to 27)

TITLE
  The WashU-Merck EST Project
JOURNAL
COMMENT
  Contact: Wilson RK
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  High quality sequence starts: 1
  High quality sequence stops: 1
  Source: IMAGE Consortium, LLNL
  This clone is available royalty-free through LLNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Trace considered overall poor quality
  Seq primer: ml3 -40 forward
  High quality sequence stop: 1.
  Location/Qualifiers
    1..27
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="GDB:3888877"
      /db_xref="taxon:9606"
      /clone="IMAGE:259171"
      /dev_stage="two placentae: one from 8 weeks and another
      from 9 weeks post conception"
      /lab_host="DH10B (ampicillin resistant)"
      /clone_lib="Soares_placenta.8to9weeks.2NbHP8to9W"
      /notes="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
      modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
      strand cDNA was primed with a Not I - oligo(dT) primer [5'
      TTTTACCAATCTGAAGTGGAGCGCGGATTTTTTTTTTTTTTTT 3'],
      double-stranded cDNA was size selected, ligated to Eco RI
      adaptors (Pharmacia), digested with Not I and cloned into
      the Not I and Eco RI sites of a modified pT7T3 vector
      (Pharmacia). Library constructed by Bento Soares and
      M.Fatima Bonaldo."

Query Match          0.8%; Score 23; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1056
N34459/c
LOCUS
DEFINITION
  N34459          27 bp      mRNA          linear      EST 16-JAN-1996
  YY13c06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
  IMAGE:271114.3' similar to gb:D00174 ALPHA-2-ANTIPLASMIN PRECURSOR
  (HUMAN);, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Homo sapiens (human)

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisan,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 16
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: m13 -40 forward
High quality sequence stop: 16.
FEATURES
source
1..27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3880756"
/db_xref="taxon:9606"
/clone="IMAGE:271114"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2NbHM"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCACCAATCGAGTGGAGCGCGCGATTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Patima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."
Query Match 0.8%; Score 23; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1057
AJ922998/c
LOCUS AJ922998 Theileria annulata piroplasm Theileria annulata cDNA clone
DEFINITION TAC20g08_gika, mRNA sequence.
ACCESSION AJ922998
VERSION AJ922998.1 GI:67493340
KEYWORDS EST.
SOURCE Theileria annulata
ORGANISM Theileria annulata
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
Theileria.
REFERENCE 1 (bases 1 to 28)
AUTHORS Pain,A., Renaud,H., Berriman,M., Murphy,L., Yeats,C.A., Weir,W.,
Kerhornou,A., Aslett,M., Bishop,R., Bouchier,C., Cochet,M.,
Coulson,R.M.R., Cronin,A., de Villiers,E., Fraser,A., Foster,N.,
Gardner,M., Goble,A., Griffiths-Jones,S., Harris,D.E., Katzer,F.,
Larke,N., Lord,A., Maser,P., McKellar,S., Mooney,P., Morton,P.,
Nene,V., O'Neil,S., Price,C., Quail,M.A., Rabinovitch,E.,
Rawlings,N.D., Rutter,S., Saunders,D., Seeger,K., Shah,T.,
Squares,R., Squares,S., Tivey,A., Walker,A.R., Woodward,J.,
Dobelaere,D.A.E., Langsley,G., Rajandream,M.-A., McKeever,D.,
Shiels,B., Tait,A., Barrell,B. and Hall,N.
TITLE The genome of the host-cell transforming parasite Theileria
annulata and a comparison with T. parva
JOURNAL Unpublished (2005)
COMMENT Contact: Pain A
The Pathogen Sequencing Unit
The Wellcome Trust Sanger Institute
Genome Campus, CB10 1SA, UNITED KINGDOM
Piroplasm cDNA library: Frank Katzer and Brian Shiels, Division of
Veterinary Infection and Immunity, ICM, University of Glasgow, UK.
FEATURES
source
1..28
/organism="Theileria annulata"
/mol_type="mRNA"
/isolate="Ankara (clone D7)"
/db_xref="taxon:5874"
/clone="TAC20g08_gika"
/dev_stages="piroplasm"
/lab_host="Bos taurus (cow)"
/clone_lib="Theileria annulata piroplasm"
/note="Country: Turkey; Ankara"
Query Match 0.8%; Score 23; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1058
DX072773
LOCUS DX072773 28 bp DNA linear GSS 10-JAN-2006
DEFINITION KBR082023F KBRB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBR082023, genomic survey
sequence.
ACCESSION DX072773
VERSION DX072773.1 GI:84767069
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 28)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.U., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBRB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBR082023
Seq primer: T7
Class: BAC ends.
FEATURES
source
1..28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chilfu"
/sub_species="pekinensis"
/db_xref="taxon:51351"

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Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM
Class: Gene Trap.

FEATURES

Source
1. .26
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/clone="A015.B4"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/note="Vector: pFLIP1"

Query Match 0.8%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 8.2e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2733
|||||
Db 26 TAACAATAAAAAAAAAAAAAAAAAA 1

RESULT 1062

CZ908520
LOCUS CZ908520 27 bp DNA linear GSS 08-AUG-2005
DEFINITION 4018003G05.2EL_y1 4018 - RescueMu Grid X Zea mays genomic, genomic survey sequence.

ACCESSION CZ908520
VERSION CZ908520.1 GI:71920521
KEYWORDS GSS.

SOURCE

Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 27)

REFERENCE

AUTHORS Walbot V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
CONTACT: Walbot V

Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221

Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4018003 row: G column: 05
Class: transposon-tagged.

FEATURES

source
1. .27
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="4018 - RescueMu Grid X"

/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid X was grown at UCSD in 2003. DNA was extracted from leaf

strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.8%; Score 22.8; DB 1; Length 27;
Best Local Similarity 92.3%; Pred. No. 8.4e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 1 AAAAATAAGAAAAAAAAAAAAAAAAA 26

RESULT 1063

CV091538/c
LOCUS CV091538 28 bp mRNA linear EST 26-AUG-2004
DEFINITION N1103_R cDNA non acclimated Bluecrop library Vaccinium corymbosum cDNA 3', mRNA sequence.

ACCESSION CV091538
VERSION CV091538.1 GI:51570877
KEYWORDS EST.

SOURCE

Vaccinium corymbosum
Vaccinium corymbosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; Ericales; Ericaceae; Vaccinioideae; Vaccinieae; Vaccinium.

REFERENCE

AUTHORS 1 (bases 1 to 28)
Dhanaraj, A.L., Alkharouf, N.W., Beard, H.S., Chouikha, I.B., Matthews, B.F. and Rowland, L.J.
TITLE Monitoring gene expression changes during cold acclimation of blueberry (Vaccinium corymbosum L.) using a cDNA microarray
JOURNAL Unpublished (2004)
COMMENT Contact: Rowland, L.J.
Fruit Lab

US Department of Agriculture (USDA), ARS, PSI
Bldg 010A, 10300 Baltimore avenue, BARC West, Beltsville, MD 20705-2350, USA
Tel: 301-504-6654
Fax: 301-504-5653
Email: rowlandj@ba.ars.usda.gov.
Location/Qualifiers

FEATURES

source
1. .28
/organism="Vaccinium corymbosum"
/mol_type="mRNA"
/cultivar="Bluecrop"
/db_xref="taxon:69266"
/tissue_type="Flower buds including bud scales"
/dev_stage="Mature plants"
/clone_lib="cDNA non acclimated Bluecrop library"
/note="Vector: pBluescript SK-; cDNA clones from Vaccinium corymbosum cv. Bluecrop, RNA for preparation of library was extracted from flower buds collected in the fall from non acclimated plants"

Query Match 0.8%; Score 22.8; DB 1; Length 28;
Best Local Similarity 85.7%; Pred. No. 8.5e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 28 ANAAAAAGTNAAAAAAAAAAAAAAAAAA 1

RESULT 1064

TA327D04P/c
LOCUS TA327D04P 28 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 327d04, forward sequence, genomic survey sequence.

ACCESSION AL497297
VERSION AL497297.1 GI:11867974
KEYWORDS GSS.

SOURCE

Trypanosoma brucei

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.8%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. NO. 8.4e+02;
Matches 23: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 |||||
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1067

AZ438069
LOCUS
DEFINITION
AZ438069
24 bp DNA linear
MW0228A10F Mouse 10kb plasmid UGCG library Mus musculus genomic
Clone UGCIM0228A10 F, genomic survey sequence.
GSS 03-OCT-2000

ACCESSION	AZ438069
VERSION	AZ438069.1
	GI:10562178

SOURCE
Mus musculus (house mouse)

Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 24)
Dunn, D., Aovagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

FEATURES
SOURCE

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 8.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2732
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAATA 24

RESULT 1068

AZ458112/c	AZ458112	24 bp	DNA	linear	GSS 04-OCT-2000
LOCUS	1M0261E24R	Mouse	10kb	plasmid	UUGCJM library
DEFINITION	clone UUGCJM0261E24 R,	genomic survey	sequence.		

ACCESSION	AZ458112
VERSION	AZ458112.1
	GI:10616237

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 24)
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

FEATURES
SOURCE

adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 8.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1069

AZ607198

LOCUS

DEFINITION 24 bp DNA linear GSS 13-DEC-2000
1M0429G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0429G03 R, genomic survey sequence.

ACCESSION

AZ607198

VERSION

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 24)

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0429 row: G column: 03

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0429G03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

source

features

source

source

source

source

source

adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 8.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 TAAATTAATAAAAAAAAAAAAAA 24

RESULT 1070

AZ621257/c

LOCUS

DEFINITION 24 bp DNA linear GSS 13-DEC-2000
1M0454E23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0454E23 F, genomic survey sequence.

ACCESSION

AZ621257

VERSION

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 24)

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0454 row: E column: 23

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0454E23"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

source

features

source

source

source

source

adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 8.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1071

DU835497/c

LOCUS 24 bp DNA linear GSS 22-DEC-2005
DEFINITION KBrS016M18F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016M18, genomic survey sequence.

ACCESSION DU835497
VERSION DU835497
KEYWORDS DU835497.1 GI:83872093

SOURCE GSS.

ORGANISM Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 24)

AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S.

TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

JOURNAL

COMMENT

Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa subsp. pekinensis Sau3AI BAC clone KBrS016M18

Seq primer: T7

Class: BAC ends.

Location/Qualifiers
1..24
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS016M18"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa subsp. pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAH."

FEATURES

source

Query Match 0.8%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 8.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1072

DX045709/c

LOCUS

DEFINITION KBrB047B17F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB047B17, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.

TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone

JOURNAL

COMMENT

Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone KBrB047B17

Seq primer: T7

Class: BAC ends.

Location/Qualifiers
1..24
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB047B17"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa subsp. pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."

FEATURES

source

Query Match 0.8%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 8.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1073

N27663/c

LOCUS

DEFINITION N27663 25 bp mRNA linear EST 30-DEC-1995
IMAGE:255706 3' similar to gb:J05032 ASPARTYL-TRNA SYNTHETASE (HUMAN); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 25)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfs, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.

TITLE

JOURNAL

PUBMED

Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
8889549

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: m13 -40 forward
High quality sequence stop: 1.

FEATURES

source
1. .25
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="CDB:3866115"
/db_xref="taxon:9606"
/clone="IMAGE:255706"
/sex="Female"
/tissue_types="olfactory epithelium"
/dev_stage="35 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Weizmann Olfactory Epithelium"
/notes="Organ: nose; Vector: pBluescript SK-; Site 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Olfactory epithelium, normal. Average insert
size: 0.8 kb; Uni-ZAP XR Vector. Library constructed by N.
Walker, D. Lancelot, Weizmann Institute of Science. -5'
adaptor sequence: 5' GAATTCGCCAGCAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

Query Match 0.8%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 8.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAA..... 27 bp mRNA linear EST 15-AUG-2003

Db 24 CTCAAAAA..... 1

RESULT 1074

CF310745 27 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--05-J07.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-J07, mRNA sequence.

ACCESSION CF310745.1 GI:33682506

VERSION 1

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 27)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1. .27

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

FEATURES

source

/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--05-J07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site_1: ECORI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.8%; Score 22.4; DB 1; Length 27;
Best Local Similarity 95.8%; Pred. No. 8.8e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAA..... 2730

Db 4 CCAAAAAA..... 27

RESULT 1075

AL039138 28 bp mRNA linear EST 06-JUL-2004
LOCUS DKF2p566L164.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DEFINITION DKF2p566L164, mRNA sequence.

ACCESSION AL039138

VERSION AL039138.1 GI:49682258

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

Bloeker,H., Boecker,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.

EST (Bloecker, et al.)

Unpublished (1999)

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

Location/Qualifiers

1. .28

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKF2p566L164"

/tissue_type="kidney"

/dev_stage="fetal"

/lab_host="Xl-2blue"

/clone_lib="566 (synonym: hfkd2)"

/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.8%; Score 22.4; DB 1; Length 28;
Best Local Similarity 95.8%; Pred. No. 8.9e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2704 GTACTAAAAA..... 2727

Db 5 GTAATAAAAAA..... 28

RESULT 1076

DX082097 28 bp DNA linear GSS 10-JAN-2006
LOCUS KBrB095E02F KBrB, Brassica rapa BamHI BAC library Brassica rapa
DEFINITION subsp. pekinensis genomic clone KBrB095E02, genomic survey
sequence.

ACCESSION DX082097

VERSION DX082097.1 GI:84776393


```

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

GSS.
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 28)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.U., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBR8) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBR8095E02
Seq primer: T7
Class: BAC ends.
FEATURES
source
1..28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chilfu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBR8095E02"
/lab_host="E.coli DH10B"
/clone_lib="KBR8, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chilfu BAC library (KBR8 BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.8%; Score 22.4; DB 1; Length 28;
Best Local Similarity 95.8%; Pred. No. 8.9e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTTAAAAA..... 2730
|||
Db 5 CTTAAAAA..... 28
|||

RESULT 1077
CF298133/c
LOCUS
DEFINITION
27 bp mRNA linear EST 15-AUG-2003
7LEAF--01-G09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--01-G09, mRNA
sequence.
ACCESSION
CF298133
VERSION
CF298133.1 GI:33669894
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 27)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

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1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 22.2; DB 1; Length 27;
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Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAA..... 2735
|||
Db 27 AAGAAAAAAGGAAAAA..... 1
|||

RESULT 1078
CF328811/c
LOCUS
DEFINITION
27 bp mRNA linear EST 18-AUG-2003
NACL--03-009.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--03-009, mRNA
sequence.
ACCESSION
CF328811
VERSION
CF328811.1 GI:33805864
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 27)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="NACL--03-G09"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 9e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAA..... 2735
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Db 27 AAAAAAAGATTAAAAA..... 1
|||

FEATURES
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1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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RESULT 1079
CF333518/c

LOCUS JMT--02-H05.g1 27 bp mRNA linear EST 18-AUG-2003
DEFINITION library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-H05, mRNA sequence.

ACCESSION CF333518.1 GI:33815326

VERSION EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 27)

REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

AUTHORS Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1..27

Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="JMT--02-H05"

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/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/notes="Vector: pCR4-TOPO; Site1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.8%; Score 22.2; DB 1; Length 27;

Best Local Similarity 88.9%; Pred. No. 9e+02;

Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2702 TTCTACTAAAAAAAAAAAAAAAAAAAAA 2728

Db 27 TTTTTTTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1080
N89936/c

LOCUS N89936 27 bp mRNA linear EST 02-APR-1996
DEFINITION zb23e12.s1 Soares_fetal_lung NBHL19W Homo sapiens cDNA clone
IMAGE:302926 3' similar to gb:X59066 ATP SYNTHASE ALPHA CHAIN,
MITOCHONDRIAL PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION N89936

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

1 (bases 1 to 27)

REFERENCE Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

AUTHORS Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maria, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL
COMMENT

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estowatson.wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: ET primer

High quality sequence stop: 8.

FEATURES
source

1..27

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:1247858"

/db_xref="taxon:9606"

/clone="IMAGE:302926"

/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal lung NBHL19W"

/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer

15'-TCTTACCAATCTGAAGTGGAGCGCCGCAATTTTTTTTTTTT-3',

double-stranded cDNA was size selected, ligated to Eco RI -

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. This library was constructed

from the same fetus as the fetal heart library, Soares

fetal heart NBHL19W."

Query Match 0.8%; Score 22.2; DB 1; Length 27;

Best Local Similarity 88.9%; Pred. No. 9e+02;

Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAA 2732

Db 27 NATGCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1081

CL654516/c

LOCUS

DEFINITION

CL654516 27 bp DNA linear GSS 09-JUL-2004

PRI0120d B08 - PRI0120d.B21 (27) Note: Recurring String Mixed stage

fosmid library of P. pacificus var. California Pristionchus

pacificus genomic, genomic survey sequence.

ACCESSION CL654516

VERSION CL654516.1

KEYWORDS GSS.

SOURCE Pristionchus pacificus

ORGANISM Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 27)

AUTHORS Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

TITLE AppADB: an AcedB database for the nematode satellite organism

JOURNAL Pristionchus pacificus

PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)

COMMENT 14681447

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: raif.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

/clone="7LEAF--04-G19"		0.8%; Score 22; DB 1; Length 22;			
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/lab_host="E.coli DH108"		0; Indels		0; Gaps	
/clone_lib="rice leaf plasmid cDNA library II (7LEAF)"					
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."					
Qy	2709	AAAAAAAAAAAAAAAAAAAAA	2730		
Db	22	AAAAAAAAAAAAAAAAAAAAA	1		
RESULT 1085					
CF310366/c					
LOCUS					
DEFINITION					
ABF--04-p14.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone					
ABF--04-p14, mRNA sequence.					
CF310366					
CF310366.1 GI:33682127					
EST.					
Oryza sativa (japonica cultivar-group)					
Oryza sativa (japonica cultivar-group)					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.					
1 (bases 1 to 22)					
REFERENCE					
AUTHORS					
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.					
Large-scale Sequencing Analysis of Rice ESTs					
Unpublished (2003)					
Contact: Nahm B.H.					
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Yongin, Gyeonggi, Korea					
Tel: 82 31 330 6193					
Fax: 82 31 321 6355					
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.					
FEATURES					
. source					
1..22					
/organism="Oryza sativa (japonica cultivar-group)"					
/mol_type="mRNA"					
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."					
Qy	2709	AAAAAAAAAAAAAAAAAAAAA	2730		
Db	22	AAAAAAAAAAAAAAAAAAAAA	1		
RESULT 1086					
CF311269/c					

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
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Email: bhnahm@bio.myongji.ac.kr.

FEATURES

source

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1. ..22
/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1088

CF312498

LOCUS

DEFINITION ABF--08-E15.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

ABF--08-E15, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 22)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.myongji.ac.kr.

FEATURES

source

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1. ..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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line."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1089

CF330679/c

LOCUS

DEFINITION NACL--06-H22.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-H22, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 22)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

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Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355

Email: bhnahm@bio.myongji.ac.kr.

FEATURES

source

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1. ..22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
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Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1090

CF333430/c

LOCUS

DEFINITION JMT--02-F04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--02-F04, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 22)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..22

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

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/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 0.8%; Score 22; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 8.5e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CF334781 22 bp mRNA linear EST 18-AUG-2003

JMT--04-D05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--04-D05, mRNA sequence.

CF334781 1 GI:33817904

CF334781

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 22)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..22

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

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/clone="JMT--04-D05"

Query Match 0.8%; Score 22; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 8.5e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CF334781 22 bp mRNA linear EST 18-AUG-2003

JMT--04-D05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 0.8%; Score 22; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 8.5e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CF336250 22 bp mRNA linear EST 18-AUG-2003

JMT--06-D20.b1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--06-D20, mRNA sequence.

CF336250 1 GI:33820891

CF336250

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 22)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..22

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

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/clone="JMT--06-D20"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 0.8%; Score 22; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 8.5e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CF337580 22 bp mRNA linear EST 18-AUG-2003

JMT--04-D05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--04-D05, mRNA sequence.

CF337580 1 GI:33817904

CF337580

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 22)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

LOCUS CF337580 22 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--08-B11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--08-B11, mRNA sequence.

ACCESSION

CF337580

VERSION

CF337580.1

KEYWORDS

GI:33823547

SOURCE

EST.

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 22)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..22

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="JMT--08-B11"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jaeminate Carboxyl methyltransferase overexpression line."

was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jaeminate Carboxyl methyltransferase overexpression line."

methyltransferase overexpression line."

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methyltransferase overexpression line."

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

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/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="RCL1--01-P07"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli SOLR"

/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"

/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730

Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1095

AW332181/c

LOCUS AW332181 22 bp mRNA linear EST 31-JAN-2000

DEFINITION SSC7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.

ACCESSION AW332181

VERSION AW332181.1

KEYWORDS GI:6828538

EST.

SOURCE Pneumocystis carinii

ORGANISM Pneumocystis carinii

Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;

Pneumocystidaceae; Pneumocystis.

1 (bases 1 to 22)

Smilian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,

Edman, J.C., Kovacs, J. and Cushion, M.

Expressed sequence tags from Pneumocystis carinii

Unpublished (2000)

Contact: Staben C

School of Biological Sciences

University of Kentucky

101 Morgan Building, University of Kentucky, Lexington, KY

40506-0225, USA

Tel: 606 257 2161

Fax: 606 257 1717

Email: staben@pop.uky.edu.

Location/Qualifiers

1..22

/organism="Pneumocystis carinii"

/mol_type="mRNA"

/db_xref="taxon:4754"

/lab_host="E. coli"

/clone_lib="AGS-1"

/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;

P. carinii organisms (3x10e9) from a single rat (99-1-6,

sacrificed on 3/17/99) at Cincinnati VA facilities.

Trizol extracted RNA. Oligo dT priming, standard

conditions described by vendor, Stratagene. Further

details see www.uky.edu/Project/Pneumocystis/

details see www.uky.edu/Project/Pneumocystis/

details see www.uky.edu/Project/Pneumocystis/

details see www.uky.edu/Project/Pneumocystis/

details see www.uky.edu/Project/Pneumocystis/

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details see www.uky.edu/Project/Pneumocystis/

details see www.uky.edu/Project/Pneumocystis/

details see www.uky.edu/Project/Pneumocystis/

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730


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Db      22  AAAAAAAAAAAAAAAAAAAAAA 1
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RESULT 1096
LOCUS   AW332399/c              22 bp  mRNA  linear  EST 31-JAN-2000
DEFINITION  SBA2 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION  AW332399
VERSION    AW332399.1  GI:6828756
SOURCE     EST.
ORGANISM   Pneumocystis carinii
            Pneumocystis carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE  1  (bases 1 to 22)
AUTHORS    Smullan,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
            Edman,J.C., Kovacs,J. and Cushman,M.
TITLE      Expressed sequence tags from Pneumocystis carinii
JOURNAL    Unpublished (2000)
COMMENT    Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.

FEATURES             source
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                    /organism="Pneumocystis carinii"
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                    /db_xref="taxon:4754"
                    /lab_host="E. coli"
                    /clone_lib="AGS-1"
                    /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
                    P. carinii organisms (3x10e9) from a single rat (99-1-6,
                    sacrificed on 3/17/99) at Cincinnati VA facilities.
                    Trizol extracted RNA. Oligo dt priming, standard
                    conditions described by vendor, Stratagene. Further
                    details see www.uky.edu/Project/Pneumocystis/"

    Query Match      0.8%; Score 22; DB 1; Length 22;
    Best Local Similarity 100.0%; Pred. No. 8.5e+02;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709  AAAAAAAAAAAAAAAAAAAAAA 2730
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Db      22  AAAAAAAAAAAAAAAAAAAAAA 1
|||||

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QY      2709  AAAAAAAAAAAAAAAAAAAAAA 2730
          |||||||
Db      22  AAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 1097
LOCUS   CN545550/c              22 bp  mRNA  linear  EST 30-APR-2004
DEFINITION  EST 17494 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
            clone B3CS00RL003D05 3', mRNA sequence.
ACCESSION  CN545550
VERSION    CN545550.1  GI:46910175
SOURCE     EST.
ORGANISM   Vitis vinifera
            Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; Vitaceae; Vitis.
REFERENCE  1  (bases 1 to 22)
AUTHORS    Abbai,P., Agase,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
TITLE      Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
JOURNAL    Unpublished (2002)
COMMENT    Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne

```

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Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES             source
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                    /organism="Vitis vinifera"
                    /mol_type="mRNA"
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                    /db_xref="taxon:29760"
                    /clone="B3CS00RL003D05"
                    /dev_stage="ripening stage"
                    /clone_lib="Ripe Grape Skin Triplex2 Library"
                    /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
                    SfiIA; Site_2: SfiIB; Oriented library"

    Query Match      0.8%; Score 22; DB 1; Length 22;
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    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709  AAAAAAAAAAAAAAAAAAAAAA 2730
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Db      22  AAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 1098
LOCUS   DN955212                22 bp  mRNA  linear  EST 04-MAY-2005
DEFINITION  it83g12.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
            sequence.
ACCESSION  DN955212
VERSION    DN955212.1  GI:63027350
KEYWORDS   EST.
SOURCE     Gnetum gnemon
ORGANISM   Gnetum gnemon
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Gnetophyta; Gnetales; Gnetales; Gnetales; Gnetum.
            1  (bases 1 to 22)
            Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
            O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W.,
            Benfey,P., Coruzzi,G. and Stevenson,D.
            Expressed tag sequences from Gnetum female cone (NYBG)
            Unpublished (2003)
            Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Seq primer: -21M13UnivRev.

FEATURES             source
    source            1..22
                    /organism="Gnetum gnemon"
                    /mol_type="mRNA"
                    /db_xref="taxon:3382"
                    /sex="female"
                    /clone_lib="Gnetum female cone (NYBG)"
                    /note="Organ: mature, unfertilized reproductive strobili;
                    Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
                    Completed 02/11/02, submitted for sequencing 02/12/02.
                    Library: Stratagene ZAP Express cDNA Synthesis Kit. The
                    library was size-fractionated to enrich for large inserts.
                    Sample: NYBG accession number #436/84"

    Query Match      0.8%; Score 22; DB 1; Length 22;
    Best Local Similarity 100.0%; Pred. No. 8.5e+02;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	2709	AAAAAAAAAAAAAAAAAAAAA	2730
Db	1	AAAAAAAAAAAAAAAAAAAAA	22
RESULT 1099			
DN955228	DN955228	22 bp mRNA linear	EST 04-MAY-2005
LOCUS	it84b02.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA		
DEFINITION	sequence.		
ACCESSION	DN955228	GI:63027366	
VERSION	DN955228.1		
KEYWORDS	EST.		
SOURCE	Gnetum gnemon		
ORGANISM	Gnetum gnemon		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Gnecotaphya; Gnecotaphida; Gnetales; Gnecotaphia; 1 (bases 1 to 22)		
AUTHORS	Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W., Benfey,P., Coruzzi,G. and Stevenson,D.		
TITLE	Expressed tag sequences from Gnetum female cone (NYBG)		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mcombie@cshl.org Seq primer: -21MI3UnivRev.		
FEATURES			
source	1..22	/organism="Gnetum gnemon"	
		/mol_type="mRNA"	
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Query Match	0.8%; Score 22; DB 1; Length 22;		
Best Local Similarity	100.0%; Pred. No. 8.5e+02;		
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Query Match	0.8%; Score 22; DB 1; Length 22;		
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Query Match	0.8%; Score 22; DB 1; Length 22;		
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Query Match	0.8%; Score 22; DB 1; Length 22;		
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		/notes="Organ: mature, unfertilized reproductive strobili; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date: Completed 02/11/02, submitted for sequencing 02/12/02. Library: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: NYBG accession number #436/84"	
Query Match	0.8%; Score 22; DB 1; Length 22;		
Best Local Similarity	100.0%; Pred. No. 8.5e+02;		
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Query Match	0.8%; Score 22; DB 1; Length 22;		
Best Local Similarity	100.0%; Pred. No. 8.5e+02;		
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
FEATURES			


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DEFINITION ik79e05.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR073458
VERSION DR073458.1 GI:67051333
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
REFERENCE 1 (bases 1 to 22)
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE Expressed tag sequences from Ginkgo female leaf (NYBG)
JOURNAL Unpublished (2005)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Original 3 prime EST has been reverse completed to be in 5 prime
direction
Seq primer: -21M13UnivRev.
Location/Qualifiers
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/mol_type="mRNA"
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/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

FEATURES
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Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 TAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1106
LOCUS DR074014/c
DEFINITION ik92d03.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR074014
VERSION DR074014.1 GI:67051943
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
REFERENCE 1 (bases 1 to 22)
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE Expressed tag sequences from Ginkgo male leaf (NYBG)
JOURNAL Unpublished (2005)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..22
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

FEATURES
source
Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 TAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1106
LOCUS DR074014/c
DEFINITION ik92d03.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR074014
VERSION DR074014.1 GI:67051943
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
REFERENCE 1 (bases 1 to 22)
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE Expressed tag sequences from Ginkgo male leaf (NYBG)
JOURNAL Unpublished (2005)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..22
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

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source
1..22
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="male"
/clone_lib="Ginkgo male leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI; Site 2:
Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large
inserts."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1107
LOCUS AZ310066/c
DEFINITION AZ310066 22 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0018D18 R, genomic survey sequence.
ACCESSION AZ310066
VERSION AZ310066.1 GI:10351682
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: D column: 18
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0018D18"
/sex="Male"
/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

```

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G[4732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1108
AZ351527
LOCUS 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0089E07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0089E07 R, genomic survey sequence.

ACCESSION AZ351527
VERSION AZ351527.1 GI:10430764
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0089 row: E column: 07

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0089E07"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G[4732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1109
AZ357630
LOCUS 22 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0099M15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0099M15 F, genomic survey sequence.

ACCESSION AZ357630
VERSION AZ357630.1 GI:10471318
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0099 row: M column: 15

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0099M15"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1110
 AZ388103
 LOCUS 22 bp DNA linear GSS 02-OCT-2000
 DEFINITION clone UUGC1M0147N14 R, genomic survey sequence.

ACCESSION AZ388103
 VERSION AZ388103.1 GI:10501811
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0147 row: N column: 14
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0147N14"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1111
 AZ401908
 LOCUS 22 bp DNA linear GSS 03-OCT-2000
 DEFINITION clone UUGC1M0169P24 R, genomic survey sequence.

ACCESSION AZ401908
 VERSION AZ401908.1 GI:10516982
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0168 row: P column: 24
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0169P24"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1112
AZ424307/c
LOCUS
DEFINITION
IM0203A24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0203A24 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: A column: 24
Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0203A24"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1113
AZ428818/c
LOCUS
DEFINITION
1M0212A05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0212A05 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: A column: 05
Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0212A05"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1114
AZ459654/c
LOCUS
DEFINITION
1M0264G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0264G12 R, genomic survey sequence.

ACCESSION
AZ459654
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus
Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: G column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
1..22
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0264G12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1115
AZ463503/c
LOCUS
DEFINITION
1M0272E24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0272E24 F, genomic survey sequence.

ACCESSION
AZ463503
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus
Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0272 row: E column: 24
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
1..22
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0272E24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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ligated to the blunt ends in high molar excess. The

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Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||
 Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1116
 AZ463652/c
 LOCUS
 DEFINITION 22 bp DNA linear GSS 04-OCT-2000
 1M0272E12R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 clone UUGCIM0272E12 R, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AZ463652
 GI:10621777
 GSS.
 Mus musculus (house mouse)
 Mus musculus

REFERENCE
 AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0272 row: E column: 12

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCIM0272E12"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydronically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G[4732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||
 Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1117
 AZ582403
 LOCUS
 DEFINITION 22 bp DNA linear GSS 13-DEC-2000
 1M0374J15R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 clone UUGCIM0374J15 R, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AZ582403
 GI:11701249
 GSS.
 Mus musculus (house mouse)
 Mus musculus

REFERENCE
 AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
 Contact: Robert B. Weiss
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 University of Utah
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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0374 row: J column: 15

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCIM0374J15"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydronically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

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Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1118
AZ607658
LOCUS 22 bp DNA linear GSS 13-DEC-2000
DEFINITION iM0430A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0430A13 F, genomic survey sequence.
ACCESSION AZ607658
VERSION AZ607658.1 GI:11729848
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0430 row: A column: 13
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0430A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

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Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1119
AZ654691
LOCUS 22 bp DNA linear GSS 14-DEC-2000
DEFINITION iM0529D05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0529D05 F, genomic survey sequence.
ACCESSION AZ654691
VERSION AZ654691.1 GI:11791837
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: D column: 05
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0529D05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

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Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1120
AZ760533
LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0554A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0554A24 F, genomic survey sequence.

ACCESSION AZ760533
VERSION AZ760533.1 GI:12868477
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0554 row: A column: 24

Seq primer: CGTTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

FEATURES Location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0554A24"
/sex="Male"

/lab host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); Purified genomic DNA from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1121
AZ779844/c

LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0016112R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0016112 R, genomic survey sequence.

ACCESSION AZ779844

VERSION AZ779844.1 GI:12910910

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0016 row: I column: 12

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

FEATURES Location/Qualifiers

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0016112"
/sex="Male"

/lab host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); Purified genomic DNA from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

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Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1122
AZ785019/c

LOCUS
DEFINITION 22 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0028E04 R, genomic survey sequence.

ACCESSION AZ785019
VERSION AZ785019.1 GI:12921341

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS 1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0028 row: E column: 04

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

FEATURES

source

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0028E04"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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0.005 inch orifice at constant velocity. The sheared DNA

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polynucleotide kinase. Adaptor oligonucleotides were

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Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1123
AZ787098/c

LOCUS
DEFINITION 22 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0033A05 F, genomic survey sequence.

ACCESSION AZ787098
VERSION AZ787098.1 GI:12925520

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS 1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0033 row: A column: 05

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

FEATURES

source

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0033A05"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1124
AZ787606/c
LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0034G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0034G12 F, genomic survey sequence.

ACCESSION AZ787606
VERSION AZ787606.1 GI:12926565
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0034 row: G column: 12

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0034G12"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male); Obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1125
AZ792704/c

LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0045A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0045A24 F, genomic survey sequence.

ACCESSION AZ792704

VERSION AZ792704.1 GI:12936911

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0045 row: A column: 24

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0045A24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male); Obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||
 Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1126
 AZ810674/c
 LOCUS
 DEFINITION 2M0076E19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0076E19 F, genomic survey sequence.
 ACCESSION AZ810674
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0076 row: E column: 19
 Seq primer: CGTTGTAACACGCGCAGT
 Class: plasmid ends

High quality sequence stop: 22.

FEATURES
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0076E19"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||
 Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1127
 AZ820439/c
 LOCUS
 DEFINITION 2M0092K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0092K13 R, genomic survey sequence.
 ACCESSION AZ820439
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0092 row: K column: 13
 Seq primer: CACACGGAACACGTATGACC
 Class: plasmid ends

High quality sequence stop: 22.

FEATURES
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0092K13"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1128

AZ841661

LOCUS

AZ841661 22 bp DNA linear GSS 20-FEB-2001
2M0139118R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0139118 R, genomic survey sequence.

ACCESSION

AZ841661

VERSION

AZ841661.1

KEYWORDS

GI:13011569

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 22)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0139 row: I column: 18

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0139118"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrotynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

FEATURES

source

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0142124"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrotynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1129

AZ843514/c

LOCUS

AZ843514 22 bp DNA linear GSS 20-FEB-2001
2M0142124F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0142124 F, genomic survey sequence.

ACCESSION

AZ843514

VERSION

AZ843514.1

KEYWORDS

GI:13013422

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 22)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0142 row: I column: 24

Seq primer: CGTTGTAAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0142124"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrotynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
DB 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1130

AZ946102

LOCUS 22 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0207D13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0207D13 R, genomic survey sequence.

ACCESSION AZ946102
VERSION
KEYWORDS
SOURCE GI:13812911
GSS.

Mus musculus
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

CONTACT: Robert B. Weiss

University of Utah

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0207 Row: D Column: 13

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

FEATURES

source

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0207D13"
/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWB42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1131

DUB34428

LOCUS 22 bp DNA linear GSS 22-DEC-2005
DEFINITION KBrS014E07F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS014E07, genomic survey sequence.

ACCESSION DUB34428
VERSION DUB34428.1 GI:83871024
KEYWORDS
SOURCE GSS.

Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 22)

REFERENCE

AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,Y.J., Seo,I.Y.J., Park,D.S., Hahn,J.H. and Park,B.S.

End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

JOURNAL

Unpublished (2005)

COMMENT

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa subsp. pekinensis Sau3AI BAC clone

KBrS014E07

Seq primer: T7

Class: BAC ends.

FEATURES

source

1..22
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS014E07"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa subsp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 22

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RESULT 1132
DUB35320
LOCUS
DEFINITION
  KBrS016H03F KBrS, Brassica rapa Sau3AI BAC library GSS 22-DEC-2005
  subsp. pekinensis genomic clone KBrS016H03, genomic survey
  sequence.
ACCESSION
DUB35320
VERSION
DUB35320.1 GI:83871916
SOURCE
GSS.
ORGANISM
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
  1 (bases 1 to 22)
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J.H. and Park,B.S.
  End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  Brassica Genomics Team
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  KBrS016H03
  BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
  Seq primer: T7
  Class: BAC ends.
  Location/Qualifiers
    1..22
      /organism="Brassica rapa subsp. pekinensis"
      /mol_type="genomic DNA"
      /cultivar="Chiifu"
      /sub_species="pekinensis"
      /db_xref="taxon:51351"
      /clone="KBrS016H03"
      /lab_host="E. coli DH10B"
      /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
      /note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
      subsp. pekinensis var. Chiifu BAC library (KBrS BAC) is
      available at NTAB."

  Query Match      0.8%; Score 22; DB 1; Length 22;
  Best Local Similarity 100.0%; Pred.No. 8.5e+02;
  Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1134
DX046124/c
LOCUS
DEFINITION
  DX046124F KBrB, Brassica rapa BamHI BAC library GSS 10-JAN-2006
  subsp. pekinensis genomic clone KBrB047K15, genomic survey
  sequence.
ACCESSION
DX046124
VERSION
DX046124.1 GI:84740421
KEYWORDS
GSS.
SOURCE
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
  1 (bases 1 to 22)
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J.H. and Park,B.S.
  End sequence of Brassica rapa BamHI (KBrB) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  Brassica Genomics Team
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  KBrB047K15
  BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
  Seq primer: T7
  Class: BAC ends.
  Location/Qualifiers
    1..22
      /organism="Brassica rapa subsp. pekinensis"
      /mol_type="genomic DNA"
      /cultivar="Chiifu"
      /sub_species="pekinensis"

  Query Match      0.8%; Score 22; DB 1; Length 22;
  Best Local Similarity 100.0%; Pred.No. 8.5e+02;
  Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1133
DX033920/c
LOCUS
DEFINITION
  DX033920 KBrB, Brassica rapa BamHI BAC library GSS 10-JAN-2006
  subsp. pekinensis genomic clone KBrB031121, genomic survey
  sequence.
ACCESSION
DX033920
VERSION
DX033920.1 GI:84728217
KEYWORDS
GSS.
SOURCE
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
  1 (bases 1 to 22)
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J.H. and Park,B.S.
  End sequence of Brassica rapa BamHI (KBrB) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  Brassica Genomics Team
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  KBrB031121
  BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
  Seq primer: T7
  Class: BAC ends.
  Location/Qualifiers
    1..22
      /organism="Brassica rapa subsp. pekinensis"
      /mol_type="genomic DNA"
      /cultivar="Chiifu"
      /sub_species="pekinensis"

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/db_xref="taxon:51351"
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 /lab_host="E.coli DH10B"
 /clone_lib="KBrB, Brassica rapa BamHI BAC library"
 /note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
 pekinensis var. Chifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730

Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1135

DX056961/C

LOCUS
 DEFINITION KBrB062A19F KBrB, Brassica rapa BamHI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBrB062A19, genomic survey
 sequence.

ACCESSION DX056961

VERSION DX056961.1 GI:84751258

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 22)

AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,

Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,

Hahn,J.H. and Park,B.S.

Title End sequence of Brassica rapa BamHI (KBrB) BAC clone

JOURNAL Unpublished (2005)

COMMENT Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa spp. pekinensis BamHI BAC clone

KBrB062A19

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. .22

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrB062A19"

/lab_host="E.coli DH10B"

/clone_lib="KBrB, Brassica rapa BamHI BAC library"

/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp

pekinensis var. Chifu BAC library (KBrB BAC) is provided

by Yong-Pyo Lim (CNU)."

Query Match 0.8%; Score 22; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 8.5e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730

Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1136

DX069868

LOCUS
 DEFINITION KBrB079A22F KBrB, Brassica rapa BamHI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBrB079A22, genomic survey
 sequence.

ACCESSION DX069868

VERSION DX069868.1 GI:84764164

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 22)

AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,

Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,

Hahn,J.H. and Park,B.S.

Title End sequence of Brassica rapa BamHI (KBrB) BAC clone

JOURNAL Unpublished (2005)

COMMENT Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa spp. pekinensis BamHI BAC clone

KBrB079A22

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. .22

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrB079A22"

/lab_host="E.coli DH10B"

/clone_lib="KBrB, Brassica rapa BamHI BAC library"

/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp

pekinensis var. Chifu BAC library (KBrB BAC) is provided

by Yong-Pyo Lim (CNU)."

Query Match 0.8%; Score 22; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 8.5e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1137

DX080494

LOCUS
 DEFINITION KBrB093A20R KBrB, Brassica rapa BamHI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBrB093A20, genomic survey
 sequence.

ACCESSION DX080494

VERSION DX080494.1 GI:84774790

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 22)

AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,

Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,

Hahn,J.H. and Park,B.S.

Title End sequence of Brassica rapa BamHI (KBrB) BAC clone

JOURNAL Unpublished (2005)

COMMENT Contact: Beom-Seok Park

```

Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB093A20
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
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        1..22
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            /clone="KBrB093A20"
            /lab_host="E.coli DH10B"
            /clone_lib="KBrB, Brassica rapa BamHI BAC library"
            /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
            pekinensis var. Chifu BAC library (KBrB BAC) is provided
            by Yong-Pyo Lim (CNU)."
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Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
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 Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1138
 AG194579
 LOCUS Pan troglodytes DNA, clone: RP43-072N05.TJ, genomic survey
 DEFINITION
 ACCESSION AG194579
 VERSION AG194579.1 GI:45226755
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM
 Eukaryota; Chordata; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Pan.

REFERENCE 1
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
 Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 BAC end sequences of Library RP-43
 Unpublished
 TITLE BAC end sequences of Library RP-43
 REFERENCE 2 (bases 1 to 22)
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
 Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 Direct Submission
 TITLE Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
 Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
 (E-mail: redstone@mail.krribb.re.kr, URL: http://phs.grc.krribb.re.kr/,
 Tel: 82-42-866-7181, Fax: 82-42-860-4409)
 COMMENT Clones are derived from the chimpanzee BAC library RP-43. This BAC
 end was generated during the R&D process and may have higher chance
 of clone tracking errors.
 PRIMERS
 Sequencing: TJ

LIBRARY
 Vector : pBACE3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.
 Location/Qualifiers
 1..22
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"

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FEATURES
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        1..22
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            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="131B09"
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Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1140
 TA329F10P
 LOCUS T. brucei sheared genomic DNA clone 329f10, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL492691
 VERSION AL492691.1 GI:11868830
 KEYWORDS GSS.

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/db_xref="taxon:9598"
/clone="RP43-072N05.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match 0.8%; Score 22; DB 1; Length 22;  

Best Local Similarity 100.0%; Pred. No. 8.5e+02;  

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730  

    |||||  

    Db 1 AAAAAAAAAAAAAAAAAAAAAA 22



RESULT 1139  

    TA131B09P  

    LOCUS T. brucei sheared genomic DNA clone 131b09, forward sequence,  

    DEFINITION genomic survey sequence.  

    ACCESSION AL464164  

    VERSION AL464164.1 GI:11834427  

    KEYWORDS GSS.  

    SOURCE Trypanosoma brucei  

    ORGANISM  

    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  

    Trypanosoma.



REFERENCE 1 (bases 1 to 22)  

    AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  

    Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  

    Melville, S.E., Rajandream, M.A. and Barrell, B.G.  

    Direct Submission  

    TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  

    JOURNAL project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  

    Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  

    nh@sanger.ac.uk  

    COMMENT Constructed at the Institute for Genomic Research (TIGR),  

    Rockville, MD. Genomic DNA isolated from a cloned population of  

    Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  

    to give a tight size distribution (  

    4 kb). The v + i method used for the library construction is  

    described in detail in Smith, H. and Venter, J.C. (Making small  

    insert libraries for whole genome shotgun sequencing projects. In  

    Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  

    Barrell, Oxford University Press, 1999).  

    Email: nelsayed@tigr.org  

    Details of T. brucei sequencing at the Sanger Centre are available  

    at http://www.sanger.ac.uk/Projects/T_brucei/.



FEATURES  

    source  

        1..22  

            /organism="Trypanosoma brucei"  

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            /strain="TREU927"  

            /db_xref="taxon:5691"  

            /clone="131B09"



Query Match 0.8%; Score 22; DB 1; Length 22;  

    Best Local Similarity 100.0%; Pred. No. 8.5e+02;  

    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730  

    |||||  

    Db 1 AAAAAAAAAAAAAAAAAAAAAA 22



RESULT 1140  

    TA329F10P  

    LOCUS T. brucei sheared genomic DNA clone 329f10, forward sequence,  

    DEFINITION genomic survey sequence.  

    ACCESSION AL492691  

    VERSION AL492691.1 GI:11868830  

    KEYWORDS GSS.


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SOURCE      Trypanosoma brucei
ORGANISM    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 22)
AUTHORS    Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT    Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES   Location/Qualifiers
            source
            1..22
                /organism="Trypanosoma brucei"
                /mol_type="genomic DNA"
                /strain="TREU927"
                /db_xref="taxon:5691"
                /clone="329f10"
Query Match      0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1141
TA35C12Q/c
LOCUS      22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 35c12, reverse sequence,
            genomic survey sequence.
ACCESSION  AL454256.1 GI:11855060
VERSION    AL454256
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 22)
AUTHORS    Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT    Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES   Location/Qualifiers
            source
            1..22
                /organism="Trypanosoma brucei"
                /mol_type="genomic DNA"
                /strain="TREU927"
                /db_xref="taxon:5691"
                /clone="329f10"
Query Match      0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1141
TA35C12Q/c
LOCUS      22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 35c12, reverse sequence,
            genomic survey sequence.
ACCESSION  AL454256.1 GI:11855060
VERSION    AL454256
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 22)
AUTHORS    Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT    Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES   Location/Qualifiers
            source
            1..22
                /organism="Trypanosoma brucei"
                /mol_type="genomic DNA"
                /strain="TREU927"
                /db_xref="taxon:5691"
                /clone="35c12"
Query Match      0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1142
TA380A07P
LOCUS      22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 380a07, forward sequence,
            genomic survey sequence.
ACCESSION  AL497713.1 GI:11873435
VERSION    AL497713
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 22)
AUTHORS    Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT    Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES   Location/Qualifiers
            source
            1..22
                /organism="Trypanosoma brucei"
                /mol_type="genomic DNA"
                /strain="TREU927"
                /db_xref="taxon:5691"
                /clone="35c12"
Query Match      0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1143
CF329694/c
LOCUS      23 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-B19.b1 Rice callus plasmid cDNA library (NACL) Oryza

```

```

sativa (japonica cultivar-group) cDNA clone NACL--05-B19, mRNA
sequence.
ACCESSION      CF329694
VERSION        CF329694.1  GI:33807601
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="NACL--05-B19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.7e-02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAA
Db 22 TAAAAA

RESULT 1144
LOCUS      CF332379/c
DEFINITION NACL--08-N21.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--08-N21, mRNA
sequence.
ACCESSION      CF332379
VERSION        CF332379.1  GI:33812983
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

```

```

1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="NACL--08-N21"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.7e-02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAA
Db 22 TAAAAA

RESULT 1145
LOCUS      DT495201
DEFINITION DT495201 BR_L03 PT-P-FL-A-2 Populus trichocarpa cDNA clone WS0112_L03
5', mRNA sequence.
ACCESSION      DT495201
VERSION        DT495201.1  GI:73892463
KEYWORDS
SOURCE
ORGANISM
Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
Populus trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE
AUTHORS      Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,
Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,
Babakaliff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,
Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglass,C., Ritland,K. and
Bohlmann,J.
TITLE        The poplar transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries
JOURNAL      Unpublished (2004)
COMMENT      Contact: Joerg Bohlmann
Genome BC forest genomics program -
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS0112 row: L column: 03
High quality sequence stop: 132
POLYA=Yes.

FEATURES
source
1..23
/organism="Populus trichocarpa"
/mol_type="mRNA"
/db_xref="taxon:3694"
/clone="WS0112_L03"
/sex="Female"
/lab_host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PT-P-FL-A-2"
/notes="Vector: pBluescript II SK (+) XR; Site 1: SstI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Phloem and
cambium from 8 year old trees harvested within the Boie
Cascade region of Washington state on May 15th, 2001. cDNA
was prepared from 20 micrograms of mRNA according to the
full-length cDNA library construction method described by

```


Carninci P. et al. (2000), Genome Research
 10(10):1617-1630 and directionally ligated into the
 pBluescript II SK (+) XR vector digested with SstI (5'
 end) and XhoI (3'). Plasmid DNA was then transformed by
 electroporation into DH10B cells (Invitrogen) for
 propagation."

Query Match 0.8%; Score 22; DB 1; Length 23;
 Best Local Similarity 95.7%; Pred. No. 8.7e+02;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2708 TAAAAA 2730
 |||||
 Db 1 TAAAAA 23

RESULT 1146

AZ425710 23 bp DNA linear GSS 03-OCT-2000
 LOCUS
 DEFINITION IM0205123R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0205123 R, genomic survey sequence.

ACCESSION AZ425710
 VERSION
 KEYWORDS
 SOURCE GSS.
 Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 23)
 DUNN, D., AOYAGI, A., BARBER, M., BEACORN, T., DUVAL, B., HAMIL, C.,
 ISLAM, H., LONGACRE, S., MAHMOUD, M., MEENEN, E., PEDERSEN, T.,
 KELLY, M., ROSE, M., ROSE, R., STOKES, R., TINGEY, A., VON
 NIEDERHAUSEN, A. and WRIGHT, D., WEISS, R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss

COMMENT

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0205 row: L column: 23

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

FEATURES

Location/Qualifiers

1..23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0205123"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAA 2730
 |||||
 Db 2 AAAAAA 23

RESULT 1147

AZ801003 23 bp DNA linear GSS 16-FEB-2001
 LOCUS
 DEFINITION 2M0059J16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0059J16 F, genomic survey sequence.

ACCESSION AZ801003
 VERSION
 KEYWORDS
 SOURCE GSS.
 Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 23)
 DUNN, D., AOYAGI, A., BARBER, M., BEACORN, T., DUVAL, B., HAMIL, C.,
 ISLAM, H., LONGACRE, S., MAHMOUD, M., MEENEN, E., PEDERSEN, T.,
 KELLY, M., ROSE, M., ROSE, R., STOKES, R., TINGEY, A., VON
 NIEDERHAUSEN, A. and WRIGHT, D., WEISS, R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0059 row: J column: 16

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

FEATURES

Location/Qualifiers

1..23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0059J16"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0079 row: A column: 23
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES

Location/Qualifiers
 1. .24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0079A23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI-. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

source

1. .24

Query Match

Best Local Similarity 0.8%; Score 22; DB 1; Length 24;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||
 Db 3 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1151

N59260/c
 LOCUS N59260 25 bp mRNA linear EST 23-FEB-1996
 DEFINITION Yz2d11.s1 Soares multiple sclerosis 2NBHMSF Homo sapiens cDNA
 clone IMAGE:289557 3' similar to gb:M77693 DIAMINE
 ACETYLTRANSFERASE (HUMAN); mRNA sequence.

ACCESSION N59260
 VERSION N59260.1 GI:1203150
 KEYWORDS EST.

SOURCE Homo sapiens
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 25)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisan,B., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 TRACE considered overall poor quality
 Seq primer: ml3 -40 forward
 High quality sequence stop: 1.

FEATURES

Location/Qualifiers
 1. .25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3905397"
 /db_xref="taxon:9606"
 /clone="IMAGE:289557"
 /sex="male"
 /tissue_type="multiple sclerosis lesions"
 /dev_stage="Age 46"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares multiple sclerosis 2NBHMSF"
 /note="vector: pT7T3D (Pharmacia) with a modified polylinker V-type: phagemid; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTACCAATCTGAAGTGGGAGCGCGCGCATTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH)."

Query Match 0.8%; Score 22; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 9e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAA 2729
 |||||
 Db 22 TAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1152

CZ914626/c
 LOCUS CZ914626 25 bp DNA linear GSS 08-AUG-2005
 DEFINITION 4013007H05.2EL.y1 4013 - RescueMu Grid O Zea mays genomic survey sequence.

ACCESSION CZ914626

VERSION CZ914626.1 GI:71931353

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 25)

REFERENCE Walbot,V.

AUTHORS Maize genomic sequences found using engineered RescueMu transposon

TITLE Unpublished (2001)

JOURNAL Contact: Walbot V

COMMENT Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4013007 row: H column: 05

Class: transposon-tagged.

Location/Qualifiers

1. .25

FEATURES

source

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.8%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 1153

LOCUS

DEFINITION C2916641 25 bp DNA linear GSS 08-AUG-2005
survey sequence.

ACCESSION C2916641

VERSION C2916641.1 GI:71934805

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 25)

Walbot, V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4021002 row: C column: 08

Class: transposon-tagged.

Location/Qualifiers

1..25

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="4021 - RescueMu Grid V"

/notes="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'http://www.mutransposon.org/project/RescueMu/'. Grid

V was grown at University of Arizona in 2003. DNA was

extracted from leaf strips, double digested using BamHI

and BglII, and ligated to form circular plasmids. DH10B

cells were transformed and then screened on LB plates with

ampicillin."

units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

Query Match 0.8%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2729
Db 4 TAAAAAAAAAAAAAAAAAAAAA 25

RESULT 1154

LOCUS

DEFINITION TA154D03P 25 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 154d03, forward sequence,
genomic survey sequence.

ACCESSION AL472971

VERSION AL472971.1 GI:11838244

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 25)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers

1..25

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="154d03"

Query Match 0.8%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 1155

LOCUS

DEFINITION AM046273 27 bp mRNA linear EST 20-SEP-2005
Schistosoma mansoni lung schistosomulum Schistosoma

mansoni cDNA clone SmlC32a10.q1k, mRNA sequence.

AM046273

AM046273

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AM046273.1 GI:75969955
EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
REFERENCE
AUTHORS Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 27)
Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katearidou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
FEATURES
source
1. .27
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC32a10.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="country: Puerto Rico"
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Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 22
RESULT 1156
CZ914111
LOCUS 27 bp DNA linear GSS 08-AUG-2005
DEFINITION 4013005E12.1EL_x1 4013 - RescueMu Grid O Zea mays genomic, genomic
survey sequence.
ACCESSION CZ914111
VERSION CZ914111.1 GI:71930546
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 27)
REFERENCE Walbot,V.
AUTHORS Zea mays genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
TITLE Contact: Walbot V
JOURNAL Department of Biological Sciences
COMMENT Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013005 row: E column: 12
Class: transposon-tagged.
Location/Qualifiers
1. .27
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
AM046273.1 GI:75969955
EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
REFERENCE
AUTHORS Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 27)
Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katearidou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
FEATURES
source
1. .27
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC32a10.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="country: Puerto Rico"
Query Match 0.8%; Score 22; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 22
RESULT 1156
CZ914111
LOCUS 27 bp DNA linear GSS 08-AUG-2005
DEFINITION 4013005E12.1EL_x1 4013 - RescueMu Grid O Zea mays genomic, genomic
survey sequence.
ACCESSION CZ914111
VERSION CZ914111.1 GI:71930546
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 27)
REFERENCE Walbot,V.
AUTHORS Zea mays genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
TITLE Contact: Walbot V
JOURNAL Department of Biological Sciences
COMMENT Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013005 row: E column: 12
Class: transposon-tagged.
Location/Qualifiers
1. .27
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"

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RESULT 1158
AW249476/c
LOCUS
DEFINITION      25 bp mRNA linear EST 07-JAN-2000
                  2821131.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821131 3',
                  mRNA sequence.
ACCESSION
VERSION          AW249476
KEYWORDS
SOURCE
ORGANISM        Homo sapiens (human)

REFERENCE
AUTHORS         NIH-MGC http://mgc.nci.nih.gov/
TITLE           National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL         Unpublished (1999)
COMMENT         Other_ESTs: 2821131.5prime
                  Contact: Robert Strausberg, Ph.D.
                  Email: cgapbs-x@mail.nih.gov
                  Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
                  Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
                  Consortium (ILML) DNA Sequencing by: Berkeley MGC sequencing
                  project Clone distribution: MGC clone distribution information can
                  be found through the I.M.A.G.E. Consortium/ILML at:
                  www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
                  Scores: PHRED from University of Washington Genome Center. Vector
                  Trimming: cross match from University of Washington Genome Center
                  PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
                  Drosophila Genome Project. University of Washington Genome Center:
                  http://www.genome.washington.edu Low Quality Sequence: 25
                  contiguous PHRED high quality bases followed vector sequence. Very
                  Low Quality Sequence: Trace file contained 25 contiguous distinct
                  peaks following vector sequence. Polyadenylation: Based upon the
                  presence of a XhoI site followed by a run of 14 or more T residues
                  at the beginning of the sequence, this cDNA insert was
                  polyadenylated.
                  Plate: L1CM6 row: A column: 4
                  High quality sequence stop: 25.
                  Location/Qualifiers
                    1..25
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2821131"
                      /issue_type="small cell carcinoma"
                      /cell_line="MGC3"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH MGC 7"
                      /notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
                      EcoRI; cDNA made by oligo-dT priming. Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGACACGAG(G). Size-selected >500bp for average
                      insert size 1.8kb. Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."
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Query Match      0.8%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 9.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAGAAATAAAAAAAAAA 1

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RESULT 1159
DN954014
LOCUS
DEFINITION      25 bp mRNA linear EST 04-MAY-2005
                  1t67e09.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
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sequence.
DN954014
VERSION          DN954014.1 GI:63026152
KEYWORDS
SOURCE
ORGANISM        Gnetum gnemon
                  Gnetum gnemon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnepophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 25)
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McComb,R.W.,
Bentley,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McComb
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccomb@cschl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
  1..25
    /organism="Gnetum gnemon"
    /mol_type="mRNA"
    /db_xref="taxon:3382"
    /sex="female"
    /clone_lib="Gnetum female cone (NYBG)"
    /notes="Organ: mature, unfertilized reproductive strobili;
    Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
    Completed 02/11/02, submitted for sequencing 02/12/02.
    Library: Stratagene ZAP Express cDNA Synthesis Kit. The
    library was size-fractionated to enrich for large inserts.
    Sample: NYBG accession number #436/84"

Query Match      0.8%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 9.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2704 GTACTAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 GTTATAAAAAAAAAAAAAAAAAAAAAA 25

RESULT 1160
AZ330737
LOCUS
DEFINITION      25 bp DNA linear GSS 29-SEP-2000
                  1M0056F09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                  clone UUGC1M0056F09 F, genomic survey sequence.
ACCESSION
VERSION          AZ330737.1 GI:10392737
KEYWORDS
SOURCE
ORGANISM        Mus musculus (house mouse)
                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Muridae; Muridae; Muridae;
1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
```



```

KBrB057C20
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .25
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB057C20"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match
Best Local Similarity 92.0%; Score 21.8; DB 1; Length 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1163
CF337311/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) EST 18-AUG-2003
JMT--07-L06.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
JMT--07-L06, mRNA sequence.
CF337311.1 GI:33823014
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 26)
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
UNPUBLISHED (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1. .25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match
Best Local Similarity 92.0%; Score 21.8; DB 1; Length 26;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

FEATURES
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1. .25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-L06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

KBrB057C20
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .25
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB057C20"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match
Best Local Similarity 92.0%; Score 21.8; DB 1; Length 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1163
CF337311/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) EST 18-AUG-2003
JMT--07-L06.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
JMT--07-L06, mRNA sequence.
CF337311.1 GI:33823014
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 26)
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
UNPUBLISHED (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1. .25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-L06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match
Best Local Similarity 92.0%; Score 21.8; DB 1; Length 26;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="JMT--07-L06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

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QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1164
CF334077/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) EST 18-AUG-2003
JMT--03-D17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
JMT--03-D17, mRNA sequence.
CF334077.1 GI:33816466
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 23)
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
UNPUBLISHED (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--03-D17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match
Best Local Similarity 95.7%; Score 21.4; DB 1; Length 23;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1165
DR072900/c
LOCUS
DEFINITION
Ginkgo biloba (maidenhair tree) EST 08-JUN-2005
ik78f03.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
DR072900.1 GI:67050748
EST.
Ginkgo biloba (maidenhair tree)
Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 23)
REFERENCE
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.

```

Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13Univrev.
Location/Qualifiers
1. .23
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: :PBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Stragatene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

	Query Match	0.8;	Score 21.4;	DB 1;	Length 23;
	Best Local Similarity	95.7;	Pred. No. 9.4e+0;		
	Matches 2;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	2708	TAAAAAAAAAAAAAAAAAAAAA	2730		
Dd	23	TAATAAAAAAAAAAAAAAAAAAGAAA	1		

RESULT	1166
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LOCUS	WS01313_BR_M18_PTxD-IL-FL-A-4 Populus trichocarpa x Populus deltoides cDNA clone WS01313_M18 5', mRNA sequence.
DEFINITION	DS7501689 23 bp mRNA linear EST 29-AUG-2005
ACCESSION	DS7501689
VERSION	DS7501689.1 GI:73898951
KEYWORDS	EST.
SOURCE	Populus trichocarpa x Populus deltoides
ORGANISM	Populus trichocarpa x Populus deltoides
REFERENCE	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus. 1 (bases 1 to 23)
AUTHORS	Ralph,S.; Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y., Kirkpatrick,K., Liu,J., Palmquist,D., Scott,J.J., Barber,S., Yang,G., Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A., Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A., Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and Bohlmann,J.
TITLE	The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
JOURNAL	Unpublished (2004)
COMMENT	Contact: Joerg Bohlmann Genome BC forest genomics program University of British Columbia Michael Smith Laboratories, 6174 University Boulevard, Rm. 237, Vancouver, British Columbia, Canada, V6T 1Z3

FEATURES	source	Location/Qualifiers
organism	1	23
organism		"/organism="Populus trichocarpa x Populus deltoides"
mol_type		"/mol_type="mRNA"
cultivar		"/cultivar="H1-11"
db_xref		"/db_xref="taxon:3695"
clone		"/clone="WS01313_M18"
sex		"/sex="Male"

/lab_host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PTX-D-IL-FL-A-4"
/notes="Vector: pBluescript II SK (+) XR; Site_1: SstI (5' end of cDNA); Site_2: XhoI (3' end of cDNA); Sapling trees one metre in height and grown under greenhouse conditions were exposed to continuous feeding by *Malacosoma disstria* Hubner (forest tent caterpillar) mid-instar larvae caged on the sapling using mesh bags. Mature leaves from within the caged region were collected 4 hours, 8 hours and 24 hours after the onset of treatment. Mature leaves were also collected above the caged region (systemic response) 4 hours, 12 hours and 48 hours after the onset of treatment. mRNA was isolated from each tissue source independently and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 20 micrograms of mRNA according to the full-length cDNA library construction method described by Carninci P. et al. (2000). Genome Research 10(10):1617-1630 and directionally ligated into the pBluescript II SK (+) XR vector digested with SstI (5' end) and XhoI (3'). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation."

	Query Match	0.8%	Score 21.4;	DB 1;	Length 23;
	Best Local Similarity	95.7%;	Pred. NO. 9.4e+02;		
	Matches 22;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
Qy	2706	ACTAAAAAAAAAAAAAAAAAAAAA	2728		
Db	1	ATTAAAAAAAAAAAAAAAAAAAAA	23		

RESULT	1167
AZ382013	
LOCUS	23 bp DNA linear GSS 02-OCT-2000
DEFINITION	IM0138M14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0138M14 R. genomic survey sequence.

ACCESSION VERSION	KEYWORDS	SOURCE	ORGANISM
A2382013	A2382013.1	GI:10495713	
	GSS.		
	Mus musculus	(house mouse)	
	Mus musculus		
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.		

REFERENCE
AUTHORS
1 (Bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, F.,
Rally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.

TITLE	JOURNAL	COMMENT
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA

Email: adam@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0138 row: M column: 14
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES	source
...g... qual...	Location/Qualifiers
	1. . 23
	/organism="Mus musculus"
	/mol_type="genomic DNA"
	/strain="C57BL/6J"
	/db_xref="taxon:10090"
	/clone="UTGCG1M0138M14"

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21.4; DB 1; Length 23;
 Best Local Similarity 95.7%; Pred. No. 9.4e+02;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
 ||||| ||||| ||||| ||||| |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1168
 AZ486853/c
 LOCUS 23 bp DNA linear GSS 05-OCT-2000
 DEFINITION 1M0315M14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315M14 R, genomic survey sequence.

ACCESSION AZ486853
 VERSION AZ486853.1 GI:10654033
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 23)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0315 row: M column: 14

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. .23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0315M14"

FEATURES
 source

1. .23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0474E01"

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21.4; DB 1; Length 23;
 Best Local Similarity 95.7%; Pred. No. 9.4e+02;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
 ||||| ||||| ||||| ||||| |||||
 Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1169
 AZ627841/c
 LOCUS 23 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0474E01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0474E01 F, genomic survey sequence.

ACCESSION AZ627841
 VERSION AZ627841.1 GI:11750127
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 23)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0474 row: E column: 01

Seq primer: CGTTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. .23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0474E01"

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|G1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.8%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT 1170

```

AZ645254/c
LOCUS      23 bp      DNA      linear      GSS 14-DEC-2000
DEFINITION mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0510005 R, genomic survey sequence.

```

```

ACCESSION  AZ645254
VERSION     AZ645254.1  GI:11774572
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)

```

ORGANISM

```

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

```

REFERENCE

```

1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

```

```

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

TITLE

```

Unpublished (2000)
Contact: Robert B. Weiss

```

JOURNAL

```

University of Utah Genome Center

```

COMMENT

```

Rm. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 595 5606
Fax: 801 595 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: 0 column: 05
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0510005"

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FEATURES

source

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Location/Qualifiers
1..23
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="vector: pEpifos-5 Fosmid vector"
Query Match      0.8%; Score 21.4; DB 1; Length 23;

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|G1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.8%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT 1171

```

CL693171
LOCUS      23 bp      DNA      linear      GSS 10-JUL-2004
DEFINITION PRI0160b_B06_2 - PRI0160b.BR (23) Note: Recurring String Mixed
            stage fosmid library of P. pacificus var. California Pristionchus
            pacificus genomic, genomic survey sequence.

```

```

ACCESSION  CL693171
VERSION     CL693171.1  GI:50215079
KEYWORDS   GSS.
SOURCE     Pristionchus pacificus

```

ORGANISM

```

Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

```

REFERENCE

```

1 (bases 1 to 23)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)

```

PUBMED

```

14681447
Contact: Sommer RJ

```

COMMENT

```

Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498

```

```

Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..23
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="vector: pEpifos-5 Fosmid vector"

```

FEATURES

source

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Location/Qualifiers
1..23
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="vector: pEpifos-5 Fosmid vector"
Query Match      0.8%; Score 21.4; DB 1; Length 23;

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```

Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 1 AAAAAAAAAAACAAAAAAAAAA 23

RESULT 1172
DU828758/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

DU828758 23 bp DNA linear GSS 22-DEC-2005
KBR5003116F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subep. pekinensis genomic clone KBR5003L16, genomic survey
sequence.
DU828758
DU828758.1 GI:83865354
GSS.
Brassica rapa subep. pekinensis
Brassica rapa subep. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 23)
REFERENCE
AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBR5003L16
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..23
/organism="Brassica rapa subep. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBR5003L16"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chifu BAC library (KBrS BAC) is
available at NTAB."

Query Match 0.8%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1173
TA55C06P
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

TA55C06P 23 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 55c06, forward sequence,
genomic survey sequence.
AL455778
AL455778.1 GI:11856729
GSS.
Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

```

```

Trypanosoma.
1 (bases 1 to 23)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
1..23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strains="TREU927"
/db_xref="taxon:5691"
/clone="55c06"

Query Match 0.8%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 1 AAAAAAAAAATAAAAAAAAAAA 23

RESULT 1174
CD743368/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CD743368 24 bp mRNA linear EST 25-JUN-2004
IRB8_E10_IRB8_072 Infected Rat Blood-fed (IRB) An.gam. 30 hr
Abdomen Library Anopheles gambiae cDNA 5', mRNA sequence.
CD743368
CD743368.1 GI:49247179
EST.
Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 24)
Dana, A.N., Lobo, N.F., Hillenmeyer, M.E. and Collins, F.H.
Hematophagy-associated gene expression patterns in adult female
Anopheles gambiae mosquitoes
Unpublished (2003)
Contact: Dana A.N.
Frank H. Collins Laboratory
University of Notre Dame
Center for Tropical Disease Research and Training, Dept. of Biol.
Sci., Notre Dame, IN 46556, USA
Tel.: 574 - 631 - 3241
Fax: 574 - 631 - 3996
Email: adana@nd.edu
PCR Primers
FORWARD: ctccggaagcgccattgtgttg
BACKWARD: ataccgactcatatagggaattgg
Seq primer: ctccggaagcgccattgtgttg.
Location/Qualifiers
1..24
/organism="Anopheles gambiae"
/mol_type="mRNA"

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/strain="4Arr"
/db_xref="taxon:7165"
/sex="female"
/tissue_type="Abdomens"
/dev_stage="Female adult 5-7 days post eclosion"
/lab_host="E. coli XLI-Blue"
/clone_lib="Infected Rat Blood-fed (IRB) An.gam. 30 hr
Abdomen Library"
/note="Vector: lambdaTriplEx2 (Clontech); Site 1: Sfi IA;
Site 2: Sfi IB; Plasmodium berghei-infected rat blood-fed
adult female An. gambiae mosquitoes were flash frozen
after a 30 hour incubation of adult mosquitoes at 19
degrees Celsius. Total RNA extracted from abdomens
separated from remaining carcasses. cDNA inserts >500 bp
cloned directionally into TriplEx2; Sfi IA site is 5'.
Non-normalized and Non-amplified phagemid library. Single
pass sequencing reactions from 5' end."
Query Match 0.8%; Score 21.4; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
| | | | | | | | | | | | | | | | | |
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1175
CF292725/c 24 bp mRNA linear EST 14-AUG-2003
LOCUS 30DGS--01-K12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION saiva (japonica cultivar-group) cDNA clone 30DGS--01-K12, mRNA
sequence.
ACCESSION CF292725
VERSION CF292725.1 GI:33661758
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel.: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 24
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--01-K12"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2702 TTGTACTAAAAAAAAAAAAA 2724

```

```

Db 23 TTGTCTAAAAAAAAAAAAA 1
| | | | | | | | | | | | | | | | | |
RESULT 1176
AZ404871
LOCUS 24 bp DNA linear GSS 03-OCT-2000
DEFINITION clone UGCG1M0173J14 R, genomic survey sequence.
ACCESSION AZ404871
VERSION AZ404871.1 GI:10528884
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0173 row: J column: 14
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0173J14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.8%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTAAAAAAAAAAAAAAA 2729

```

```

Db      2  CTCAAAAAAAAAAAAAAAAAAAA 24

RESULT 1177
AZ486788      24 bp  DNA      linear      GSS 05-OCT-2000
LOCUS      1M031512F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION  clone UGCM031512 F, genomic survey sequence.
ACCESSION  AZ486788
VERSION    AZ486788.1 GI:10653906
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 24)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0315 row: 1 column: 22
            Seq Primer: CGTGTAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES   source
            1..24
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGCIM0315122"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UGCM library"
            /notes="Vector: FWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydronamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adapted DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWB42 [gi|4732114|gb|AF129072.1], a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adapted mouse DNA was annealed to
            adapted vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
            Query Match      0.8%; Score 21.4; DB 1; Length 24;
            Best Local Similarity 95.7%; Pred. No. 9.5e+02;
            Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2708 TAAAAAAAAAAAAAAAAAAAAA 2730

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```

Db      23 TAAATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1178
AU265663/c
LOCUS      AU265663 VS Dictyostelium discoideum cDNA clone VSF713 5', mRNA
DEFINITION  sequence.
ACCESSION  AU265663
VERSION    AU265663.1 GI:20524461
KEYWORDS   EST.
SOURCE     Dictyostelium discoideum
ORGANISM   Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
REFERENCE  1 (bases 1 to 25)
AUTHORS   Uruehira,H., Morio,T., Saito,T., Kohara,Y., Koriki,E., Ochiai,H.,
            Maeda,M., Williams,J.G., Takeuchi,I. and Tanaka,Y.
TITLE     Analyses of cDNAs from growth and slug stages of Dictyostelium
            discoideum
JOURNAL    Nucleic Acids Res. 32 (5), 1647-1653 (2004)
PUBMED    15010511
COMMENT    Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES   source
            1..25
            /organism="Dictyostelium discoideum"
            /mol_type="mRNA"
            /strain="AX4"
            /db_xref="taxon:44689"
            /clone="VSF713"
            /sex="mat A"
            /dev_stage="vegetative"
            /clone_lib="VS"
            Query Match      0.8%; Score 21.4; DB 1; Length 25;
            Best Local Similarity 95.7%; Pred. No. 9.7e+02;
            Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2731

Db      24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1179
AV737092
LOCUS      AV737092 CB Homo sapiens cDNA clone CBFBI11 5', mRNA sequence.
DEFINITION  EST.
ACCESSION  AV737092
VERSION    AV737092.1 GI:10854673
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 25)
AUTHORS   Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
            Chen,S., Mao,M. and Chen,Z.
TITLE     Homo sapiens CB library cDNA clones
JOURNAL    Unpublished (2000)
COMMENT    Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490
            Fax: 86-21-64743206
            Email: mbshi@ms.stn.sh.cn
            This clone is available at Shanghai Hematology Institute in

```


Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

FEATURES

source
1. .25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CBFIB11"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="CB"
/note="Vector: pBluescript; Site 1: EcoRI; The insert is cloned randomly with the EcoRI digestion"

Query Match 0.8%; Score 21.4; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2707 CTAAAAAAGAAAAAAGAAAAA 2731
DB 1 CNAANAAAAAAGAAAAAAGAAAAA 25

RESULT 1180

CG726337 25 bp DNA linear GSS 20-OCT-2003
1119089E12.2EL_Y1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.

ACCESSION CG726337.1 GI:37764992
VERSION
KEYWORDS
SOURCE

ORGANISM

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)

JOURNAL

Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221

Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119089 row: E column: 12
Class: transposon-tagged.

FEATURES

source
1. .25
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmndb.iaestate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids.

DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.8%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAAAGAAAAAAGAAAAA 2729
DB 24 CCAAAAAAAGAAAAAAGAAAAA 2

RESULT 1181

AG194089 26 bp DNA linear GSS 06-MAR-2004
LOCUS Pan troglodytes DNA, clone: RP43-071013.TJ, genomic survey sequence.
DEFINITION

ACCESSION AG194089
VERSION AG194089.1 GI:45226265

KEYWORDS

SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.

REFERENCE

1 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J., Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43 Unpublished

JOURNAL

REFERENCE 2 (bases 1 to 26)

AUTHORS

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J., Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail: redetson@mail.kribb.re.kr, URL: http://phs.grc.kribb.re.kr/, Tel: 82-42-866-7181, Fax: 82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: TJ

LIBRARY

Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.

FEATURES

source

1. .26
Location/Qualifiers
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clones="RP43-071013.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match 0.8%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 9.9e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAGAAAAAAGAAAAA 2730
DB 4 TAAAAAAGAAAAAAGAAAAA 26

RESULT 1182

AM043942 26 bp mRNA linear EST 11-AUG-2005
LOCUS AM043942 Schistosoma mansoni lung Schistosomulum Schistosoma mansoni cDNA clone Smlc11b03.q1k, mRNA sequence.
DEFINITION

ACCESSION

```

VERSION AM043942.1 GI:72292305
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni

REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
AUTHORS Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 26)
Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
source
1..26
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="Smlc1lb03.glk"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1e+03;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2701 TTGTGTAACAAAAA 2726
|||
1 TTTTATTTTAAAAA 26

Db 1 TTTTATTTTAAAAA 26

RESULT 1183
CF280688/c
LOCUS CF280688 26 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--07-H09-g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ORYZA SATIVA (japonica cultivar-group) cDNA clone 14ETL--07-H09,
mRNA sequence.
ACCESSION CF280688
VERSION CF280688.1 GI:33658074
KEYWORDS EST.
ORGANISM Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..26
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--07-H09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"

/Note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1e+03;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2703 TGTACTAAAAA 2728
|||
26 TTTTCCAAAAA 1

Db 26 TTTTCCAAAAA 1

RESULT 1184
AW333508/c
LOCUS AW333508 26 bp mRNA linear EST 31-JAN-2000
DEFINITION S22F8 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION AW333508
VERSION AW333508.1 GI:6829865
KEYWORDS EST.
ORGANISM Pneumocystis carinii
SOURCE Pneumocystis carinii
Pneumocystidaceae; Pneumocystis.
1 (bases 1 to 26)
Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
Edman,J.C., Kovacs,J. and Cushion,M.
TITLE Expressed sequence tags from Pneumocystis carinii
JOURNAL Unpublished (2000)
COMMENT Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.

FEATURES
source
1..26
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"

/Note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat (59-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1e+03;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2701 TTTTACTAAAAA 2726
|||
26 TTTTATTTTAAAAA 1

Db 26 TTTTATTTTAAAAA 1

RESULT 1185
AZ358846/c
LOCUS AZ358846 26 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0101M24F Mouse 10kb plasmid UUG1M library Mus musculus genomic
clone UUG1M0101M24 F, genomic survey sequence.
ACCESSION AZ358846
VERSION AZ358846.1 GI:10472546
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```


Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

```

source
  1. .21
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    /mol_type="mRNA"
    /db_xref="taxon:9823"
    /clone="C0005212.D02"
    /tissue_type="embryo"
    /clone_lib="KN277"
    /notes="vector: pBlueScriptII(SK+); Site 1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."
  
```

```

Query Match      0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  
```

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21
  
```

RESULT 1188

```

AJ666203
LOCUS AJ666203 CSQRAN09 Sus scrofa cDNA clone C000033_C15, mRNA
DEFINITION
ACCESSION AJ666203
VERSION AJ666203.1 GI:49350654
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 21)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
  
```

FEATURES

```

source
  1. .21
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    /organism="Sus scrofa"
    /mol_type="mRNA"
    /db_xref="taxon:9823"
    /clone="C000033_C15"
    /tissue_type="placenta"
    /clone_lib="CSEQRAN09"
    /notes="vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."
  
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Query Match      0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  
```

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QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21
  
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RESULT 1189

```

AL048777
LOCUS AL048777 21 bp mRNA linear EST 04-SEP-2003
DEFINITION DKF2566N053_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION DKF2566N053, mRNA sequence.
VERSION AL048777
KEYWORDS AL048777.1 GI:4727848
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 21)
Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehrer, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
  
```

FEATURES

```

source
  1. .21
  Location/Qualifiers
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="DKF2p566N053"
    /tissue_type="kidney"
    /dev_stage="fetal"
    /lab_host="X1-2blue"
    /clone_lib="566 (synonym: hfkd2)"
    /notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
  
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Query Match      0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  
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QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 21
  
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RESULT 1190

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AM047262/c
LOCUS AM047262 21 bp mRNA linear EST 11-AUG-2005
DEFINITION AM047262 Schistosoma mansoni lung schistosomulum Schistosoma
ACCESSION AM047262
VERSION AM047262.1 GI:72293372
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 21)
Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
  
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FEATURES

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    /mol_type="mRNA"
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    /dev_stage="lung schistosomulum"
    /clone_lib="Schistosoma mansoni lung schistosomulum"
  
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Query Match	0.8%;	Score 21;	DB 1; Length 21;					
Best Local Similarity	100.0%;	Pred. No. 9.5e+02;						
Matches	21;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;					
Qy	2709	AAAAAAAAAAAAAAAAAAAAA 2729						
Db	21	AAAAAAAAAAAAAAAAAAAAA 1						
RESULT 1191								
CF282216								
LOCUS								
DEFINITION	CF282216 21 bp mRNA linear EST 14-AUG-2003							
ACCESSION	14ETL--09-K01.g1 Rice etiolated leaf plasmid cDNA library (14ETL)							
VERSION	Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-K01,							
KEYWORDS	mRNA sequence.							
SOURCE	CF282216.1 GI:33659603							
ORGANISM	Oryza sativa (japonica cultivar-group)							
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.								
REFERENCE	1 (bases 1 to 21)							
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.							
TITLE	Large-scale Sequencing Analysis of Rice ESTs							
JOURNAL	Unpublished (2003)							
COMMENT	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University							
Yongin, Kyeonggi, Korea								
Tel: 82 31 330 6193								
Fax: 82 31 321 6355								
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.								
Location/Qualifiers								
1. .21								
/organism="Oryza sativa (japonica cultivar-group)"								
/mol_type="mRNA"								
/cultivar="Nackdong"								
/db_xref="taxon:39947"								
/clone="14ETL--09-K01"								
/tissue_type="leaf"								
/dev_stages="14 days after germination"								
/lab_host="E.coli DH10B"								
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"								
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."								
Query Match	0.8%;	Score 21;	DB 1; Length 21;					
Best Local Similarity	100.0%;	Pred. No. 9.5e+02;						
Matches	21;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;					
Qy	2709	AAAAAAAAAAAAAAAAAAAAA 2729						
Db	21	AAAAAAAAAAAAAAAAAAAAA 1						
RESULT 1193								
CF295642/c								
LOCUS								
DEFINITION	CF295642 21 bp mRNA linear EST 14-AUG-2003							
ACCESSION	30DGS--05-K20.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza							
VERSION	sativa (japonica cultivar-group) cDNA clone 30DGS--05-K20, mRNA							
KEYWORDS	sequence.							
SOURCE	CF295642.1 GI:33664675							
ORGANISM	Oryza sativa (japonica cultivar-group)							
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.								
REFERENCE	1 (bases 1 to 21)							
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.							
TITLE	Large-scale Sequencing Analysis of Rice ESTs							
JOURNAL	Unpublished (2003)							
COMMENT	Contact: Nahm B.H.							
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University								
Yongin, Kyeonggi, Korea								
Tel: 82 31 330 6193								
Fax: 82 31 321 6355								
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.								
Location/Qualifiers								
1. .21								
/organism="Oryza sativa (japonica cultivar-group)"								
/mol_type="mRNA"								
/cultivar="Nackdong"								
/db_xref="taxon:39947"								
/clone="14ETL--09-K01"								
/tissue_type="leaf"								

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/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1194
CF297615
LOCUS
DEFINITION
30DGS--08-J10.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--08-J10, mRNA
sequence.
ACCESSION
CF297615
VERSION
CF297615.1 GI:336666648
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
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TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
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Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--01-K14"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1196
CF300809/c
LOCUS
DEFINITION
7LEAF--05-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--05-G20, mRNA
sequence.
ACCESSION
CF300809
VERSION
CF300809.1 GI:33672570
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--08-J10"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1195
CF298322/c
LOCUS
DEFINITION
7LEAF--01-K14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--01-K14, mRNA
sequence.
ACCESSION
CF298322

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CF298322.1 GI:33670083
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--01-K14"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1196
CF300809/c
LOCUS
DEFINITION
7LEAF--05-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--05-G20, mRNA
sequence.
ACCESSION
CF300809
VERSION
CF300809.1 GI:33672570
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

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1. .21
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||

Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1200

CF327391
LOCUS
DEFINITION
NACL--01-N18.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-N18, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

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1. .21
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/mol_type="mRNA"
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1201

CF332956/c
LOCUS
DEFINITION
JMT--01-K14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source
1. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||

Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1202

CF338057
LOCUS
DEFINITION
JMT--08-M03.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;


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cDNA clone B3CS57RB007G04 3', mRNA sequence.
CN546504
VERSION CN546504.1 GI:46911129
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 21)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1..21
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007G04"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1206
CN546595/c
LOCUS 21 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18739 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS58RB008G02 3', mRNA sequence.
CN546595
ACCESSION CN546595.1 GI:46911220
VERSION EST.
KEYWORDS Vitis vinifera
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 21)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France

```

```

Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1..21
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58RB008G02"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1207
CO779794/c
LOCUS 21 bp mRNA linear EST 05-AUG-2004
DEFINITION BL007D E05 6-Day Axolotl Tail Blastema (6DAXBL) Ambystoma mexicanum
cDNA 5' similar to hypothetical protein, mRNA sequence.
CO779794
ACCESSION CO779794.1 GI:50995774
VERSION EST.
KEYWORDS Ambystoma mexicanum (axolotl)
SOURCE Ambystoma mexicanum
ORGANISM Ambystoma mexicanum
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.
1 (bases 1 to 21)
Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
TITLE An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
JOURNAL Genome Biol. (2004) In press
COMMENT Contact: Elly M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pfothenhauerstrasse 108, 01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: BL007D row: 05 column: E
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
Location/Qualifiers
1..21
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Tail Blastema"
/cell_type="regenerating tail blastema"
/clone_lib="6-Day Axolotl Tail Blastema (6DAXBL)"
/notes="Vector: pCMVSPORT6; Site_1: NotI; Site_2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydt primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.67 kb.
TAG_LTB-6DAXBL"

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1208

DR063419/c
 LOCUS ip65b04.g1 Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA
 DEFINITION sequence.
 ACCESSION DR063419 21 bp mRNA linear EST 06-JUN-2005
 VERSION DR063419.1 GI:66986987
 KEYWORDS EST.
 SOURCE Ginkgo biloba (maidenhair tree)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W., Benfey,P., Coruzzi,G. and Stevenson,D.
 TITLE Expressed tag sequences from Ginkgo megasporophyll (NYBG)
 JOURNAL Unpublished (2005)
 COMMENT Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Seq primer: -21M13UnivRev.

FEATURES

source
 1..21

/organism="Ginkgo biloba"
 /mol_type="mRNA"
 /db_xref="taxon:3311"
 /sex="Female"
 /clone_lib="Ginkgo megasporophyll (NYBG)"
 /note="Organ: megasporophyll; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1209

DR072918/c
 LOCUS ik79c11.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
 DEFINITION sequence.
 ACCESSION DR072918 21 bp mRNA linear EST 08-JUN-2005
 VERSION DR072918 GI:67050766
 KEYWORDS EST.
 SOURCE Ginkgo biloba (maidenhair tree)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W., Benfey,P., Coruzzi,G. and Stevenson,D.
 TITLE Expressed tag sequences from Ginkgo female leaf (NYBG)
 JOURNAL Unpublished (2005)
 COMMENT Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Seq primer: -21M13UnivRev.

FEATURES

source

1..21
 Location/Qualifiers
 /organism="Ginkgo biloba"
 /mol_type="mRNA"
 /db_xref="taxon:3311"
 /sex="female"
 /clone_lib="Ginkgo female leaf (NYBG)"
 /note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1210

AZ348593 21 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0085A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0085A13 F, genomic survey sequence.
 ACCESSION AZ348593
 VERSION AZ348593.1 GI:10427830
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0085 row: A column: 13
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

source

1..21
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0085A13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1211

AZ350611
LOCUS 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0088C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0088C14 F, genomic survey sequence.

ACCESSION AZ350611
VERSION AZ350611.1 GI:10429848
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0088 row: C column: 14

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0088C14"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1212

AZ386711
LOCUS 21 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0145016R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0145016 R, genomic survey sequence.

ACCESSION AZ386711
VERSION AZ386711.1 GI:10500411
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0145 row: O column: 16

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0145016"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
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DB 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1213

AZ386794

LOCUS

DEFINITION AZ386794 21 bp DNA linear GSS 02-OCT-2000
clone UUGC1M0145022 R, genomic survey sequence.

ACCESSION

AZ386794

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0145 row: 0 column: 22

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0145022"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1214

AZ389287

LOCUS

DEFINITION AZ389287 21 bp DNA linear GSS 02-OCT-2000
clone UUGC1M0149A13 R, genomic survey sequence.

ACCESSION

AZ389287

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0149 row: A column: 13

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

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/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0149A13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1215
AZ389687
LOCUS
DEFINITION
1M0150B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0150B10 R, genomic survey sequence.

ACCESSION
AZ389687
VERSION
AZ389687.1 GI:105033395
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: B column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0150B10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1216
AZ406936/C

LOCUS
DEFINITION
1M0176E24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0176E24 F, genomic survey sequence.

ACCESSION
AZ406936
VERSION
AZ406936.1 GI:10530949
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0176 row: E column: 24
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.

Location/Qualifiers
1. .21

FEATURES
source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0176E24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1217
AZ412739/c
LOCUS
DEFINITION
1M0186023F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0186023 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
(house mouse)

REFERENCE
AUTHORS
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0186 row: D column: 23
Seq primer: CGTTGTAAACACGCGCAGT

Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21

FEATURES
source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0186023"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1218
AZ412931/c
LOCUS
DEFINITION
1M0186N08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0186N08 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
(house mouse)

REFERENCE
AUTHORS
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A., and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0186 row: N column: 08
Seq primer: CACACGAAACACGCTATGACC

Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21

FEATURES
source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0186N08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1219
AZ415029
LOCUS
DEFINITION
IM0189M07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0189M07 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0189 row: M column: 07

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0189M07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1220

AZ465890/c

LOCUS

DEFINITION

IM0276F07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0276F07 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0276 row: F column: 07

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0276F07"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1221
AZ611116
LOCUS
DEFINITION
21 bp DNA linear GSS 13-DEC-2000
clone U0436N02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION
AZ611116
VERSION
AZ611116.1 GI:11733306
KEYWORDS
GSS.

SOURCE
Mus musculus
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0436 row: N column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

Location/Qualifiers

FEATURES
source

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0436N02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1222
AZ6111423
LOCUS
DEFINITION
21 bp DNA linear GSS 13-DEC-2000
clone U0437E13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION
AZ6111423
VERSION
AZ6111423.1 GI:11733613
KEYWORDS
GSS.

SOURCE
Mus musculus
ORGANISM
Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0437 row: E column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

Location/Qualifiers

FEATURES
source

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0437E13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1223
AZ615628/c
LOCUS
DEFINITION
1M0444M19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0444M19 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ615628 1 GI:11737734
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0444 row: M column: 19

Seq primer: CACACAGGAACACGATGACC
Class: plasmid ends
High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0444M19"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: FWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

features

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
1 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1224

AZ627843/c

LOCUS

DEFINITION

1M0474H03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0474H03 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AZ627843 1 GI:11750129

Mus musculus (house mouse)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

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plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0474 row: H column: 03

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0474H03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: FWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1225
AZ627845/c
LOCUS
DEFINITION
1M0474G11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0474G11 F, genomic survey sequence.

ACCESSION
AZ627845
VERSION
AZ627845.1 GI:11750131
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0474 row: G column: 11

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0474G11"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1226
AZ657727

LOCUS

DEFINITION

1M0534B07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

Clone UUGC1M0534B07 F, genomic survey sequence.

ACCESSION

AZ657727

VERSION

AZ657727.1 GI:11794873

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0534 row: B column: 07

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0534B07"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1227
AZ766552
LOCUS 21 bp DNA linear GSS 16-FEB-2001
DEFINITION IM056401LF Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M056401 F, genomic survey sequence.

ACCESSION AZ766552
VERSION AZ766552.1 GI:12883741
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH
Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0564 row: 0 column: 11

Seq primer: CGTTGTAACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M056401"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1228

AZ769976

LOCUS 21 bp DNA linear GSS 16-FEB-2001

DEFINITION IM057111LF Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M057111 F, genomic survey sequence.

ACCESSION AZ769976

VERSION AZ769976.1 GI:12890681

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0571 row: L column: 11

Seq primer: CGTTGTAACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21
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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M057111"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

```

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
    |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1229
A2793486/c
LOCUS
DEFINITION
2M0046G18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0046G18 R, genomic survey sequence.
ACCESSION
A2793486
VERSION
A2793486.1 GI:12938487
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 21)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0046 row: G column: 18
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0046G18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
    |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1230
A2799327
LOCUS
DEFINITION
2M0056C09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0056C09 R, genomic survey sequence.
ACCESSION
A2799327
VERSION
A2799327.1 GI:12950331
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 21)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: C column: 09
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0056C09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

```


Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1231
AZ810054
LOCUS 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0074E19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0074E19 F, genomic survey sequence.

ACCESSION AZ810054
VERSION AZ810054.1 GI:12976935
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0074 row: E column: 19
Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends
High quality sequence stop: 21.

FEATURES
Location/Qualifiers
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source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0074E19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: FW42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1232

AZ815424

LOCUS 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0083H1LR Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0083H11 R, genomic survey sequence.

ACCESSION AZ815424

VERSION AZ815424.1 GI:12985332

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0083 row: H column: 11

Seq primer: CACACAGGAACGATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES
Location/Qualifiers
1..21
source

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0083H11"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1233
AZ819181
LOCUS
DEFINITION
2M0089110R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0089110 R, genomic survey sequence.

ACCESSION
AZ819181
VERSION
AZ819181.1 GI:12989089
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: 1 column: 10
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

Location/Qualifiers
1..21

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0089110"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

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(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1234
AZ832198
LOCUS

DEFINITION
2M0112P20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0112P20 F, genomic survey sequence.

ACCESSION
AZ832198
VERSION
AZ832198.1 GI:13002106
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

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Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0112 row: P column: 20

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

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/sex="Male"

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/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1235
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LOCUS
DEFINITION
2M0142106R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0142106 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
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plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
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University of Utah
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84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0142 row: 1 column: 06
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 21.
Location/Qualifiers
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1236

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LOCUS
DEFINITION
2M0228A01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0228A01 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
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plasmid inserts

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COMMENT
Unpublished (2000)
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University of Utah
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84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0228 row: A column: 01
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Class: plasmid ends

High quality sequence stop: 21.
Location/Qualifiers
1. .21

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/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1237
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LOCUS 2M0288020R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION Clone UUGC2M0288020 R, genomic survey sequence.

ACCESSION BH000837
VERSION BH000837.1 GI:13872063
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0288 row: 0 column: 20

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

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/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

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/clone="UUGC2M0288020"

/sex="Female"

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/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

source

Query Match 0.8%; Score 21; DB 1; Length 21;

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1238
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LOCUS DU828985/21 bp DNA linear GSS 22-DEC-2005

DEFINITION KBrS004C05F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa

subsp. pekinensis genomic clone KBrS004C05, genomic survey

sequence.

ACCESSION DU828985

VERSION DU828985.1 GI:83865581

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 21)

AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

Hahn, J. H. and Park, B.S.

End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

Unpublished (2005)

JOURNAL

COMMENT Contact: Beom-Seok Park

Brassica Genomics Team

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225 Seodun-Dong, Suwon, 441-707, Korea

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Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone

KBrS004C05

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. .21

/organism="Brassica rapa subsp. pekinensis"

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/note="Vector: pCUGBAC1; Site_1: Sau3AI; Brassica rapa

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available at NIAB."

Query Match 0.8%; Score 21; DB 1; Length 21;

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Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

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DEFINITION DUB32906 21 bp DNA linear GSS 22-DEC-2005
subsp. pekinensis genomic clone KBrS006C07, genomic survey
sequence.
ACCESSION DUB32906
VERSION DUB32906.1 GI:83866695
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 21)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS006C07
Seq primer: M13 Reverse
Class: BAC ends.
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/sub_species="pekinensis"
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/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chifu BAC library (KBrS BAC) is
available at NIAB."
Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1240
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LOCUS DUB32906
DEFINITION DUB32906 21 bp DNA linear GSS 22-DEC-2005
subsp. pekinensis genomic clone KBrS011B18, genomic survey
sequence.
ACCESSION DUB32906
VERSION DUB32906.1 GI:83869502
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 21)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS011B18
Seq primer: M13 Reverse
Class: BAC ends.
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Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
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QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1241
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subsp. pekinensis genomic clone KBrS014K05, genomic survey
sequence.
ACCESSION DUB34573
VERSION DUB34573.1 GI:83871169
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 21)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS014K05
Seq primer: T7

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
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Hahn,J. H. and Park,B.S.
Hahn,J. H. and Park,B.S.
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COMMENT Contact: Beom-Seok Park
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National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS011B18
Seq primer: M13 Reverse
Class: BAC ends.
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/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chifu BAC library (KBrS BAC) is
available at NIAB."
Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1241
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DEFINITION DUB34573 21 bp DNA linear GSS 22-DEC-2005
subsp. pekinensis genomic clone KBrS014K05, genomic survey
sequence.
ACCESSION DUB34573
VERSION DUB34573.1 GI:83871169
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 21)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
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National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS014K05
Seq primer: T7

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VERSION				
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DEFINITION				
ACCESSION				
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TITLE				
JOURNAL				
COMMENT				
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/sub_species="pekinensis"				
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Best Local Similarity				
Matches				
21; Conservative				
0; Mismatches				
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Db	21	AAAAAAAAAAAAAAAAAAAAA	1	
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DX035098/c				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
source				
1. .21				
/organism="Brassica rapa subsp. pekinensis"				
/mol_type="genomic DNA"				
/cultivar="Chiifu"				
/sub_species="pekinensis"				
/db_xref="taxon:51351"				
/clone="KB-R047K19"				
/lab_host="E.coli DH10B"				
/clone_lib="KB-R, Brassica rapa Sau3AI BAC library"				
/note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa spp pekinensis var. Chiifu BAC library (KB-R BAC) is available at NTAB."				
Query Match				
Best Local Similarity				
Matches				
21; Conservative				
0; Mismatches				
0; Indels				
0; Gaps				
0;				
QY	2709	AAAAAAAAAAAAAAAAAAAAA	2729	
Db	21	AAAAAAAAAAAAAAAAAAAAA	1	
RESULT 1242				
DX035098/c				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
source				
1. .21				
/organism="Brassica rapa subsp. pekinensis"				
/mol_type="genomic DNA"				
/cultivar="Chiifu"				
/sub_species="pekinensis"				
/db_xref="taxon:51351"				
/clone="KB-R047K19				

REFERENCE	1 (bases 1 to 21)
AUTHORS	Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
TITLE	End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL	Unpublished (2005)
COMMENT	Contact: Beom-Seok Park Brassica Genomics Team National Institute of Agricultural Biotechnology 225 Seodun-Dong, Suwon, 441-707, Korea Tel: +82-31-299-1670 Fax: +82-31-299-1672 Email: pbeom@da.go.kr BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone KBrB052P02 Seq primer: T7 Class: BAC ends.
FEATURES	Location/Qualifiers
source	1..21
	/organism="Brassica rapa subsp. pekinensis" /mol_type="genomic DNA" /cultivar="Chiifu" /sub_species="pekinensis" /db_xref="taxon:51351" /clone="KBrB052P02" /lab_host="E.coli DH10B" /notes="Vector: PCUGTBAC1; Site 1: BamHI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."
Query Match	0.8%; Score 21; DB 1; Length 21;
Best Local Similarity	100.0%; Pred.No. 9.5e+02;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db	1 AAAAAAAAAAAAAAAAAAAAAA 21
RESULT 1245	
DX056929/c	
LOCUS	DX056929 21 bp DNA linear GSS 10-JAN-2006
DEFINITION	KBrB061P24R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB061P24, genomic survey sequence.
ACCESSION	DX056929
VERSION	DX056929.1 GI:84751226
KEYWORDS	GSS.
SOURCE	Brassica rapa subsp. pekinensis
ORGANISM	Brassica rapa subsp. pekinensis Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE	1 (bases 1 to 21)
AUTHORS	Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
TITLE	End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL	Unpublished (2005)
COMMENT	Contact: Beom-Seok Park Brassica Genomics Team National Institute of Agricultural Biotechnology 225 Seodun-Dong, Suwon, 441-707, Korea Tel: +82-31-299-1670 Fax: +82-31-299-1672 Email: pbeom@da.go.kr BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone KBrB061P24 Seq primer: M13 Reverse Class: BAC ends.
FEATURES	Location/Qualifiers
source	1..21

RESULT 1247

DX075742
LOCUS
DEFINITION
21 bp DNA linear GSS 10-JAN-2006
KBrB086M24F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB086M24, genomic survey
sequence.

ACCESSION

VERSION
KEYWORDS
SOURCE
ORGANISM

DX075742.1 GI:84770038
GSS.
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.

TITLE

JOURNAL
COMMENT
End sequence of Brassica rapa BamHI (KBrB) BAC clone

UNPUBLISHED (2005)

Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBrB086M24

Seq primer: T7

Class: BAC ends.

FEATURES

source

1. .21
Location/Qualifiers

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrB086M24"

/lab_host="E.coli DH10B"

/clone_lib="KBrB, Brassica rapa BamHI BAC library"

/note="Vector: PCUGIBAC1; Site 1: BamHI; Brassica rapa ssp

pekinensis var. Chiifu BAC library (KBrB BAC) is provided

by Yong-Pyo Lim (CNU)."

Query Match 0.8%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729

Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1248

DX082155/c
LOCUS
DEFINITION
21 bp DNA linear GSS 10-JAN-2006
KBrB095F12F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB095F12, genomic survey
sequence.

ACCESSION

VERSION
KEYWORDS
SOURCE
ORGANISM

DX082155.1 GI:84776451
GSS.
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

TITLE

JOURNAL

COMMENT

Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBrB095F12

Seq primer: T7

Class: BAC ends.

FEATURES

source

1. .21
Location/Qualifiers

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrB095F12"

/lab_host="E.coli DH10B"

/clone_lib="KBrB, Brassica rapa BamHI BAC library"

/note="Vector: PCUGIBAC1; Site 1: BamHI; Brassica rapa ssp

pekinensis var. Chiifu BAC library (KBrB BAC) is provided

by Yong-Pyo Lim (CNU)."

Query Match 0.8%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729

Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1249

DX082624

LOCUS

DEFINITION

21 bp DNA linear GSS 10-JAN-2006

KBrB095P24F KBrB, Brassica rapa BamHI BAC library Brassica rapa

subsp. pekinensis genomic clone KBrB095P24, genomic survey

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 21)

Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

Hahn, J.H. and Park, B.S.

End sequence of Brassica rapa BamHI (KBrB) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBrB095P24

Seq primer: T7

Class: BAC ends.

FEATURES

source

1. .21
Location/Qualifiers

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

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/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB095924"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
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Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
1 AAAAAAAAAAAAAAAAAAAAAA 21

Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1250

AL038477

LOCUS DXFZP566C1646_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DEFINITION DXFZP566C1646, mRNA sequence.

ACCESSION AL038477

VERSION AL038477.1 GI:49692139

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

AUTHORS Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.

TITLE EST (Ottenwaelder, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

IngoIstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1. .22
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566C1646"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_hosts="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/notes="Vector: pAMF1; Site_1: NotI; Site_2: SalI"

Query Match 0.8%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2728
2 TAAAAAAAAAAAAAAAAAAAAA 22

Db 2 TAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1251

CF282024/c

LOCUS 14ETL--09-F13.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F13,
mRNA sequence.

ACCESSION CF282024

VERSION CF282024.1 GI:33659411

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

```

clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
```

FEATURES
source
1. .22
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--09-F13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
1 AAAAAAAAAAAAAAAAAAAAAA 21

Db 2 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1252

CO778290

LOCUS CO778290 22 bp mRNA linear EST 05-AUG-2004
DEFINITION BL003B_H01 6-Day Axolotl Tail Blastema (GDAXBL) Ambystoma mexicanum
cDNA 5' similar to hypothetical protein, mRNA sequence.

ACCESSION CO778290

VERSION CO778290.1 GI:509994270

KEYWORDS EST.

SOURCE Ambystoma mexicanum (axolotl)

ORGANISM Ambystoma mexicanum

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.

AUTHORS Habermann, B., Bebin, A.G., Herklotz, S., Volkmer, M., Eckelt, K.,
Pehlke, K., Epperlein, H.H., Schackert, H.K., Wiebe, G. and Tanaka, E.M.

TITLE An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries

JOURNAL Genome Biol. (2004) In press

COMMENT Contact: Elly M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pflotenauerstrasse 108, 01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: BL003B row: 01 column: H
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

FEATURES
source
1. .22
Location/Qualifiers
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"

/tissue_type="Tail Blastema"
 /cell_type="regenerating tail blastema"
 /clone_lib="6-Day Axolotl Tail Blastema (6DaxBL)"
 /note="Vector: pCMVSPORT6; Site_1: NotI; Site_2: SalI;
 Unnormalized cDNA plasmid library prepared by invitrogen.
 Size fractionated mRNA was polydT primed and cloned into
 NotI-SalI site of pCMVSPORT6. Bacterial host is
 EMDH10B-TONA. Average insert size is 1.67 kb.
 TAG_LIB=6DAXBL"

Query Match 0.8%; Score 21; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
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 Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1253
 AZ304806
 LOCUS 22 bp DNA linear GSS 29-SEP-2000
 DEFINITION IM0005K17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0005K17 F, genomic survey sequence.

ACCESSION AZ304806
 VERSION
 KEYWORDS

SOURCE GI:10341191

ORGANISM Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Mus;

1 (bases 1 to 22)

REFERENCE
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Bescorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0005 row: K column: 17

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0005K17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnates/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 [gil4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
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 Db 2 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1254

AZ374487

LOCUS 22 bp DNA linear GSS 02-OCT-2000

DEFINITION IM0127H16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0127H16 F, genomic survey sequence.

ACCESSION AZ374487

VERSION

KEYWORDS

SOURCE GI:10488187

ORGANISM Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Mus;

1 (bases 1 to 22)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0127 row: H column: 16

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0127H16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnates/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 2 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1255
AZ505769
LOCUS 22 bp DNA linear GSS 05-OCT-2000
DEFINITION lM0346A10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ505769
VERSION 1 GI:10687085
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0346 row: A column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 22.
Location/Qualifiers
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0346A10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

FEATURES
source

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 2 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1256
AZ823875
LOCUS 22 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0098K07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ823875
VERSION 1 GI:12993795
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0098 row: K column: 07
Seq primer: CGTGTGTAACGACGCGCCAGT
Class: plasmid ends

High quality sequence stop: 22.
Location/Qualifiers
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0098K07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

FEATURES
source

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1257
AL048776
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
1. .23
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566N213"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkcd2)"
/note="Vector: pMPL; Site_1: NotI; Site_2: Sali"
Query Match 0.8%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2728
|||||
DB 3 TAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1258
DT503381
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Populus trichocarpa x *Populus deltoides*
Populus trichocarpa x *Populus deltoides*
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; *Populus*.

REFERENCE

AUTHORS
1 (bases 1 to 23)
Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y., Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G., Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A., Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A., Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and Bohlmann,J.

TITLE
The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries

JOURNAL
COMMENT
Unpublished (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia

Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS0136 row: G column: 19
High quality sequence stop: 104
POLYA=Yes.

FEATURES

Location/Qualifiers
1. .23
/organism="Populus trichocarpa x *Populus deltoides*"
/mol_type="mRNA"
/cultivar="Hil-11"
/db_xref="taxon:3695"
/clone="WS0136_G19"
/sex="Male"
/lab_host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PTXD-IL-FL-A-4"
/note="Vector: pBluescript II SK (+) XR; Site 1: SstI (5' end of cDNA); Site 2: XhoI (3' end of cDNA); Sapling trees one metre in height and grown under greenhouse conditions were exposed to continuous feeding by *Malacosoma disstria* Hubner (forest tent caterpillar) mid-instar larvae caged on the sapling using mesh bags. Mature leaves from within the caged region were collected 4 hours, 8 hours and 24 hours after the onset of treatment. Mature leaves were also collected above the caged region (systemic response) 4 hours, 12 hours and 48 hours after the onset of treatment. mRNA was isolated from each tissue source independently and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 20 micrograms of mRNA according to the full-length cDNA library construction method described by Carninci P. et al. (2000). Genome Research 10(10):1617-1630 and directionally ligated into the pBluescript II SK (+) XR vector digested with SstI (5' end) and XhoI (3'). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation."

Query Match 0.8%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2728
|||||
DB 3 TAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1259

AL037096
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
DKFZp564I2164_r1 564 (synonym: hEbr2) *Homo sapiens* cDNA clone
DKFZp564I2164, mRNA sequence.
AL037096
AL037096.1 GI:49681938
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

```

REFERENCE
AUTHORS      Hominiidae; Homo.
TITLE        1 (bases 1 to 26)
JOURNAL      Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
COMMENT      Wiemann,S.
              EST (Duesterhoeft, et al.)
              Unpublished (1999)
              Contact: MIPS
              MIPS
              Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
  1..26
  Location/Qualifiers
    .organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="DKFP564L2164"
    /tissue_type="brain"
    /dev_stage="fetal"
    /lab_host="X1-2blue"
    /clone_lib="564 (synonym: hfr2)"
    /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.8%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
      |||||
Db 6 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 1260
TA321G11P
LOCUS      TA321G11P
DEFINITION T. brucei sheared genomic DNA clone 321g11, forward sequence,
            genomic survey sequence.
ACCESSION  AL492371
VERSION    AL492371.1 GI:11867375
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma
            1 (bases 1 to 26)
            Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
            Direct Submission
            Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
            Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
  1..26
  /organism="Trypanosoma brucei"
  /mol_type="genomic DNA"
  /strain="TREU927"
  /db_xref="taxon:5691"
  /clone="321g11"

Query Match      0.8%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+03;

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
      |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1261
AZ626101/c
LOCUS      AZ626101
DEFINITION 1M0466J07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0466J07 F, genomic survey sequence.
ACCESSION  AZ626101
VERSION    AZ626101.1 GI:11748291
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
            1 (bases 1 to 24)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0466 row: J column: 07
            Seq primer: CGTTGTAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 24.

FEATURES
source
  1..24
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="CS7BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC1M0466J07"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UUGC1M library"
  /note="Vector: PWD42nv; Purified genomic DNA from M.
  musculus CS7BL/6J (male) was obtained from the Jackson
  Laboratory Mouse DNA Resource
  (http://www.jax.org/resources/documents/dnares/). The DNA
  was hydrodynamically sheared by repeated passage through a
  0.005 inch orifice at constant velocity. The sheared DNA
  was blunt end-repaired with T4 DNA polymerase and T4
  polynucleotide kinase. Adaptor oligonucleotides were
  ligated to the blunt ends in high molar excess. The
  adaptor DNA was purified and size-selected for a 9.5 to
  10.5 kb range using preparative agarose gel
  electrophoresis. Vector DNA was prepared from a derivative
  of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
  inducible derivative of plasmid R1. The vector was ligated
  with adaptors complementary to the insert adaptors and
  purified. The sheared, adaptor mouse DNA was annealed to
  adaptor vector DNA, and transformed into
  chemically-competent E. coli XL10-Gold (Stratagene) cells
  and selected for ampicillin resistance."

Query Match      0.8%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1e+03;

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	Matches	22;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	2709	AAAAAAAAAAAAAAAAAAAAA	AAAAA	2732						
Db	24	AAAAAAAAAAAAAAAAAAAAA	AGAA	1						

RESULT	1262
AZ627850	
LOCUS	AZ627850 24 bp DNA linear GSS 13-DEC-2000
DEFINITION	1M0474N20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0474N20 F, genomic survey sequence.

VERSION	A2627850.1	GI:11750136
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.	

REFERENCE
AUTHORS
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacore, T., Duval, B., Hamil, C.,
Islan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokess, R., Tingey, A., von
Niederhausen, A. and Wright, D. Weiss, R.

TITLE	JOURNAL	COMMENT
Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SL 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: gdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: N column: 20
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
Hitc quality sequence stop: 24.

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FEATURES
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1. .24
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUC1M0474N20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Query Match 0.8%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1e+03;

	Matches	22;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	2709	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	2732							
Db	1	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	24							

RESULT	1263
CL693181	
LOCUS	
CL693181	24 bp DNA linear GSS 10-JUL-2004
DEFINITION	PRI0160C.A02_2 - PRI0160C.BR (24) Note: Recurring Sring Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

Accession	CL693181
Version	CL693181.1
Keywords	GSS.
Source	<i>Pristionchus pacificus</i>
Organism	<i>Pristionchus pacificus</i> Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; <i>Pristionchus</i> .

REFERENCE
AUTHORS
TITLE
JOURNAL

14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES	source	Location/Qualifiers
		1. .24
		/organism="Pristionchus pacificus"
		/mol_type="genomic DNA"
		/strain="California"
		/db_xref="taxon:54126"
		/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
		/note="Vector: pToifog-5 Fosmid vector"

Query Match 0.8%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1e+03;
Matches 22: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	2709	AAAAAAAAAAAAAAAAAAAAAAAAA	2732
Dp	1	AAACCAAAAAAAAAAAAAAAAAA	24

RESULT	1264
DUB829360/c	
LOCUS	DUB829360
DEFINITION	KBrS004M04R KB-S, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS004M04, genomic survey sequence.
	24 bp DNA linear GSS 22-DEC-2005

ACCESSION
 VERSION
 DU829360.
 DU829360.1
 GI:83865956
 KEYWORDS
 GSS.
 SOURCE
 Brassica rapa subsp. pekinensis
 ORGANISM
 Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE
 1 (bases 1 to 24)
 Yang, T.-J., Kwon, S.-J., Kim, J.-A., Kim, K.-B., Jin, M., Park, J.-Y., Lim, M.-H., Kim, H.-I., Choi, B.-S., Seol, Y.-J., Park, D.-S.,

TITLE
JOURNAL
COMMENT

Hahn, J. H. and Park, B. S.
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeon@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS004M04

Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers

FEATURES

source

1. .24

/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS004M04"
/lab_host="E. coli DH10B"
/clone_lib="KBrS_Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAH."

Query Match 0.8%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
Db 24 AAAAAAAAAAGAAAAATAAAAA 1

RESULT 1265
AZ476141/c
LOCUS
DEFINITION
1M0294M10R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0294M10 R, genomic survey sequence.

ACCESSION AZ476141 GI:10634266
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0294 row: M column: 10
Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers

FEATURES

source

1. .25

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0294M10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.8%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
Db 24 AAAAAAAAAACAAAAACAAAAA 1

RESULT 1266

CZ910207
LOCUS
DEFINITION
4012001F09.1EL_Y1 4012 - RescueMu Grid BB Zea mays genomic, genomic
survey sequence.

ACCESSION CZ910207
VERSION
KEYWORDS
SOURCE
ORGANISM

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS
1 (bases 1 to 25)
Walbot V.

Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4012001 row: F column: 09
Class: transposon-tagged

FEATURES

source

1. .25

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"

```

/lab_host="DH10B"
/clone_lib="4012 - RescueMu Grid BB"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid BB was grown at UC Berkeley in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

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Query Match      0.8%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2731
      |||||||||||||||||||
Db 1 TAAAAAAAAAAAAAAAAAAAAAAAAACAGA 24

```

RESULT 1267

```

CZ917081      25 bp      DNA      linear      GSS 08-AUG-2005
LOCUS      4021004807.2ELy1 4021 - RescueMu Grid V Zea mays genomic, genomic
DEFINITION      survey sequence.

```

```

ACCESSION      CZ917081
VERSION
KEYWORDS
SOURCE      GSS.
ORGANISM      Zea mays

```

```

REFERENCE
AUTHORS      Walbot,V.
TITLE      Maize genomic sequences found using engineered RescueMu transposon
JOURNAL      Unpublished (2001)
COMMENT      Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021004 row: B column: 07
Class: transposon-tagged.

```

```

FEATURES
source
1..25
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"

```

```

/clone_lib="4021 - RescueMu Grid v"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with

```

```

ampicillin."

```

```

Query Match      0.8%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732
      |||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAAGAGAGAAAA 24

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RESULT 1268

```

AZ437459/c      26 bp      DNA      linear      GSS 03-OCT-2000
LOCUS      1M0225B15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0225B15 R, genomic survey sequence.

```

```

ACCESSION      AZ437459
VERSION
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus

```

```

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0225 row: B column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.

```

```

FEATURES
source
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0225B15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [gil4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

```


84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0287 row: L column: 21

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

FEATURES

source

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0287L21"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/notes="Vector: FWD42nv; Purified genomic DNA from M.

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydronamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 [G14732114|GB|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match

Best Local Similarity 95.5%; Pred. No. 1e+03; Length 22;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

2709 AAAAAAAAAAAAAAAAAAAAAA 2730

|||||

1 AAAAAAAAAAAAAAAAAAAGA 22

RESULT 1274

DU835072/c

LOCUS

DEFINITION 22 bp DNA linear GSS 22-DEC-2005

subsp. pekinensis genomic clone KBR066D14, genomic survey

sequence.

DU835072

DU835072.1 GI:83871682

SOURCE

Brassica rapa subsp. pekinensis

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 22)

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

Hahn, J. H. and Park, B.S.

End sequence of Brassica rapa Sau3AI (KBR-S) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBR015P15

Seq primer: T7

Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..22

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBR015P15"

/lab_host="E. coli DH10B"

/clone_lib="KBR-S, Brassica rapa Sau3AI BAC library"

/note="Vector: PCUGIBAC1; Site_1: Sau3AI; Brassica rapa

ssp pekinensis var. Chiifu BAC library (KBR-S BAC) is

available at NIAB."

Query Match 0.7%; Score 20.4; DB 1; Length 22;

Best Local Similarity 95.5%; Pred. No. 1e+03; Length 22;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

2709 AAAAAAAAAAAAAAAAAAAAAA 2730

|||||

22 AAAAAAAAAAAAAAAAAA 1

RESULT 1275

DX060105

LOCUS

DEFINITION

22 bp DNA linear GSS 10-JAN-2006

KBR066D14F KBR-S, Brassica rapa BamHI BAC library Brassica rapa

subsp. pekinensis genomic clone KBR066D14, genomic survey

sequence.

DX060105

DX060105.1 GI:84754401

SOURCE

GSS.

ORGANISM

Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 22)

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

Hahn, J.H. and Park, B.S.

End sequence of Brassica rapa BamHI (KBR-B) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBR066D14

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..22

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBR066D14"

/lab_host="E.coli DH10B"

/clone_lib="KBR-B, Brassica rapa BamHI BAC library"

/note="Vector: PCUGIBAC1; Site_1: BamHI; Brassica rapa spp

pekinensis var. Chiifu BAC library (KBR-B BAC) is provided

by Yong-Pyo Lim (CNU)."

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Query Match      0.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.e+03; Mismatches 0; Gaps 0;
Matches 21; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
      |||||
Db 1 AAAAAAAAAAAAAAAAAACAAA 22

RESULT 1276
TA303G05P      22 bp DNA linear GSS 13-DEC-2000
LOCUS          T. brucei sheared genomic DNA clone 303g05, forward sequence,
DEFINITION     genomic survey sequence.
ACCESSION      AL497383
VERSION        AL497383.1 GI:11865504
KEYWORDS       GSS.
SOURCE         Trypanosoma brucei
ORGANISM       Trypanosoma brucei
               Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
               Trypanosoma.
REFERENCE      1 (bases 1 to 22)
AUTHORS        Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
               Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
               Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE          Direct Submission
JOURNAL        Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
               project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
               Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
               nh1@sanger.ac.uk
COMMENT        Constructed at the Institute for Genomic Research (TIGR),
               Rockville, MD. Genomic DNA isolated from a cloned population of
               Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared
               to give a tight size distribution (
               4 kb). The v + i method used for the library construction is
               described in detail in Smith, H. and Venter, J.C. (Making small
               insert libraries for whole genome shotgun sequencing projects. In
               Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
               Barrell, Oxford University Press, 1999).
               Email: nelsayed@tigr.org
               Details of T. brucei sequencing at the Sanger Centre are available
               at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES       source
               1..22
               /organism="Trypanosoma brucei"
               /mol_type="genomic DNA"
               /strain="TREU927"
               /db_xref="taxon:5691"
               /clone="303g05"

Query Match      0.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.e+03; Mismatches 0; Gaps 0;
Matches 21; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
      |||||
Db 1 AAAAAAAAAAGAAAAAAAAA 22

RESULT 1277
AL038397
LOCUS          DKFZp566N082_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DEFINITION     DKFZp566N082, mRNA sequence.
ACCESSION      AL038397
VERSION        AL038397.1 GI:49682109
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.

```

```

REFERENCE      1 (bases 1 to 23)
AUTHORS        Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
               Wiemann, S.
TITLE          EST (Ottenwaelder, et al.)
JOURNAL        Unpublished (1999)
COMMENT        Contact: MIPS
               MIPS
               Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES       source
               1..23
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="DKFZp566N082"
               /tissue_type="kidney"
               /dev_stage="fetal"
               /lab_host="Xl-2blue"
               /clone_lib="566 (synonym: hfkd2)"
               /note="Vector: pAMPl; Site_1: NotI; Site_2: SalI"

Query Match      0.7%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.1e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2705 TACTATAAAAAAAAAAAAAA 2726
      |||
Db 2 TACAAAAAAAAAAAAA 23

RESULT 1278
AL038592
LOCUS          DKFZp566G1446_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DEFINITION     DKFZp566G1446, mRNA sequence.
ACCESSION      AL038592
VERSION        AL038592.1 GI:49682166
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE      1 (bases 1 to 23)
AUTHORS        Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
               Wiemann, S.
TITLE          EST (Ottenwaelder, et al.)
JOURNAL        Unpublished (1999)
COMMENT        Contact: MIPS
               MIPS
               Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES       source
               1..23
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="DKFZp566G1446"
               /tissue_type="kidney"
               /dev_stage="fetal"
               /lab_host="Xl-2blue"
               /clone_lib="566 (synonym: hfkd2)"
               /note="Vector: pAMPl; Site_1: NotI; Site_2: SalI"

Query Match      0.7%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.1e+03; Mismatches 1; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2705 TACTATAAAAAAAAAAAAAA 2726
      |||
Db 2 TACAAAAAAAAAAAAA 23

RESULT 1279
AL038609

```



```

Db      3  TCAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1285
CF326993
LOCUS   NACL--01-E17, g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--01-E17, mRNA
sequence.
ACCESSION CF326993
VERSION   1 GI:33802241
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzaceae; Oryza.
          1 (bases 1 to 24)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS   Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
TITLE     Contact: Nahm B.H.
JOURNAL   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT   of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..24
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-01-E17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/notes="lib=Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db      3  AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1286
DT496307
LOCUS   WS01123.AL5 PT-P-FL-A-2 Populus trichocarpa cDNA clone
DEFINITION Oryza sativa (japonica cultivar-group)
ACCESSION DT496307
VERSION   1 GI:73893569
KEYWORDS  EST.
SOURCE    Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
ORGANISM  Populus trichocarpa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids 1; Malpighiales; Salicaceae; Populus.
          1 (bases 1 to 24)
REFERENCE Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,
AUTHORS   Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,
          Babakiaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,
          Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
          Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
          Bohlmann,J.

The poplar transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries
Unpublished (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS01123 row: A column: 15
High quality sequence stop: 124
POLYA=Yes.

Location/Qualifiers
1..24
/organism="Populus trichocarpa"
/mol_type="mRNA"
/cultivar="383-2499 (Nisqually-1)"
/db_xref="taxon:3694"
/clone="WS01123_AL5"
/sex="Female"
/lab_host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PT-P-FL-A-2"
/notes="Vector: pBluescript II SK (+) XR; Site 1: SstI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Phloem and
cambium from 8 year old trees harvested within the Boise
Cascade region of Washington state on May 15th, 2001. cDNA
was prepared from 20 micrograms of mRNA according to the
full-length cDNA library construction method described by
Carninci P. et al. (2000), Genome Research
10(10):1617-1630 and directionally ligated into the
pBluescript II SK (+) XR vector digested with SstI (5'
end) and XhoI (3'). Plasmid DNA was then transformed by
electroporation into DH10B cells (Invitrogen) for
propagation."

Query Match 0.7%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2707 CTAAAAAAAAAAAAAAAAAAAA 2728
Db      3  CCAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1287
CF310471/c
LOCUS   ABF--05-C07.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION CF310471
VERSION   1 GI:33682232
KEYWORDS  EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzaceae; Oryza.
          1 (bases 1 to 25)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS   Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
TITLE     Contact: Nahm B.H.
JOURNAL   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT   of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

```

Query Match 0.7%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;

TITLE
JOURNAL

COMMENT
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="12f02"

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Best Local Similarity 88.0%; Pred. No. 1.1e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2701 TTGTACTAAAAA 2725
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Db 1 TTTTAAAAA 25

RESULT 1293
AJ666402/c

LOCUS
AJ666402 CSEQRAN09 Sus scrofa cDNA clone C000033_C23, mRNA

DEFINITION
sequence.

ACCESSION
AJ666402

VERSION
AJ666402.1 GI:49350853

KEYWORDS
EST.

SOURCE
Sus scrofa (pig)

ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE
1 (bases 1 to 20)
Anderson S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

TITLE
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector: pBluescriptII (KS+). R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
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/clone_lib="CSEQRAN09"
/note="Vector: pBluescriptII (KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library

constructed from pooled tissue from day 30 placentas."

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAA 2728
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Db 20 AAAAAAAAAA 1

RESULT 1294
AL038427

LOCUS
AL038427 DKFP566A1746_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone

DEFINITION
DKFP566A1746, mRNA sequence.

ACCESSION
AL038427

VERSION
AL038427.1 GI:49682121

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 20)
Ottewaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Ottewaelder, et al.)
Unpublished (1999)
Contact: MIPS

TITLE
JOURNAL

COMMENT
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
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/organism="Homo sapiens"
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OY 2708 TAAAAA 2727
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Db 1 TAAAAA 20

RESULT 1295
AL038429

LOCUS
AL038429 DKFP566A1946_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone

DEFINITION
DKFP566A1946, mRNA sequence.

ACCESSION
AL038429

VERSION
AL038429.1 GI:49682123

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 20)
Ottewaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Ottewaelder, et al.)
Unpublished (1999)
Contact: MIPS

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2708 TAAAAA 2727
|||||
Db 1 TAAAAA 20

RESULT 1295
AL038429

LOCUS
AL038429 DKFP566A1946_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone

DEFINITION
DKFP566A1946, mRNA sequence.

ACCESSION
AL038429

VERSION
AL038429.1 GI:49682123

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 20)
Ottewaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Ottewaelder, et al.)
Unpublished (1999)
Contact: MIPS

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FEATURES
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    100.0%; Pred. No. 1.1e+03;
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    20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 TAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1296
AL038570
LOCUS
  AL038570 20 bp mRNA linear EST 06-JUL-2004
DEFINITION
  DKFP566F1746_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
  DKFP566F1746, mRNA sequence.
ACCESSION
  AL038570
VERSION
  AL038570.1 GI:49682159
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
  1 (bases 1 to 20)
  Ortenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
  Wiemann,S.
  EST (Ottenwaelder, et al.)
  Unpublished (1999)
  Contact: MIPS
  MIPS

  Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
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Qy 2708 TAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 TAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1297
AL038750
LOCUS
  AL038750 20 bp mRNA linear EST 06-JUL-2004
DEFINITION
  DKFP566M1146_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
  DKFP566M1146, mRNA sequence.
ACCESSION
  AL038750
VERSION
  AL038750.1 GI:49682199
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
  1 (bases 1 to 20)
  Ortenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
  Wiemann,S.
  EST (Ottenwaelder, et al.)
  Unpublished (1999)
  Contact: MIPS
  MIPS

  Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
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    /clone_lib="566 (synonym: hfkd2)"
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    20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 TAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1298
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LOCUS
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DEFINITION
  14ETL--07-M07.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
  Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-M07,
  mRNA sequence.
ACCESSION
  CF280913
VERSION
  CF280913.1 GI:33658299
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
    clade; Ehrhartoideae; Oryzeae; Oryza.
  1 (bases 1 to 20)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
    1..20
    /organism="Oryza sativa (japonica cultivar-group)"
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    /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
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ORGANISM
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
  1 (bases 1 to 20)
  Ortenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
  Wiemann,S.
  EST (Ottenwaelder, et al.)
  Unpublished (1999)
  Contact: MIPS
  MIPS

  Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
  Location/Qualifiers
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    /db_xref="taxon:9606"
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    /dev_stage="fetal"
    /lab_host="X1-2blue"
    /clone_lib="566 (synonym: hfkd2)"
    /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

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    100.0%; Pred. No. 1.1e+03;
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Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1298
AL038913
LOCUS
  AL038913 20 bp mRNA linear EST 14-AUG-2003
DEFINITION
  14ETL--07-M07.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
  Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-M07,
  mRNA sequence.
ACCESSION
  CF280913
VERSION
  CF280913.1 GI:33658299
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
    clade; Ehrhartoideae; Oryzeae; Oryza.
  1 (bases 1 to 20)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
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RT-PCR."

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 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1299

CF282035 20 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ETL--09-F19.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F19,
 mRNA sequence.

ACCESSION CF282035.1 GI:33659422

VERSION EST.

KEYWORDS Oryza sativa (japonica cultivar-group)

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 20)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES

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/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

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(14ETL)"

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with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.7%; Score 20; DB 1; Length 20;
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
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 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1300

CF282414 20 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ETL--09-F19.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F19,
 mRNA sequence.

ACCESSION CF282414

VERSION CF282414.1 GI:33659801

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE
AUTHORSTITLE
JOURNAL
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 20)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES

source

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/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

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(14ETL)"

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 with oligoribonucleotides and then used as templates for

RT-PCR."

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1301

CF299822/c

LOCUS 7LEAF--03-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--03-P22, mRNA

sequence.

ACCESSION CF299822

VERSION CF299822.1 GI:33671583

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 20)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES

source

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/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

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Db	20 AAAAAAAAAAAAAAAAAAAAAA 1		
<p>RESULT 1302</p> <p>CF301720/c</p> <p>LOCUS</p> <p>DEFINITION</p> <p>7LEAF--06-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-L01, mRNA sequence.</p>			
<p>ACCESSION</p> <p>VERSION</p> <p>KEYWORDS</p> <p>SOURCE</p> <p>ORGANISM</p>			
<p>CF301720.1 GI:33673481</p> <p>EST.</p> <p>Oryza sativa (japonica cultivar-group)</p> <p>Oryza sativa (japonica cultivar-group)</p> <p>Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.</p>			
<p>REFERENCE</p> <p>AUTHORS</p> <p>Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.</p> <p>Large-scale Sequencing Analysis of Rice ESTs</p> <p>Unpublished (2003)</p> <p>Contact: Nahm B.H.</p> <p>Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University</p> <p>Yongin, Kyeonggi, Korea</p> <p>Tel: 82 31 330 6193</p> <p>Fax: 82 31 321 6355</p> <p>Email: bhnaem@gbio.com, bhnaem@bio.myongji.ac.kr.</p>			
<p>FEATURES</p> <p>source</p> <p>1..20</p> <p>/organism="Oryza sativa (japonica cultivar-group)"</p> <p>/mol_type="mRNA"</p> <p>/cultiivar="Nackdong"</p> <p>/db_xref="taxon:39947"</p> <p>/clone="7LEAF--06-L01"</p> <p>/tissue_type="leaf"</p> <p>/dev_stage="7 days after germination"</p> <p>/lab_host="E.coli DH10B"</p> <p>/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"</p> <p>/note=vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."</p>			
<p>Query Match</p> <p>Best Local Similarity 100.0%; Score 20; DB 1; Length 20;</p> <p>Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>		<p>/tissue_type="leaf"</p> <p>/dev_stage="7 days after germination"</p> <p>/lab_host="E.coli DH10B"</p> <p>/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"</p> <p>/note=vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."</p>	
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Db	20 AAAAAAAAAAAAAAAAAAAAAA 1		
<p>RESULT 1303</p> <p>CF302027/c</p> <p>LOCUS</p> <p>DEFINITION</p> <p>7LEAF--07-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C16, mRNA sequence.</p>			

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Db      1 AAAAAAAAAAAAAAAAAAAAAA 20
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RESULT 1306
CF313569/c
LOCUS   CF313569                20 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION HD--01-L22.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION HD--01-L22, mRNA sequence.
VERSION    CF313569
KEYWORDS   CF313569.1 GI:33685330
SOURCE     EST.
ORGANISM   Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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         /clone_lib="OSHDA1-overexpressing transgenic rice plasmid
         cDNA library (HD)"
         /note="vector: pCR4-TOPO; Site_1: EcoRI; Callus was
         treated with ABA(20um) for 1hr. Oligo-capped mRNA was
         reverse transcribed and then used for PCR. mRNA was
         derived from rice Histone Deacetylase overexpression
         line."

Query Match          0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
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QY      2709 AAAAAAAAAAAAAAAAAAAA 2728
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Db      20 AAAAAAAAAAAAAAAAAAAA 1
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CF319133/c
LOCUS   CF319133                20 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION HD--09-I13.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION HD--09-I13, mRNA sequence.
VERSION    CF319133
KEYWORDS   CF319133.1 GI:33690894
SOURCE     EST.
ORGANISM   Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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         line."

Query Match          0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YV      2709 AAAAAAAAAAAAAAAAAAAA 2728
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TITLE
JOURNAL
COMMENT

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
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cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1308

CF321721/c
LOCUS
DEFINITION
CF321721 20 bp mRNA linear EST 15-AUG-2003
HD-13-B05-g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD-13-B05, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source
1..20
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/lab_host="E.coli DH10B"

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cDNA library (HD)"
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
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Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1309

CF328565
LOCUS
DEFINITION
CF328565 20 bp mRNA linear EST 18-AUG-2003
NACL-03-II4.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL-03-II4, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
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QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1310

CF333173/c
LOCUS
DEFINITION
CF333173 20 bp mRNA linear EST 18-AUG-2003
JMT--01-P11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--01-P11, mRNA sequence.

ACCESSION CF333173
 VERSION CF333173.1 GI:33814617
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 20)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1311
 CF334170/c
 LOCUS
 DEFINITION JMT--03-F17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--03-F17, mRNA sequence.
 ACCESSION CF334170
 VERSION CF334170.1 GI:33816671
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 20)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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 Query Match 0.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1312
 CF33525/c
 LOCUS
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 ACCESSION CF33525
 VERSION CF33525.1 GI:33821425
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 20)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
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 QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

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Db      20  AAAAAAAAAAAAAAAAAAAAAA 1
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CF337494/c
LOCUS
DEFINITION
JMT--07-P04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--07-P04, mRNA sequence.
CF337494
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP.
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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cDNA library (JMT)"
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Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.le+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1315
CN545446/c
LOCUS
DEFINITION
EST 17390 Green Grape Skin Triplex2 Library Vitis vinifera CDNA
clone B3CS00GL005C02 3', mRNA sequence.
CN545446
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE
1 (bases 1 to 20)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaidechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 17.
Location/Qualifiers
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Query Match 0.7%; Score 20; DB 1; Length 20;

Db      20  AAAAAAAAAAAAAAAAAAAAAA 1
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RESULT 1314
AW334823/c
LOCUS
DEFINITION
S39P5 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
AW334823
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pneumocystis carinii
Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
REFERENCE
1 (bases 1 to 20)
Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
Contact: Staben C

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Db      20  AAAAAAAAAAAAAAAAAAAAAA 1
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RESULT 1313
CF337494/c
LOCUS
DEFINITION
JMT--07-P04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--07-P04, mRNA sequence.
CF337494
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP.
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1. .20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-P04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.le+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1314
AW334823/c
LOCUS
DEFINITION
S39P5 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
AW334823
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pneumocystis carinii
Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
REFERENCE
1 (bases 1 to 20)
Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
Unpublished (2000)
Contact: Staben C

```

```

School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.
Location/Qualifiers
1. .20
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/notes="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat [99-1-6,
sacrificed on 3/17/99] at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/project/Pneumocystis/"
Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.le+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1315
CN545446/c
LOCUS
DEFINITION
EST 17390 Green Grape Skin Triplex2 Library Vitis vinifera CDNA
clone B3CS00GL005C02 3', mRNA sequence.
CN545446
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE
1 (bases 1 to 20)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaidechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 17.
Location/Qualifiers
1. .20
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00GL005C02"
/dev_stage="green stage"
/clone_lib="Green Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"
Query Match 0.7%; Score 20; DB 1; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1316
CN545501/c
LOCUS
DEFINITION 20 bp mRNA linear EST 30-APR-2004
clone B3CS00GL005H02 3', mRNA sequence.

ACCESSION CN545501
VERSION
KEYWORDS
SOURCE CN545501.1 GI:46910126
ORGANISM
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 20)
AUTHORS Abbal, P., Agasse, A., Ageorges, A., Atanasova, R., Barrieu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
JOURNAL Contact: Hamdi S.
COMMENT UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France

Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7

FEATURES
source
1..20
Location/Qualifiers
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00GL005H02"
/dev_stage="green stage"
/clone_lib="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1317
DN953918
LOCUS
DEFINITION 20 bp mRNA linear EST 04-MAY-2005
1t66c07.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.

ACCESSION DN953918
VERSION
KEYWORDS
SOURCE DN953918.1 GI:63026056
ORGANISM
Gnetum gnemon
Gnetum gnemon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetophyta; Gnetales; Gnetales; Gnetum.
REFERENCE 1 (bases 1 to 20)
AUTHORS Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,

O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)

CONTACT: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
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Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES
source
1..20
Location/Qualifiers

/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
/note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1318
DN954281/c

LOCUS
DEFINITION 20 bp mRNA linear EST 04-MAY-2005
DN954281
Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.

ACCESSION DN954281
VERSION
KEYWORDS
SOURCE DN954281.1 GI:63026419
ORGANISM
Gnetum gnemon
Gnetum gnemon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetophyta; Gnetales; Gnetales; Gnetum.
REFERENCE 1 (bases 1 to 20)
AUTHORS Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)

CONTACT: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES
source
1..20
Location/Qualifiers

/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
/note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.

Query Match

Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1322
DR073130/c
LOCUS
DEFINITION 20 bp mRNA linear EST 08-JUN-2005
ik86h03.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.

ACCESSION DR073130
VERSION DR073130
KEYWORDS
SOURCE DR073130.1 GI:67050981

ORGANISM
Ginkgo biloba (maidenhair tree)

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

1 (bases 1 to 20)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.

Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)

CONTACT: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884
Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.

Location/Qualifiers

1..20

/organism="Ginkgo biloba"

/mol_type="mRNA"

/db_xref="taxon:3311"

/sex="female"

/clone_lib="Ginkgo female leaf (NYBG)"

/note="Organ: Leaf; Vector: pBK-CMV; Site 1: XhoI;

Site 2: Eco RI; Stragene ZAP Express cDNA Synthesis Kit.

The library was size-fractionated to enrich for large

inserts."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1323
DT493556
LOCUS
DEFINITION 20 bp mRNA linear EST 29-AUG-2005
WS0111_BR_L11 PT-P-FL-A-2 Populus trichocarpa cDNA clone WS0111_L11
5', mRNA sequence.

ACCESSION DT493556
VERSION DT493556
KEYWORDS
SOURCE DT493556.1 GI:73890818

ORGANISM
Populus trichocarpa (Populus balsamifera subsp. trichocarpa)

Populus trichocarpa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.

1 (bases 1 to 20)

Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,

Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,

Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,

Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,

TITLE

JOURNAL

COMMENT

Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
Bohlmann,J.

The poplar transcriptome: Analysis of expressed sequence tags from

multiple cDNA libraries

Unpublished (2004)

Contact: Joerg Bohlmann

Genome BC forest genomics program

University of British Columbia

Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,

Vancouver, British Columbia, Canada, V6T 1Z3

Tel: 1-604-822-0282

Fax: 1-604-822-2114

Email: bohlmann@msl.ubc.ca

Plate: WS0111 row: L column: 11

High quality sequence stop: 139

POlyA=yes.

FEATURES

source

1..20

/organism="Populus trichocarpa"

/mol_type="mRNA"

/cultivar="383-2499 (Nisqually-1)"

/db_xref="taxon:3694"

/clones="WS0111_L11"

/sex="Female"

/lab_hosts="E. coli DH10B T1 phage resistant cells"

/clone_lib="PT-P-FL-A-2"

/note="Vector: pBluescript II SK (+) XR; Site 1: SacI (5'

end of cDNA); Site 2: XhoI (3' end of cDNA); Phiom and

cambium from 8 year old trees harvested within the Boise

Cascade region of Washington state on May 15th, 2001. cDNA

was prepared from 20 micrograms of mRNA according to the

full-length cDNA library construction method described by

Carninci,P. et al. (2000), Genome Research

10(10):1617-1630 and directionally ligated into the

pBluescript II SK (+) XR vector digested with SetI (5'

end) and XhoI (3'). Plasmid DNA was then transformed by

electroporation into DH10B cells (Invitrogen) for

propagation."

Query Match 0.7%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1324

T50579/c

LOCUS

DEFINITION

T50579

IMAGE:77095

5' similar to contains

L1 repetitive element, mRNA

sequence.

ACCESSION

T50579

VERSION

T50579.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa;

Chordata; Craniata;

Vertebrata; Euteleostomi;

Mammalia; Eutheria;

Euarchontoglires; Primates;

Carnivora; Homini

1 (bases 1 to 20)

REFERENCE

AUTHORS

Hillier,L.,

Lennon,G.,

Becker,M.,

Bonaldo,M.F.,

Chiapelli,B.,

Chissoe,S.,

Dietrich,N.,

DuBuque,T.,

Favello,A.,

Gish,W.,

Hawkins,M.,

Hultman,M.,

Kucaba,T.,

Lacy,M.,

Le,M.,

Le,N.,

Mardis,E.,

Moore,B.,

Morris,M.,

Parsons,J.,

Prange,C.,

Rifkin,L.,

Rohlfing,T.,

Schellenberg,K.,

Soares,M.B.,

Tan,F.,

Thierry-Mieg,J.,

Trevaaskis,E.,

Underwood,K.,

Wohlmann,P.,

Waterston,R.,

Wilson,R.,

and Maria,M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

PUBMED

8889549

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RPI
High quality sequence stop: 20.

FEATURES

source

1. .20
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:506824"
/db_xref="taxon:9606"
/clone="IMAGE:77095"
/sex="female"
/dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/notes="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI;
Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt.
Total ovary tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR vector; ~5' adaptor sequence: 5'
GAATTCGGACGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3'"

Query Match 0.7%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1325

AZ307671/c

LOCUS

1M0009M20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0009M20 R, genomic survey sequence.

ACCESSION

AZ307671

VERSION

AZ307671.1 GI:10346897

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 20)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: M column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

FEATURES

source

1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0009M20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1326

AZ333980/c

LOCUS

AZ333980 20 bp DNA linear GSS 29-SEP-2000
1M0063K10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0063K10 F, genomic survey sequence.

ACCESSION

AZ333980

VERSION

AZ333980.1 GI:10400856

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 20)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0063 row: K column: 10
Seq primer: CGTTGTAACGACGCCGACG
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

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source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0063K10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1327
AZ341530
LOCUS
DEFINITION
AZ341530 20 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0073N21 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: N column: 21
Seq primer: CACACAGAAACAGTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
Location/Qualifiers

```

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source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0076F13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1329
AZ351273
LOCUS
DEFINITION
1M0089B18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0089B18 F, genomic survey sequence.
ACCESSION
AZ351273
VERSION
AZ351273.1 GI:10430510
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: B column: 18
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
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1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0089B18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1330
AZ357623
LOCUS
DEFINITION
1M0099A20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0099A20 F, genomic survey sequence.
ACCESSION
AZ357623
VERSION
AZ357623.1 GI:10471335
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: A column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
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1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0099A20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|Gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1331
AZ369734
LOCUS
DEFINITION
AZ369734 20 bp DNA linear GSS 02-OCT-2000
clone UUGC1M0120024 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0120 row: 0 column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: C column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

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source      1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0145C11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709  AAAAAAAAAAAAAAAAAAAAAA 2728
Db      1  AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1333
AZ396481
LOCUS      20 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION      1M0161K02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0161K02 F, genomic survey sequence.
ACCESSION      AZ396481
VERSION      AZ396481.1 GI:10511553
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0161 row: K column: 02
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

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source      1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0161K02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709  AAAAAAAAAAAAAAAAAAAAAA 2728
Db      1  AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1334
AZ442328
LOCUS      20 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION      1M0236B11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0236B11 F, genomic survey sequence.
ACCESSION      AZ442328
VERSION      AZ442328.1 GI:10566341
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0236 row: B column: 11
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

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source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0236B11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1335
A2463331/c
LOCUS
DEFINITION
clone UUC1M0272006 F, genomic survey sequence.
ACCESSION
A2463331
VERSION
A2463331.1 GI:10621456
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0272 row: 0 column: 06
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

source
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0272006"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1335
A2463331/c
LOCUS
DEFINITION
clone UUC1M0272006 F, genomic survey sequence.
ACCESSION
A2463331
VERSION
A2463331.1 GI:10621456
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0272 row: 0 column: 06
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

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source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0297E23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
| | | | | | | | | | | | | | | | | |
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1337
AZ479464/c
LOCUS
DEFINITION
1M0300P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0300P01 F, genomic survey sequence.
ACCESSION
AZ479464
VERSION
AZ479464.1 GI:10638941
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0300 row: P column: 01
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 10.
Location/Qualifiers
FEATURES

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source
1. .20
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0300P01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
| | | | | | | | | | | | | | | | | |
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1338
AZ486784/c
LOCUS
DEFINITION
1M0315C20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315C20 F, genomic survey sequence.
ACCESSION
AZ486784
VERSION
AZ486784.1 GI:10653898
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: C column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
FEATURES

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source
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0315C20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2727
DB 20 TAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1339
AZ498625/c
LOCUS
DEFINITION
  AZ498625 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0336E05 F, genomic survey sequence.
ACCESSION
  AZ498625
VERSION
  AZ498625.1 GI:10676657
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 20)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0336 row: E column: 05
  Seq primer: CGTTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 20.
  Location/Qualifiers

FEATURES
  Location/Qualifiers

source
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0336E05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1340
AZ514729
LOCUS
DEFINITION
  AZ514729 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0361E11 R, genomic survey sequence.
ACCESSION
  AZ514729
VERSION
  AZ514729.1 GI:10696045
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 20)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0361 row: E column: 11
  Seq primer: CACACAGGAACACGTATGACC
  Class: plasmid ends
  High quality sequence stop: 20.
  Location/Qualifiers

FEATURES
  Location/Qualifiers

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source      1. .20
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1341
AZ581208
LOCUS      20 bp DNA linear GSS 13-DEC-2000
DEFINITION      1M0369P15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0369P15 R, genomic survey sequence.
ACCESSION      AZ581208
VERSION        AZ581208.1 GI:11695991
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE      1 (bases 1 to 20)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0369 row: P column: 15
                Seq primer: CACACAGAAACAGCTATGACC
                Class: plasmid ends
                High quality sequence stop: 20.
                Location/Qualifiers

FEATURES

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/strain="C57BL/6J"
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/clone="UUGC1M0369P15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1342
AZ588011
LOCUS      20 bp DNA linear GSS 13-DEC-2000
DEFINITION      1M0396A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0396A13 F, genomic survey sequence.
ACCESSION      AZ588011
VERSION        AZ588011.1 GI:11710297
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE      1 (bases 1 to 20)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0396 row: A column: 13
                Seq primer: CGTTGTAAACGACGCCAGT
                Class: plasmid ends
                High quality sequence stop: 20.
                Location/Qualifiers

FEATURES

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source

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/organism="Mus musculus"
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/clone="UUGC1M0396A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match 0.7%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1343

AZ607328

LOCUS

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AZ607328 20 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0429A14 R, genomic survey sequence.

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ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE

AUTHORS

```

1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

```

TITLE

```

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

JOURNAL

COMMENT

```

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

```

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0429 row: A column: 14

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

FEATURES

source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0429A14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match 0.7%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1344

AZ623155/c

LOCUS

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AZ623155 20 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0460K05 R, genomic survey sequence.

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ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE

AUTHORS

```

1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

```

TITLE

```

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

JOURNAL

COMMENT

```

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

```

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0460 row: K column: 05

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

FEATURES

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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0460K05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G[14732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1345
AZ623214/c
LOCUS
DEFINITION
1M0460L12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0460L12 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

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/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="UUGC1M0460L12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G[14732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1346
AZ643992
LOCUS
DEFINITION
1M0507D18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0507D18 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

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1. .20
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0507D18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1347
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LOCUS
DEFINITION
20 bp DNA linear GSS 14-DEC-2000
clone UUGC1M0511D03 R, genomic survey sequence.
ACCESSION
AZ645829
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: D column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1347
AZ645829/c
LOCUS
DEFINITION
20 bp DNA linear GSS 14-DEC-2000
clone UUGC1M0511D03 R, genomic survey sequence.
ACCESSION
AZ645829
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
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University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: D column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0520C21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%  Score 20;  DB 1;  Length 20;
Best Local Similarity 100.0%;  Pred. No. 1.1e+03;
Matches 20;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  2709  AAAAAAAAAAAAAAAAAAAAAA 2728
      ||||||||||||||||||
Db    1  AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1349
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LOCUS
DEFINITION
  1M0554A24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0554A24 R, genomic survey sequence.
ACCESSION
  AZ760838
VERSION
  AZ760838.1  GI:12869112
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 20)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: dunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0554 row: A column: 24
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 20.
  Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0554A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%  Score 20;  DB 1;  Length 20;
Best Local Similarity 100.0%;  Pred. No. 1.1e+03;
Matches 20;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  2709  AAAAAAAAAAAAAAAAAAAAAA 2728
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Db    1  AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1350
AZ764504
LOCUS
DEFINITION
  1M0560M02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0560M02 R, genomic survey sequence.
ACCESSION
  AZ764504
VERSION
  AZ764504.1  GI:12879535
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 20)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: dunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0560 row: M column: 02
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 20.
  Location/Qualifiers

FEATURES

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/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1351
AZ765211/c
LOCUS
DEFINITION
  AZ765211 20 bp DNA linear GSS 16-FEB-2001
  clone UUGC1M0562H04 F, genomic survey sequence.
ACCESSION
  AZ765211 GI:12880970
VERSION
  AZ765211.1
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0562 row: H column: 04
  Seq primer: CGTTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 20.
  Location/Qualifiers

FEATURES
  Location/Qualifiers

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M056M02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1351
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DEFINITION
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  clone UUGC1M0562H04 F, genomic survey sequence.
ACCESSION
  AZ765211 GI:12880970
VERSION
  AZ765211.1
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
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  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
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  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0562 row: H column: 04
  Seq primer: CGTTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 20.
  Location/Qualifiers

FEATURES
  Location/Qualifiers

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1353
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DEFINITION
2M0015M18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0015M18 R, genomic survey sequence.
ACCESSION
VERSION AZ779425.1 GI:12910066
KEYWORDS
SOURCE
MUS musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0015 row: M column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1354
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DEFINITION
2M0026B21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0026B21 F, genomic survey sequence.
ACCESSION
VERSION AZ784041.1 GI:12919375
KEYWORDS
SOURCE
MUS musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: B column: 21
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

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/clone="UUGC2M0026B21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1355
AZ793467/c
LOCUS
DEFINITION
2M0046C16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0046C16 R, genomic survey sequence.
ACCESSION
AZ793467
VERSION
AZ793467.1 GI:12938450
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0046 row: C column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1355
AZ793467/c
LOCUS
DEFINITION
2M0055G19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0055G19 F, genomic survey sequence.
ACCESSION
AZ798529
VERSION
AZ798529.1 GI:12948718
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0055 row: G column: 19
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1357
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LOCUS      20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0066L14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0066L14 F, genomic survey sequence.
ACCESSION  AZ805163
VERSION     AZ805163.1 GI:12965890
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0066 row: L column: 14
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            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers

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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1358
AZ806521
LOCUS      20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0068C08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0068C08 R, genomic survey sequence.
ACCESSION  AZ806521
VERSION     AZ806521.1 GI:12969953
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0068 row: C column: 08
            Seq primer: CACACAGGAACGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers

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/strain="C57BL/6J"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1359
AZ806585
LOCUS
DEFINITION
2M0068C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0068C15 R, genomic survey sequence.
ACCESSION
AZ806585
VERSION
AZ806585.1 GI:12970081
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0068 row: C column: 15
Seq primer: CACACAGGAAACAGTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

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/strain="C57BL/6J"
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/clones="UUGC2M0068C15"
/sex="Male"
/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1360
AZ809306
LOCUS
DEFINITION
2M0073D15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0073D15 F, genomic survey sequence.
ACCESSION
AZ809306
VERSION
AZ809306.1 GI:12975468
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: D column: 15
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0073D15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1361
AZ810986
LOCUS      20 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M0076120R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0076120 R, genomic survey sequence.
ACCESSION  AZ810986
VERSION     AZ810986.1  GI:12978793
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: I column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

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source      1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0073D15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1361
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LOCUS      20 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M0076120R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0076120 R, genomic survey sequence.
ACCESSION  AZ810986
VERSION     AZ810986.1  GI:12978793
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: I column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

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source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0081F21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1363
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LOCUS
DEFINITION
2M0086C20R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0086C20 R, genomic survey sequence.
ACCESSION
AZ817323
VERSION
AZ817323.1 GI:12987327
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: C column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0086C20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1364
AZ817414
LOCUS
DEFINITION
2M0086K08R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0086K08 R, genomic survey sequence.
ACCESSION
AZ817414
VERSION
AZ817414.1 GI:12987238
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: K column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

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source      1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0086K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1365
AZ817467
LOCUS      20 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M0086J15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0086J15 R, genomic survey sequence.
ACCESSION  AZ817467
VERSION     AZ817467.1 GI:12987291
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0086 row: J column: 15
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers

FEATURES

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source      1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0086J15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1366
AZ817608/c
LOCUS      20 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M0087K08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0087K08 F, genomic survey sequence.
ACCESSION  AZ817608
VERSION     AZ817608.1 GI:12987516
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0087 row: K column: 08
            Seq primer: CGTTGTAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers

FEATURES

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source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0087K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1367
AZ818489/c
LOCUS
DEFINITION
  AZ818489 20 bp DNA linear GSS 20-FEB-2001
  clone UUGC2M008K01 R, genomic survey sequence.
ACCESSION
  AZ818489
VERSION
  AZ818489.1 GI:12988397
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 20)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunne@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0088 row: K column: 01
  Seq primer: CACACAGGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 20.
  Location/Qualifiers

FEATURES
  Location/Qualifiers

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source      1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0089M05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1369
AZ837491
LOCUS      20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0132K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0132K13 R, genomic survey sequence.
ACCESSION  AZ837491
VERSION     AZ837491.1 G1:13007399
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D..Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0132 row: K column: 13
            Seq primer: CACACAGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers

FEATURES

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source      1. .20
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0132K13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1370
AZ841342
LOCUS      20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0139H16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0139H16 F, genomic survey sequence.
ACCESSION  AZ841342
VERSION     AZ841342.1 G1:13011250
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D..Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0139 row: H column: 16
            Seq primer: CGTTGTAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers

FEATURES

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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0139H16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1371
A2841558/c
LOCUS
DEFINITION
2M0139A10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0139A10 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
GI:13011466
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: A column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: O column: 03
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

source
1. .20
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0139A10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1372
A2858052
LOCUS
DEFINITION
2M0163003F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0163003 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
GSS.
GI:13050813
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: O column: 03
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: O column: 03
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

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source      1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0163003"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
| | | | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1373
AZ858419
LOCUS      20 bp      DNA      linear      GSS 21-FEB-2001
DEFINITION 2M0163003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0163003 R, genomic survey sequence.
ACCESSION  AZ858419
VERSION     AZ858419.1  GI:13051545
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
JOURNAL
COMMENT    Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0163 row: 0 column: 03
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 20.
          Location/Qualifiers

FEATURES

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source      1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0163003"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2727
| | | | | | | | | | | | | | | | | | | |
Db 1 TAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1374
AZ936914
LOCUS      20 bp      DNA      linear      GSS 26-APR-2001
DEFINITION 2M0193G23R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0193G23 R, genomic survey sequence.
ACCESSION  AZ936914
VERSION     AZ936914.1  GI:13795495
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
JOURNAL
COMMENT    Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0193 row: G column: 23
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 20.
          Location/Qualifiers

FEATURES

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source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0193G23"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1375
AZ949180/c
LOCUS
DEFINITION
2M0212102R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0212102 R, genomic survey sequence.
ACCESSION
AZ949180
VERSION
AZ949180.1 GI:13820407
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: I column: 02
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0212102"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1376
AZ963973/c
LOCUS
DEFINITION
2M0233J01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0233J01 F, genomic survey sequence.
ACCESSION
AZ963973
VERSION
AZ963973.1 GI:13835200
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: J column: 01
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

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1. .20

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0233J01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Query Match          0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT	1377
CW979138	
LOCUS	
DEFINITION	CW979138 20 bp DNA linear GSS 28-DEC-2004 KBrH001K19R KB+H, Brassica rapa HindIII BAC library subsp. pekinensis genomic clone KBrH001K19, genomic survey

REFERENCE
AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Lim, Y.P. and Park, B.S.
TITLE
End sequence of *Brassica rapa* HindIII BAC library (KBrH)
JOURNAL
Unpublished (2004)
COMMENT
Contact: Beom-Seok Park

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FEATURES
source
    Location/Qualifiers
    1..20
    /organism="Brassica rapa subsp. pekinensis"
    /mol_type="genomic DNA"
    /cultivar="Chifu"

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/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBRH001K19"
/tissue_type="young leaves"
/lab_host="E.coli DH10B"
/clone_lib="KBRH, Brassica rapa HindIII BAC library"
/note="Vector: pCUGIBac1; Site 1: HindIII; Brassica rapa
    spp. pekinensis inbred line Chiifu BAC library (KBRH BAC)
    is provided by Yong-Pyo Lim."

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```
Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 1378
DUG34188/c
LOCUS
DUB34188 20 bp DNA linear GSS 22-DEC-2005
DEFINITION
KRS013J15F KRSrS, *Brassica rapa* Sau3AI BAC library *Brassica rapa*
subsp. *pekinensis* genomic clone KRS013J15, genomic survey
sequence.

```
Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

RESULT 1379
DU835125
LOCUS      20 bp      DNA      linear      GSS 22-DEC-2005
DEFINITION KBRs016A17f KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBRs016A17, genomic survey
            sequence.
ACCESSION  DU835125
VERSION     DU835125.1  GI:839871721
KEYWORDS   GSS.
SOURCE     Brassica rapa subsp. pekinensis
ORGANISM   Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J.H. and Park,B.S.
TITLE     End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL   Unpublished (2005)
COMMENT   Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1672
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone
            KBRs016A17
            Seq primer: T7
            Class: BAC ends.
            Location/Qualifiers
                source
                1..20
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                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBRs016A17"
                /lab_host="E. coli DH10B"
                /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                subsp. pekinensis var. Chiifu BAC library (KBrS BAC) is
                available at NTAB."

FEATURES             source
    Oy      2709  TAAAAAAAAAAAAAAAAAAA 2728
    Db      1  TAAAAAAAAAAAAAAAAAAA 20

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1380
DU835125
LOCUS      20 bp      DNA      linear      GSS 10-JAN-2006
DEFINITION KBRs047C15F KBrB, Brassica rapa BamHI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBRs047C15, genomic survey
            sequence.
ACCESSION  DU835125
VERSION     DU835125.1  GI:84740048
KEYWORDS   GSS.
SOURCE     Brassica rapa subsp. pekinensis
ORGANISM   Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J.H. and Park,B.S.
TITLE     End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL   Unpublished (2005)
COMMENT   Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1672
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone
            KBRs047C15
            Seq primer: M13 Reverse
            Class: BAC ends.
            Location/Qualifiers
                source
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                /organism="Brassica rapa subsp. pekinensis"
                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBRs047C15"
                /lab_host="E. coli DH10B"
                /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                subsp. pekinensis var. Chiifu BAC library (KBrS BAC) is
                available at NTAB."

FEATURES             source
    Oy      2709  TAAAAAAAAAAAAAAAAAAA 2728
    Db      1  TAAAAAAAAAAAAAAAAAAA 20

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1381
DU835125
LOCUS      20 bp      DNA      linear      GSS 10-JAN-2006
DEFINITION KBRs060D05R KBrB, Brassica rapa BamHI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBRs060D05, genomic survey
            sequence.
ACCESSION  DX055580
VERSION     DX055580.1  GI:84749877
KEYWORDS   GSS.
SOURCE     Brassica rapa subsp. pekinensis
ORGANISM   Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J.H. and Park,B.S.
TITLE     End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL   Unpublished (2005)
COMMENT   Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1672
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone
            KBRs060D05
            Seq primer: M13 Reverse
            Class: BAC ends.
            Location/Qualifiers
                source
                1..20
                /organism="Brassica rapa subsp. pekinensis"
                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBRs060D05"
                /lab_host="E. coli DH10B"
                /clone_lib="KBrB, Brassica rapa BamHI BAC library"
                /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa subsp.
                pekinensis var. Chiifu BAC library (KBrB BAC) is provided
                by Yong-Pyo Lim (CNU)."

FEATURES             source
    Oy      2708  TAAAAAAAAAAAAAAAAAAA 2727
    Db      1  TAAAAAAAAAAAAAAAAAAA 20

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/clone="KBrB060D05"
 /lab_host="E.coli DH10B"
 /clone_lib="KBrB, Brassica rapa BamHI BAC library"
 /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
 pekinensis var. Chiifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 0.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 |||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1382

DX070282/c

LOCUS DX070282 20 bp DNA linear GSS 10-JAN-2006
 DEFINITION KBrB079J23F KBrB, Brassica rapa BamHI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBrB079J23, genomic survey
 sequence.

ACCESSION DX070282

VERSION DX070282.1 GI:84764578

KEYWORDS GSS.

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis
 Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
 Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
 Hahn, J.H. and Park, B.S.

TITLE

End sequence of Brassica rapa BamHI (KBrB) BAC clone

JOURNAL

Unpublished (2005)

COMMENT

Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea
 Tel: +82-31-293-1670
 Fax: +82-31-293-1672
 Email: pbeom@da.go.kr
 BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
 KBrB079J23
 Seq primer: T7
 Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..20
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrB079J23"
 /lab_host="E.coli DH10B"
 /clone_lib="KBrB, Brassica rapa BamHI BAC library"
 /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
 pekinensis var. Chiifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 0.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 |||
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1383

BX556006/c

LOCUS

BX556006 21 bp mRNA linear EST 10-OCT-2003

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J.Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'

end of the cDNA all q1c reads are from

the 3' end.

Location/Qualifiers

1..21

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clone="Tse24c09_p1c"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected

gut"

/notes="country: Zimbabwe; EST from adult gut infected with

T.brucei"

Query Match 0.7%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

|||

Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1384

CF276638/c

LOCUS

DEFINITION

Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--01-N19,

mRNA sequence.

ACCESSION CF276638

VERSION CF276638.1 GI:33654024

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzoideae; Oryza.

1 (bases 1 to 21)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

10-OCT-2003

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL-01-N19"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1385

CF311914/c
LOCUS
DEFINITION
ABF--07-G07.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--07-G07, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--07-G07"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1386

CF318152/c
LOCUS
DEFINITION
HD--08-C11.bi OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--08-C11, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--08-C11"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1387

CX000923/c
LOCUS
DEFINITION
CX000923
mRNA sequence.
CX000923.1 GI:56272339

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Canis familiaris (dog)
Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 21)

AUTHORS Baliya,V.S., Naecimento,L.U. and McCombie,W.R.

TITLE ESTs from Canis familiaris left cardiac ventricle (dog)

JOURNAL Unpublished (2004)

COMMENT

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org.

Location/Qualifiers

FEATURES

source

1. .21

/organism="Canis familiaris"

/mol_type="mRNA"

/db_xref="taxon:9615"

/sex="Unknown"

/tissue_type="Cardiac muscle"

/dev_stage="3 month old normal canine"

/lab_host="X110 Gold"

/clone_lib="Left Cardiac Ventricle (DOGE5T7)"

/note="Organ: Heart; Vector: pBluescript II SK; Site: 1:

EcoRI; Site: 2: XhoI; Library constructed using pBluescript

XR kit from Stratagene. Cloned cDNA was size selected

between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,

Pathology and Medical Genetics, School of Veterinary

Medicine, University of Pennsylvania, 3800 Spruce Street,

Philadelphia, PA 19104-6051"

Query Match

Best Local Similarity 0.7%; Score 20; DB 1; Length 21;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2727

Db 20 TAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1388

DT496709

LOCUS

DEFINITION WS01124.BR D19 PT-FL-A-2 Populus trichocarpa cDNA clone

EST. 21 bp mRNA linear EST 29-AUG-2005

ACCESSION DT496709

KEYWORDS DT496709.1 GI:73893971

SOURCE EST.

ORGANISM Populus trichocarpa (Populus balsamifera subsp. trichocarpa)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.

1 (bases 1 to 21)

Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,

Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,

Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,

Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,

Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and

Bohmann,J.

The poplar transcriptome: Analysis of expressed sequence tags from

multiple cDNA libraries

Unpublished (2004)

Contact: Joerg Bohmann

Genome BC forest genomics program

University of British Columbia

Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,

Vancouver, British Columbia, Canada, V6T 1Z3

Tel: 1-604-822-0282

Fax: 1-604-822-2114

Email: bohmann@msl.ubc.ca

Plate: WS01124 row: D column: 19

High quality sequence stop: 116
POLYA=Yes.

FEATURES

source

Location/Qualifiers

1. .21

/organism="Populus trichocarpa"

/mol_type="mRNA"

/cultivar="383-2499 (Nisqually-1)"

/db_xref="taxon:3694"

/clone="WS01124_D19"

/sex="Female"

/lab_host="E. coli DH10B T1 phage resistant cells"

/clone_lib="PT-P-FL-A-2"

/note="Vector: pBluescript II SK (+) XR; Site: 1: SstI (5'

end of cDNA); Site: 2: XhoI (3' end of cDNA); Phloem and

cambium from 8 year old trees harvested within the Boise

Cascade region of Washington state on May 15th, 2001. cDNA

was prepared from 20 micrograms of mRNA according to the

full-length cDNA library construction method described by

Carninci P. et al. (2000), Genome Research

10(10):1617-1630 and directionally ligated into the

pBluescript II SK (+) XR vector digested with SstI (5'

end) and XhoI (3'). Plasmid DNA was then transformed by

electroporation into DH10B cells (Invitrogen) for

propagation."

Query Match

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

Db 2 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1389

AZ461824

LOCUS

DEFINITION 1M0267B23R Mouse 10kb plasmid UUGCIM library Mus musculus genomic

clone UUGCIM0267B23 R, genomic survey sequence.

ACCESSION AZ461824

KEYWORDS AZ461824.1 GI:10619949

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0267 row: B column: 23

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="CS7BL/6J"

```

/db_xref="taxon:10090"
/clone="UUGC1M0267B23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1390
AZ493766
LOCUS      21 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION      1M0328C11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0328C11 R, genomic survey sequence.
ACCESSION      AZ493766
VERSION      AZ493766.1 GI:10667750
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 21)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0328 row: C column: 11
Seq primer: CACACAGAAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

FEATURES
source

```

```

/db_xref="taxon:10090"
/clone="UUGC1M0328C11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2727
      |||||||
Db 2 TAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1391
DX056270/c
LOCUS      21 bp      DNA      linear      GSS 10-JAN-2006
DEFINITION      KBrB061B22F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB061B22, genomic survey
sequence.
ACCESSION      DX056270
VERSION      DX056270.1 GI:84750567
KEYWORDS      GSS.
SOURCE      Brassica rapa subsp. pekinensis
ORGANISM      Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 21)
AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE      End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pheom@da.go.kr
BAC end sequence of Brassica rapa sep. pekinensis BamHI BAC clone
KBrB061B22
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..21
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB061B22"

FEATURES
source

```

/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1392

DX081159 21 bp DNA linear GSS 10-JAN-2006
LOCUS KBrB093P23R KBrB, Brassica rapa BamHI BAC library Brassica rapa
DEFINITION subsp. pekinensis genomic clone KBrB093P23, genomic survey
sequence.

ACCESSION DX081159
VERSION DX081159.1 GI:84775455
KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eutrosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 21)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.

TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone

JOURNAL

COMMENT Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672

Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB093P23

Seq primer: M13 Reverse
Class: BAC ends.

Location/Qualifiers

FEATURES

1..21
source
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB093P23"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 2 TAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1393

CF310486 22 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--05-C16.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION

library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-C16, mRNA sequence.
ACCESSION CF310486
VERSION CF310486.1 GI:33682247
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..22
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF-05-C16"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"

/note="Vector: pCR4-TOPO. Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.7%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 3 TAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1394

DR073660 22 bp mRNA linear EST 08-JUN-2005
LOCUS ik82h05.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
DEFINITION sequence.

ACCESSION DR073660

VERSION DR073660.1 GI:67051563

KEYWORDS EST.

SOURCE Ginkgo biloba (maidenhair tree)

ORGANISM

Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

REFERENCE

1 (bases 1 to 22)
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martensen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)

JOURNAL

COMMENT Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874

Email: mcombie@cshl.org
Original 3 prime EST has been reverse completed to be in 5 prime direction
Seq primer: -21M13UnivRev.

FEATURES

Location/Qualifiers
1. .22
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."

Query Match 0.7%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2727
|||||
DB 3 TAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1395

AL587621/c 23 bp mRNA linear EST 02-MAR-2001
LOCUS BP Chicken Brain Library Gallus gallus cDNA clone
DEFINITION ROS059H07, mRNA sequence.

ACCESSION AL587621.1 GI:13192655

VERSION EST.

KEYWORDS Gallus gallus (chicken)

SOURCE Gallus gallus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

1 (bases 1 to 23)

REFERENCE

Murray, F.

BP Chicken Brain Library

Unpublished (2001)

Contact: Frazer Murray

Dept. Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UK

Tel: +44 (0)131 527 4200

Fax: +44 (0)131 440 0434

Email: frazer.murray@bbrc.ac.uk

CGGCGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech

(*6854-

Seq primer: M13P.

FEATURES

Location/Qualifiers
1. .23
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059H07"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPori1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGCGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech (*6854-1)"

Query Match 0.7%; Score 20; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729

Db 23 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1396

AZ315640

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0033 row: 0 column: 04

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. .23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0033004"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 [gi|4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728


```

Db      4 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1397
AZ621676
LOCUS   AZ621676
DEFINITION 23 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0455J07 F, genomic survey sequence.
ACCESSION AZ621676
VERSION   AZ621676.1 GI:11743962
KEYWORDS  GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE    Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL  Unpublished (2000)
COMMENT  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0455 row: J column: 07
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0455J07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

```

```

Db      1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1398
AZ817623
LOCUS   AZ817623
DEFINITION 23 bp DNA linear GSS 20-FEB-2001
clone UUGC2M0087N09 F, genomic survey sequence.
ACCESSION AZ817623
VERSION   AZ817623.1 GI:12987531
KEYWORDS  GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE    Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL  Unpublished (2000)
COMMENT  Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0087 row: N column: 09
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0087N09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

```

```

Db      1  AAAAAAAAAAAAAAAAAAAAAA 20
|||||
|||||

RESULT 1399
DX064291/c
LOCUS   DX064291 23 bp DNA linear GSS 10-JAN-2006
DEFINITION
subsp. pекinensis genomic clone KBrB071L16, genomic survey
sequence.
ACCESSION
VERSION  DX064291.1 GI:84758587
KEYWORDS
SOURCE    GSS.
ORGANISM  Brassica rapa subsp. pекinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 23)
AUTHORS   Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE     End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL   Unpublished (2005)
COMMENT   Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbecm@da.go.kr
BAC end sequence of Brassica rapa ssp. pекinensis BamHI BAC clone
KBrB071L16
Seq primer: T7
Class: BAC ends.

FEATURES             Location/Qualifiers
     source           1..23
     /organism="Brassica rapa subsp. pекinensis"
     /mol_type="genomic DNA"
     /cultivar="Chifu"
     /sub_species="pекinensis"
     /db_xref="taxon:51351"
     /clone="KBrB071L16"
     /lab_host="E.coli DH10B"
     /clone_lib="KBrB, Brassica rapa BamHI BAC library"
     /note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pекinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
```

Query Match 0.7%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      2709  AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
|||||

RESULT 1400
AJ668301/c
LOCUS   AJ668301 24 bp mRNA linear EST 28-JUN-2004
DEFINITION
sequence.
ACCESSION
VERSION  AJ668301.1 GI:49352752
KEYWORDS
SOURCE    EST.
ORGANISM  Sus scrofa (pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1 (bases 1 to 24)
AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
```

Query Match 0.7%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      2708  TAAAAAAAAAAAAAAAAAAAAA 2727
|||||
|||||

RESULT 1401
AJ663467
LOCUS   AJ663467 25 bp mRNA linear EST 28-JUN-2004
DEFINITION
sequence.
ACCESSION
VERSION  AJ663467.1 GI:49347590
KEYWORDS
SOURCE    Sus scrofa (pig)
ORGANISM  Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1 (bases 1 to 25)
AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE     Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL   Unpublished (2004)
COMMENT   Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
```

Query Match 0.7%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2708  TAAAAAAAAAAAAAAAAAAAAA 2727
|||||
|||||

FEATURES             Location/Qualifiers
     source           1..25
     /organism="Sus scrofa"
     /mol_type="mRNA"
     /db_xref="taxon:9823"
     /clone="C0000045_P10"
     /tissue_type="placenta"
     /clone_lib="CSEQAN09"
     /note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
```

Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

```

NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

Query Match      0.7%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1402
DX071965/c
LOCUS
DEFINITION
KBrB081N24F KBrB, Brassica rapa BamHI BAC library GSS 10-JAN-2006
subsp. pekinensis genomic clone KBrB081N24, genomic survey
sequence.
ACCESSION
DX071965.1 GI:84766261
VERSION
DX071965
SOURCE
GSS.
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 25)
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-298-1670
Fax: +82-31-298-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa esp. pekinensis BamHI BAC clone
KBrB081N24
Seq primer: T7
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1..25
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB081N24"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
```

Query Match 0.7%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 25 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 1403
BX568055/c
LOCUS
DEFINITION
BX568055 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse91f03_pic, mRNA sequence.
ACCESSION
BX568055.1 GI:33434952

```

KEYWORDS
SOURCE
Glossina morsitans morsitans
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 23)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
PUBMED
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
FEATURES
Location/Qualifiers
source
1..23
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse91f03_pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match 0.7%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAAAAAAAAAAA 2730
Db 23 TATATAAAAAAAAAAAAAAAAAA 1

RESULT 1404
CF297907/c
LOCUS
DEFINITION
CF297907
ACCESSION
CF297907
VERSION
CF297907.1 GI:33669668
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
```

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

```

FEATURES
    source
        Location/Qualifiers
            1..23
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="7LEAF-01-205"
                /tissue_type="leaf"
                /dev_stage="7 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

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Query Match      0.7%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 1405
CF314322/c
LOCUS
DEFINITION
    HD--02-M20.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA
    library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
    HD--02-M20, mRNA sequence.
ACCESSION
CF314322
VERSION
CF314322.1 GI:33686083
KEYWORDS
EST.
SOURCE
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
    clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
    1 (bases 1 to 23)
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    Large-scale Sequencing Analysis of Rice ESTs
    Unpublished (2003)
    Contact: Nahm B.H.
    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
    of Bioscience and Bioinformatics, Myongji University
    Yongin, Kyeonggi, Korea
    Tel: 82 31 330 6193
    Fax: 82 31 321 6355
    Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.
    Location/Qualifiers
        1..23
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="HD--02-M20"
            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 2 weeks"
            /lab_host="E.coli DH10B"
            /clone_lib="OshDACL1-overexpressing transgenic rice plasmid
            cDNA library (HD)"
            /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
            treated with ABA(20um) for 1hr. Oligo-capped mRNA was
            reverse transcribed and then used for PCR. mRNA was
            derived from rice Histone Deacetylase overexpression
            line."

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FEATURES
    source
        Location/Qualifiers
            1..23
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                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="HD--02-M20"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                /lab_host="E.coli DH10B"
                /clone_lib="OshDACL1-overexpressing transgenic rice plasmid
                cDNA library (HD)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
                treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                reverse transcribed and then used for PCR. mRNA was
                derived from rice Histone Deacetylase overexpression
                line."

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```

Query Match      0.7%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2703 TGTACTATAAAAAAAAAAAAAA 2725
Db 23 TGTATAAAAAAAAAAAAAAAAAA 1

```

```

RESULT 1406
CF318266/c
LOCUS
DEFINITION
    HD--08-F07.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
    library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
    HD--08-F07, mRNA sequence.
ACCESSION
CF318266
VERSION
CF318266.1 GI:33690027
KEYWORDS
EST.
SOURCE
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
    clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
    1 (bases 1 to 23)
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    Large-scale Sequencing Analysis of Rice ESTs
    Unpublished (2003)
    Contact: Nahm B.H.
    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
    of Bioscience and Bioinformatics, Myongji University
    Yongin, Kyeonggi, Korea
    Tel: 82 31 330 6193
    Fax: 82 31 321 6355
    Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.
    Location/Qualifiers
        1..23
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="HD--08-F07"
            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 2 weeks"
            /lab_host="E.coli DH10B"
            /clone_lib="OshDACL1-overexpressing transgenic rice plasmid
            cDNA library (HD)"
            /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
            treated with ABA(20um) for 1hr. Oligo-capped mRNA was
            reverse transcribed and then used for PCR. mRNA was
            derived from rice Histone Deacetylase overexpression
            line."

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```

FEATURES
    source
        Location/Qualifiers
            1..23
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                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="HD--08-F07"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                /lab_host="E.coli DH10B"
                /clone_lib="OshDACL1-overexpressing transgenic rice plasmid
                cDNA library (HD)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
                treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                reverse transcribed and then used for PCR. mRNA was
                derived from rice Histone Deacetylase overexpression
                line."

```

```

Query Match      0.7%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

```

```

RESULT 1407
AW334124/c
LOCUS
DEFINITION
    S30G5 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION
AW334124
VERSION
AW334124.1 GI:6830481
KEYWORDS
EST.
SOURCE
    Pneumocystis carinii
    Pneumocystis carinii
    Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
    Pneumocystidaceae; Pneumocystis.
REFERENCE
    1 (bases 1 to 23)
    Smilian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
    Edman,J.C., Kovacs,J. and Cushion,M.
    Expressed sequence tags from Pneumocystis carinii

```

JOURNAL
COMMENT

Unpublished (2000)
Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.
Location/Qualifiers

FEATURES
source

1. .23
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.7%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAACCAA 1

RESULT 1408

AZ447220
LOCUS
IM0244E15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0244E15 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0244 row: E column: 15

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

FEATURES

source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0244E15"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1:4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAATAAAAAAAAAAAAA 23

RESULT 1409

AZ662734
LOCUS
IM0542D04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0542D04 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0542 row: D column: 04

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

FEATURES

source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0542D04"


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/clone_lib="566 (synonym: hfkd2)"
/notes="vector: pAMPl; Site_1: NotI; Site_2: SalI"

Query Match
Best Local Similarity 0.7%; Score 19.4; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 TCAAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1413
BX548564/c
LOCUS
DEFINITION
BX548564 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse101g03_plc, mRNA sequence.
ACCESSION
BX548564
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 21)
Lehane, M.J., Aksoy, S., Gibson, M., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
JOURNAL
PUBMED
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
source
Location/Qualifiers
1..21
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/db_xref="taxon:37546"
/clone="Tse101g03_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match
Best Local Similarity 0.7%; Score 19.4; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db 21 AAAAAAAAAAAAAAAAAAGAAAAA 1

RESULT 1414
CF276747/c
LOCUS
DEFINITION
CF276747 21 bp mRNA linear EST 14-AUG-2003
14ETL--02-A06.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--02-A06,
mRNA sequence.

/clone_lib="566 (synonym: hfkd2)"
/notes="vector: pAMPl; Site_1: NotI; Site_2: SalI"

Query Match
Best Local Similarity 0.7%; Score 19.4; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAA 2726
Db 21 ACCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1415
CF296213/c
LOCUS
DEFINITION
CF296213 21 bp mRNA linear EST 14-AUG-2003
30DGS--06-H19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--06-H19, mRNA
sequence.
ACCESSION
CF296213
VERSION
CF296213.1 GI:33665246
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--02-A06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: ECORI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 0.7%; Score 19.4; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAA 2726
Db 21 ACCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1415
CF296213/c
LOCUS
DEFINITION
CF296213 21 bp mRNA linear EST 14-AUG-2003
30DGS--06-H19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--06-H19, mRNA
sequence.
ACCESSION
CF296213
VERSION
CF296213.1 GI:33665246
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..21
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/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="14ETL--02-A06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: ECORI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS-06-H19"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match
Best Local Similarity 0.7%; Score 19.4; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
| | | | | | | | | | | | | | | | | | | | |
Db 21 AAAAAAAAAACAAAAAAAAAAAA 1

RESULT 1416
CF302218/c
LOCUS
DEFINITION
7LEAF--07-117.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-117, mRNA
sequence.
ACCESSION
CF302218.1 GI:33673979
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 21)
REFERENCE
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-02-L11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
created with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match
Best Local Similarity 0.7%; Score 19.4; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
| | | | | | | | | | | | | | | | | | | | |
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1418
DR073305/c
LOCUS
DEFINITION
ik77a11.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION
DR073305.1 GI:67051167
KEYWORDS
SOURCE
Ginkgo biloba (maidenhair tree)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 21)
REFERENCE
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory

```

```

CF314260/c
LOCUS
DEFINITION
HD--02-L11.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--02-L11, mRNA sequence.
ACCESSION
CF314260
VERSION
CF314260.1 GI:33686021
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 21)
REFERENCE
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-02-L11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
created with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match
Best Local Similarity 0.7%; Score 19.4; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
| | | | | | | | | | | | | | | | | | | | |
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1418
DR073305/c
LOCUS
DEFINITION
ik77a11.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION
DR073305.1 GI:67051167
KEYWORDS
SOURCE
Ginkgo biloba (maidenhair tree)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 21)
REFERENCE
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory

```

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mconbie@cshl.org

Original 3 prime EST has been reverse completed to be in 5 prime

direction

Seq primer: -21M13UnivRev.

Location/Qualifiers

1. .21

/organism="Ginkgo biloba"

/mol_type="mRNA"

/db_xref="taxon:3311"

/sex="female"

/clone_lib="Ginkgo female leaf (NYBG)"

/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;

Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.

The library was size-fractionated to enrich for large

inserts."

Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2728

Db 1 TCAAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1419

AZ317208/C

LOCUS

DEFINITION AZ317208 21 bp DNA linear GSS 29-SEP-2000

clone UUGC1M0035J02 R, genomic survey sequence.

ACCESSION AZ317208

VERSION AZ317208.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Muridae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0035 row: J column: 02

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0035J02"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729

Db 21 AAAAAAGAAAAAAAAAAAAAAAAA 1

RESULT 1420

AZ486776/C

LOCUS

DEFINITION AZ486776 21 bp DNA linear GSS 05-OCT-2000

clone UUGC1M0315M10 F, genomic survey sequence.

ACCESSION AZ486776

VERSION AZ486776.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Muridae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0315 row: M column: 10

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0315M10"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19.4; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 ||||| ||||| ||||| ||||| |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1421
 AZ792613/c
 LOCUS 2M0045M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0045M12 F, genomic survey sequence.

ACCESSION AZ792613
 VERSION AZ792613.1 GI:12936725
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0045 row: M column: 12
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends

High quality sequence stop: 21.
 Location/Qualifiers

FEATURES
 source
 1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0045M12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19.4; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2706 ACTAAAAAAAAAAAAAAAAAAAAA 2726
 ||||| ||||| ||||| ||||| |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1422
 AZ822825

LOCUS 2M0096I20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0096I20 F, genomic survey sequence.

ACCESSION AZ822825
 VERSION AZ822825.1 GI:12992733
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0096 row: 1 column: 20
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends

High quality sequence stop: 21.
 Location/Qualifiers

FEATURES
 source
 1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0096I20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732141|gb|AF129072.1|, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match      0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY	2709	AAAAAAAAAAAAAAAAAAAA	2729
DB	1	AAAAAAAAAAAAAAAAAAAA	21

RESULT 1424
CL693165
LOCUS
CL693165 21 bp DNA linear GSS 10-JUL-2004
DEFINITION
PRI0160a.G10.2 - PRI0160a.BR (21) Note: Recurring String Mixed
stage fosmid library of *P. pacificus* var. *California* Pristionchus
pacificus genomic, genomic survey sequence.

Accession number, genome survey sequence.

ACCESSION	CL693165	
VERSION	CL693165.1	GI:50215073
KEYWORDS	GSS.	
SOURCE	<i>Pristionchus pacificus</i>	
ORGANISM	<i>Pristionchus pacificus</i>	
	Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.	
REFERENCE	1 (bases 1 to 21)	
AUTHORS	Srinivasan,J., Otto,G.W., Kahlow,U., Geiseler,R. and Sommer,R.J.	
TITLE	APRABD: an AcedB database for the nematode satellite organism <i>Pristionchus pacificus</i>	
JOURNAL	Nucleic Acids Res. 32 (1), D421-D422 (2004)	
PUBMED	14681447	
COMMENT	Contact: Sommer RJ	

Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: raif.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seg primer: T7
Class: fosmid ends.

```

Query Match          0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

2709 AAAAAAAAAAAAAAAAAAAAAA 2729

```


Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2728
Db 22 TATAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1428
CL693160
LOCUS
DEFINITION
CL693160 22 bp DNA linear GSS 10-JUL-2004
PRI0160a.F09.2 - PRI0160a.BR (22) Note: Recurring String Mixed
stage fosmid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 22)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source
1..22
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

Query Match 0.7%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1429
AJ666332/c
LOCUS
DEFINITION
AJ666332 CSEQAN09 Sus scrofa cDNA clone C0000033_H19, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 23)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and

embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1;
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
source
1..23
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_H19"
/tissue_type="placenta"
/clone_lib="CSEQAN09"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

Query Match 0.7%; Score 19.4; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAAAAAA 2727
Db 21 CCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1430
AL048745
LOCUS
DEFINITION
AL048745 23 bp mRNA linear EST 04-SBP-2003
DKFZp566K213_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AL048745.1 GI:4727816
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo;
1 (bases 1 to 23)
Koehler,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehler, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..23
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566K213"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site 1: NotI; Site 2: SalI"

Query Match 0.7%; Score 19.4; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2728
Db 3 TCAAAAAAAAAAAAAAAAAAAAAA 23

```

RESULT 1431
CF333801/c
LOCUS
DEFINITION
JMT--02-N11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-N11, mRNA sequence.
CF333801
CF333801.1 GI:33815910
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--02-N11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.7%; Score 19.4; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2728
DB 22 TAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1432
AM043222
LOCUS
DEFINITION
AM043222 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC13h07.g1k, mRNA sequence.
ACCESSION
AM043222
VERSION
AM043222.1 GI:75970086
KEYWORDS
EST.
SOURCE
Schistosoma mansoni
ORGANISM
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeida; Schistosomatidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 24)
Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
Contact: Ivens AC

FEATURES
source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0005124"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

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Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
1..24
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC13h07.g1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="country: Puerto Rico"

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2701 TTTTCTACTAAAAAAAAAAAAAAAAA 2724
DB 1 TTTTCTACTAAAAAAAAAAAAAAAAA 24

RESULT 1433
AZ304870/c
LOCUS
DEFINITION
AZ304870 Mouse 10kb plasmid UGC1M library Mus musculus genomic
clone UGC1M0005124 F, genomic survey sequence.
ACCESSION
AZ304870
VERSION
AZ304870.1 GI:10341320
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Iellam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0005 row: I column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0005124"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 693 ATGAAGAAGCAGAGGAGAGACAG 716

Db 24 AAGAAGAAGTAGAGGAAGAAGAAG 1

RESULT 1434

AZ309553
LOCUS
DEFINITION
1M0016B10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0016B10 F, genomic survey sequence.

ACCESSION
AZ309553

VERSION
AZ309553.1

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0016 row: B column: 10

Seq primer: CGTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

FEATURES

Location/Qualifiers

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0016B10"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male); was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2703 TGTACTAAAAA 2726

Db 1 TTTTAAAAA 24

RESULT 1435

AZ448207

LOCUS

DEFINITION
1M0245E16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0245E16 R, genomic survey sequence.

ACCESSION
AZ448207

VERSION
AZ448207.1

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0245 row: E column: 16

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 24.

FEATURES

Location/Qualifiers

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0245E16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male); was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.7%;	Score 19.2;	DB 1;	Length 24;
Best Local Similarity	87.5%;	Pred. No. 1.3e+03;		
Matches	21;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
Qy	2709	AAAAAAAAAAAAAAAAAAAAA	2732	
Db	24	AAAAAAAAAGAAAGAAAAAAGAA	1	

RESULT 1437	
CL676551/c	
LOCUS	24 bp DNA linear GSS 09-JUL-2004
DEFINITION	PRI0118d.H07.2 - PRI0118d.BR (24) Mixed stage foetid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION	CL676551
VERSION	CL676551.1
KEYWORDS	GI:50182197
SOURCE	GSS.
ORGANISM	Pristionchus pacificus
REFERENCE	Pristionchus pacificus
AUTHORS	Pristionchus pacificus
TITLE	Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
JOURNAL	1 (bases 1 to 24)
PUBLISHED	Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J. Appabid: an Acedb database for the nematode satelite organism Pristionchus pacificus
COMMENT	Nucleic Acids Res. 32 (1), D421-D422 (2004) 14681447 Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371 Fax: 00497071601498 Email: ralf.sommer@tuebingen.mpg.de This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.

```

Class: Fosmid ends.
Location/Qualifiers
1. .24
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

Query Match          0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
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Db 24 AAAAAAAAAAAAAAAAAAGCAAAA 1

RESULT 1438
AJ668179/c

```

```

LOCUS      AJ668179          19 bp      mRNA      linear      EST 28-JUN-2004
DEFINITION AJ668179 CSEQRAN09 Sus scrofa cDNA clone C0000045_L19, mRNA
sequence.
ACCESSION  AJ668179
VERSION     AJ668179.1  GI:49352630
KEYWORDS   EST.
SOURCE     Sus scrofa (pig)
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
            1 (bases 1 to 19)
REFERENCE  Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
AUTHORS    Development of cDNA and EST resources for studying reproduction and
TITLE      embryo development in pigs and cattle
JOURNAL    Unpublished (2004)
COMMENT    Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross match with the -minscore 20
            and -mismatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
            EcoRI R. Site 2: NotI Description: Normalised library constructed
            from pooled tissue from day 30 placentas. Clones available from UK
            Centre for Functional Genomics in Farm Animals, Roslin Institute,
            Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES   Location/Qualifiers
            1..19
            /organism="Sus scrofa"
            /mol_type="mRNA"
            /db_xref="taxon:9823"
            /clone="C0000045_L19"
            /tissue_type="placenta"
            /clone_lib="CSEQRAN09"
            /note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2:
            NotI; Single pass sequencing. Normalised library
            constructed from pooled tissue from day 30 placentas."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db   19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1439
LOCUS      AJ669138          19 bp      mRNA      linear      EST 28-JUN-2004
DEFINITION AJ669138 CSEQRAN09 Sus scrofa cDNA clone C0000048_O12, mRNA
sequence.
ACCESSION  AJ669138
VERSION     AJ669138.1  GI:49353592
KEYWORDS   EST.
SOURCE     Sus scrofa (pig)
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
            1 (bases 1 to 19)
REFERENCE  Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
AUTHORS    Development of cDNA and EST resources for studying reproduction and
TITLE      embryo development in pigs and cattle
JOURNAL    Unpublished (2004)
COMMENT    Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -mismatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:

```

```

EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES   Location/Qualifiers
            1..19
            /organism="Sus scrofa"
            /mol_type="mRNA"
            /db_xref="taxon:9823"
            /clone="C0000048_O12"
            /tissue_type="placenta"
            /clone_lib="CSEQRAN09"
            /note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2:
            NotI; Single pass sequencing. Normalised library
            constructed from pooled tissue from day 30 placentas."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db   19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1440
LOCUS      BQ588729          19 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION S013713-024-014-B24-T7 MP12-ADIS-024-storage root Beta vulgaris
CDNA Clone 024-014-B24 3-PRIME, mRNA sequence.
ACCESSION  BQ588729
VERSION     BQ588729.1  GI:26118312
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Amaranthaceae; Beta.
            1 (bases 1 to 19)
REFERENCE  Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
AUTHORS    Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.,
            Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
            12472698
            Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weissshaar@mpiz-koeln.mpg.de
            Insert Length: 19 Std Error: 0.00
            Plate: 14 row: B column: 24
            Seq primer: T7; GTAATACGACTCACTATAGGGC.

FEATURES   Location/Qualifiers
            1..19
            /organism="Beta vulgaris"
            /mol_type="mRNA"
            /cultivar="KWS2320 (double haploid, monogerm breeding
            line)"
            /db_xref="GABI:187281"
            /db_xref="taxon:161934"
            /clone="024-014-B24"
            /tissue_type="storage root"
            /lab_host="EMDH108"
            /clone_lib="MP12-ADIS-024-storage root"
            /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzaucht AG Binbeck, Germany, contact:
            b.schul@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

```

Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1441

CB174047/c

LOCUS

DEFINITION OR 2032F05 010529_Y1 Adult mouse olfactory epithelium library Mus

musculus cDNA clone 2032F05 5', mRNA sequence.

ACCESSION CB174047

VERSION CB174047.1

SOURCE GI:37592676

KEYWORDS EST.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sclurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Young, J.M., Shykind, B.M., Lane, R.P., Tonnes-Priiddy, L., Ross, J.A.,

Walker, M., Williams, E.M. and Trask, B.J.

TITLE Odorant receptor expressed sequence tags demonstrate olfactory

expression of over 400 genes, extensive alternate splicing and

unequal expression levels

Genome Biol. 4 (11), R71.1-R71.15 (2003)

CONTACT: Young JM

Trask Lab, Division of Human Biology

Fred Hutchinson Cancer Research Center

1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA

98109-1024, USA

Tel: 206 667 1471

Fax: 206 667 6524

Email: jayoung@fhcrc.org

Seq primer: M33 Reverse

Location/Qualifiers

i..19

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="2032F05"

/tissue_type="olfactory and respiratory epithelium"

/dev_stage="Adult"

/clone_lib="Adult mouse olfactory epithelium library"

/note="Organ: Olfactory turbinates; Vector:

LambdaZAPII-XR; Site 1: EcoRI; Site 2: XhoI; This library

was provided by Leslie Vossall. mRNA was prepared from

the olfactory and respiratory epithelium of an adult

mouse. Oligo-dT primed cDNA was directionally cloned into

Stratagene's lambdaZAPII-XR vector."

Query Match 0.7%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1442

CF279008/c

LOCUS

DEFINITION 14ETL--05-C13.b1 Rice etiolated leaf plasmid cDNA library (14ETL)

Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-C13,

EST 14-AUG-2003

Query Match 0.7%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 1

mRNA sequence.

ACCESSION CF279008

VERSION CF279008.1

KEYWORDS GI:33656394

SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

i..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ETL--05-C13"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH108"

/clone_lib="Rice etiolated leaf plasmid cDNA library

(14ETL)"

/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.7%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727

|||||

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1443

CF291089/c

LOCUS

DEFINITION 14ROOT--01-G03.b1 Rice root plasmid cDNA library (14ROOT) Oryza

sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G03, mRNA

sequence.

ACCESSION CF291089

VERSION CF291089.1

KEYWORDS GI:33660122

SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

i..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ETL--05-C13"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH108"

/clone_lib="Rice etiolated leaf plasmid cDNA library

(14ETL)"

/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

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source      1. .19
/organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nackdong"
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1444
CF291090
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G03, mRNA
sequence.
CF291090.1 GI:33660123
EST.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .19
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RT-PCR."

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1444
CF291090
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G03, mRNA
sequence.
CF291090.1 GI:33660123
EST.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 1445
CF299598/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K23, mRNA
sequence.
CF299598.1 GI:33671359
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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FEATURES
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1446
CF302327/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-L24, mRNA
sequence.
CF302327.1 GI:33674088
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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```

```

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. 19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stages="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1447
CF304589/c
LOCUS
DEFINITION
ABF1--05-G10.g1 ABF3-overexpressing transgenic rice lambda phage
CDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA
clone ABF1--05-G10, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. 19
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/lab_host="E.coli SOLR"
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phage cDNA library (ABF1)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match
0.7%; Score 19; DB 1; Length 19;

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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1448
CF309801/c
LOCUS
DEFINITION
ABF--04-C04.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--04-C04, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
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/organism="Oryza sativa (japonica cultivar-group)"
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cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1449
CF309943
LOCUS
DEFINITION
ABF--04-F15.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--04-F15, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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REFERENCE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS	1. (bases 1 to 19) Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Gyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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FEATURES
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cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1450
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LOCUS
DEFINITION
CF311496 19 bp mRNA linear EST 15-AUG-2003
ABF-06-L18.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF-06-L18, Oryza sativa (japonica cultivar-group) cDNA clone
ABF-06-L18, Oryza sativa (japonica cultivar-group) cDNA clone
CF311496.1 GI:33683257
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1. (bases 1 to 19)
Kim, J.-S., Jun, K.-M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B. H.
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Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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source
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"

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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2727
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Db       19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1451
CF311513/c
LOCUS
DEFINITION
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library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-M03, mRNA sequence.
CF311513
CF311513.1 GI:33683274
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B. H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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FEATURES

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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
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Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

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RESULT 1452
CF312403
LOCUS
DEFINITION
ABF--08-C07.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--08-C07, mRNA sequence.
ACCESSION
CF312403
VERSION
CF312403.1 GI:33684164
SOURCE
EST.
ORGYZA sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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cDNA library (ABF)"
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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19
RESULT 1453
CF315299
LOCUS
DEFINITION
HD--04-C17.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--04-C17, mRNA sequence.
ACCESSION
CF315299
VERSION
CF315299.1 GI:33687060
SOURCE
EST.
ORGYZA sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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cDNA library (ABF)"
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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

```

```

COMMENT
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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cDNA library (HD)"
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 1454
CF316480
LOCUS
DEFINITION
HD--05-M14.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-M14, mRNA sequence.
ACCESSION
CF316480
VERSION
CF316480.1 GI:33688241
SOURCE
EST.
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was

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Query Match 0.7%; Score 19; DB 1; Length 19;
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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
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 Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1455
 CF318788
 LOCUS
 DEFINITION HD--09-A23.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
 VERSION CF318788.1 GI:33690549
 SOURCE
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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 /clone="NACL--05-109"
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 /lab_host="E.coli DH10B"
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 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
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 Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1457
 CF332063/c
 LOCUS
 DEFINITION NACL--08-G19.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-G19, mRNA sequence.

ACCESSION
 VERSION CF332063.1 GI:33812347
 SOURCE
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Query Match 0.7%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1456
 CF329986
 LOCUS
 DEFINITION NACL--05-109.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-109, mRNA sequence.

CF329986
 CF329986.1 GI:33808194
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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Query Match 0.7%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1457
 CF332063/c
 LOCUS
 DEFINITION NACL--08-G19.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-G19, mRNA sequence.

ACCESSION
 VERSION CF332063.1 GI:33812347
 SOURCE
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
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 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..19
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db    19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1458
CF333507
LOCUS     CF333507             19 bp      mRNA          linear      EST 18-AUG-2003
DEFINITION JMT--02-G23.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
WMT--02-G23, mRNA sequence.
CF333507
ACCESSION CF333507.1 GI:33815309
VERSION   CF333507.1
KEYWORDS  Oryza sativa (japonica cultivar-group)
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT   Nahm B.H.
GENOMICS  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/tissue_type="leaf"
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/lab_host="E.coli DH10B"
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cDNA library (JMT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

FEATURES             source
source
Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db    1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1460
CF334014/c
LOCUS     CF334014/c         19 bp      mRNA          linear      EST 18-AUG-2003
DEFINITION JMT--03-C09.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
WMT--03-C09, mRNA sequence.
CF334014
ACCESSION CF334014.1 GI:33816333
VERSION   CF334014.1
KEYWORDS  Oryza sativa (japonica cultivar-group)
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT   Nahm B.H.
GENOMICS  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/lab_host="E.coli DH10B"
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cDNA library (JMT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db    1 AAAAAAAAAAAAAAAAAAAAAA 19

```

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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methyltransferase overexpression line."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1461

CN545602/c
LOCUS
DEFINITION
EST 17546 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL003H10 3', mRNA sequence.

ACCESSION
CN545602
VERSION
CN545602.1 GI:46910227
KEYWORDS
EST.
SOURCE
Vitis vinifera
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

REFERENCE
AUTHORS
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)

TITLE
JOURNAL
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
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Db 19 AAAAAAAAAAAAAAAAAA 1

FEATURES

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/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1462

CN545922/c
LOCUS
DEFINITION
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clone B3CS00RL006D07 3', mRNA sequence.

ACCESSION
CN545922
VERSION
CN545922.1 GI:46910547
KEYWORDS
EST.
SOURCE
Vitis vinifera
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

REFERENCE
AUTHORS
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)

TITLE
JOURNAL
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
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Db 19 AAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 19; DB 1; Length 19;
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QY 2709 AAAAAAAAAAAAAAAAAA 2727
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Db 19 AAAAAAAAAAAAAAAAAA 1

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
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Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1463

CN545964/c
LOCUS
DEFINITION
EST 17912 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL006H10 3', mRNA sequence.

ACCESSION
CN545964
VERSION
CN545964.1 GI:46910589
KEYWORDS
EST.
SOURCE
Vitis vinifera
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
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Db 19 AAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE 1 (bases 1 to 19)
 AUTHORS Abbal, P., Agase, A., Ageorges, A., Atanasova, R., Barrieu, F.,
 Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
 Hamdi, S., Romieu, C. and Terrier, N.
 TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 JOURNAL Unpublished (2002)
 COMMENT Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES
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 SfiIA; Site_2: SfiIB; Oriented library"

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 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
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 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1464
 CN546303/c
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 DEFINITION cDNA clone B3CS1XGB015E10 3', mRNA sequence.
 CN546303
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Vitis vinifera
 Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Abbal, P., Agase, A., Ageorges, A., Atanasova, R., Barrieu, F.,
 Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
 Hamdi, S., Romieu, C. and Terrier, N.
 TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 JOURNAL Unpublished (2002)
 COMMENT Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES
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 /clone="B3CS1XGB015E10"
 /dev_stage="green stage"
 /clone_lib="Green Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda
 Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.7%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1465
 CX003880
 LOCUS EST 19 bp mRNA linear EST 03-DEC-2004
 DEFINITION iv25a12.bl Brain - Cerebellum Library (DOGE8T8) Canis familiaris
 CDNA, mRNA sequence.
 ACCESSION CX003880
 VERSION CX003880.1 GI:56275296
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Balijs, V., Nascimento, L.U. and McCombie, W.R.
 TITLE ESTs from Canis familiaris cerebellum (dog)
 JOURNAL Unpublished (2004)
 COMMENT Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org.

FEATURES
 source
 1..19
 Location/Qualifiers
 /organism="Canis familiaris"
 /mol_type="mrna"
 /db_xref="taxon:9615"
 /sex="Unknown"
 /tissue_type="Cerebellum"
 /dev_stage="3 month old normal canine"
 /lab_host="XL10 Gold"
 /clone_lib="Brain - Cerebellum Library (DOGE8T8)"
 /note="Organ: Brain; Vector: pBluescript II SK; Site_1:
 EcoRI; Site_2: XhoI; Library constructed using pBluescript
 XR kit from Stratagene. Cloned cDNA was size selected
 between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
 Medical Genetics, School of Veterinary Medicine,
 University of Pennsylvania, 3800 Spruce Street,
 Philadelphia, PA 19104-6051"

Query Match 0.7%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1466
 CX007355/c
 LOCUS EST 19 bp mRNA linear EST 06-DEC-2004
 DEFINITION io27h10.g1 Whole Heart Library (DOGE8T5) Canis familiaris cDNA,
 mRNA sequence.
 ACCESSION CX007355

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VERSION      CX007355.1  GI:56389584
KEYWORDS     EST.
SOURCE       Canis familiaris (dog)
ORGANISM     Canis familiaris
              Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
              Canis.
REFERENCE    1 (bases 1 to 19)
AUTHORS      Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE        ESTs from Canis familiaris whole heart (dog)
JOURNAL      Unpublished (2004)
COMMENT      Contact: W. Richard McCombie
              Lita Annenberg Hazen Genome Sequencing Center
              Cold Spring Harbor Laboratory
              PO Box 100, Cold Spring Harbor, NY 11724, USA
              Tel: 516 367 8884
              Fax: 516 367 8874
              Email: mccombie@cshl.org.
FEATURES     Location/Qualifiers
              source
                1..19
                /organism="Canis familiaris"
                /mol_type="mRNA"
                /db_xref="taxon:9615"
                /sex="Unknown"
                /dev_stage="3 month old normal canine"
                /lab_hosts="XL10 Gold"
                /clone_lib="Whole Heart Library (DOGESTS)"
                /note="Organ: Heart; Vector: pBluescript II SK; Site 1:
                EcoRI; Site 2: XhoI; Library constructed using pBluescript
                XR kit from Stratagene. Cloned cDNA was size selected
                between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
                Medical Genetics, School of Veterinary Medicine,
                University of Pennsylvania, 3800 Spruce Street,
                Philadelphia, PA 19104-6051"
Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1467
DN954273/c
LOCUS      it71a04.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
DEFINITION
ACCESSION  DN954273
VERSION     DN954273.1  GI:63026411
KEYWORDS    EST.
SOURCE      Gnetum gnemon
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
              1 (bases 1 to 19)
REFERENCE    Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
              O'Shaughnessy,A.L., Ballia,V., Martienssen,R.A., McCombie,R.W.,
              Benfey,P., Coruzzi,G. and Stevenson,D.
              Expressed tag sequences from Gnetum female cone (NYBG)
              Unpublished (2003)
              Contact: W. Richard McCombie
              Lita Annenberg Hazen Genome Sequencing Center
              Cold Spring Harbor Laboratory
              PO Box 100, Cold Spring Harbor, NY 11724, USA
              Tel: 516 367 8884
              Fax: 516 367 8874
              Email: mccombie@cshl.org
              Seq primer: -21M13UnivRev.
              Location/Qualifiers
                1..19
                /organism="Gnetum gnemon"
                /mol_type="mRNA"
                /db_xref="taxon:3382"
                /sex="female"
                /clone_lib="Gnetum female cone (NYBG)"
                /note="Organ: mature, unfertilized reproductive strobili;
                Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
                Completed 02/11/02, submitted for sequencing 02/12/02.
                Library: Stratagene ZAP Express cDNA Synthesis Kit. The
                library was size-fractionated to enrich for large inserts.
                Sample: NYBG accession number #436/84"
Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1469
DN955630
LOCUS      it91f11.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
DEFINITION

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/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
/note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"
Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1468
DN955154/c
LOCUS      it82g11.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
DEFINITION
ACCESSION  DN955154
VERSION     DN955154.1  GI:63027292
KEYWORDS    EST.
SOURCE      Gnetum gnemon
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
              1 (bases 1 to 19)
REFERENCE    Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
              O'Shaughnessy,A.L., Ballia,V., Martienssen,R.A., McCombie,R.W.,
              Benfey,P., Coruzzi,G. and Stevenson,D.
              Expressed tag sequences from Gnetum female cone (NYBG)
              Unpublished (2003)
              Contact: W. Richard McCombie
              Lita Annenberg Hazen Genome Sequencing Center
              Cold Spring Harbor Laboratory
              PO Box 100, Cold Spring Harbor, NY 11724, USA
              Tel: 516 367 8884
              Fax: 516 367 8874
              Email: mccombie@cshl.org
              Seq primer: -21M13UnivRev.
              Location/Qualifiers
                1..19
                /organism="Gnetum gnemon"
                /mol_type="mRNA"
                /db_xref="taxon:3382"
                /sex="female"
                /clone_lib="Gnetum female cone (NYBG)"
                /note="Organ: mature, unfertilized reproductive strobili;
                Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
                Completed 02/11/02, submitted for sequencing 02/12/02.
                Library: Stratagene ZAP Express cDNA Synthesis Kit. The
                library was size-fractionated to enrich for large inserts.
                Sample: NYBG accession number #436/84"
Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1469
DN955630
LOCUS      it91f11.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
DEFINITION

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sequence.
ACCESSION DN955630
VERSION DN955630.1 GI:63027768
KEYWORDS EST.
SOURCE Gnetum gnemon
ORGANISM Gnetum gnemon
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Gnetophyta; Gnetales; Gnetales; Gnetales; Gnetum.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
/vector="Org: mature, unfertilized reproductive strobili;
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1470
LOCUS DR062165 19 bp mRNA linear EST 06-JUN-2005
DEFINITION iq09e02.g1 Cycas sporophyll (w/o ovule) (NYBG) Cycas rumphii cDNA
ACCESSION DR062165
VERSION DR062165.1 GI:66985731
KEYWORDS EST.
SOURCE Cycas rumphii
ORGANISM Cycas rumphii
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Cycadophyta; Cycadales; Cycadales; Cycas.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Cycas ovules (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Cycas rumphii"
/mol_type="mRNA"
/db_xref="taxon:58031"
/sex="female"
/clone_lib="Cycas ovule (NYBG)"
/vector="Org: Ovules; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1470
LOCUS DR062165 19 bp mRNA linear EST 06-JUN-2005
DEFINITION iq09e02.g1 Cycas sporophyll (w/o ovule) (NYBG) Cycas rumphii cDNA
ACCESSION DR062165
VERSION DR062165.1 GI:66985731
KEYWORDS EST.
SOURCE Cycas rumphii
ORGANISM Cycas rumphii
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Cycadophyta; Cycadales; Cycadales; Cycas.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Cycas ovules (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Cycas rumphii"
/mol_type="mRNA"
/db_xref="taxon:58031"
/sex="female"
/clone_lib="Cycas ovule (NYBG)"
/vector="Org: Ovules; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1470
LOCUS DR063459 19 bp mRNA linear EST 06-JUN-2005
DEFINITION iq24h10.g1 Cycas ovule (NYBG) Cycas rumphii cDNA 3', mRNA sequence.
ACCESSION DR063041
VERSION DR063041.1 GI:66986609
KEYWORDS EST.
SOURCE Cycas rumphii
ORGANISM Cycas rumphii
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Cycadophyta; Cycadales; Cycadales; Cycas.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Cycas ovules (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Cycas rumphii"
/mol_type="mRNA"
/db_xref="taxon:58031"
/sex="female"
/clone_lib="Cycas ovule (NYBG)"
/vector="Org: Ovules; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1470
LOCUS DR063459/c 19 bp mRNA linear EST 06-JUN-2005
DEFINITION iq24h10.g1 Cycas ovule (NYBG) Cycas rumphii cDNA 3', mRNA sequence.
ACCESSION DR063041
VERSION DR063041.1 GI:66986609
KEYWORDS EST.
SOURCE Cycas rumphii
ORGANISM Cycas rumphii
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Cycadophyta; Cycadales; Cycadales; Cycas.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Cycas ovules (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Cycas rumphii"
/mol_type="mRNA"
/db_xref="taxon:58031"
/sex="female"
/clone_lib="Cycas ovule (NYBG)"
/vector="Org: Ovules; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

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/organism="Cycas rumphii"
/mol_type="mRNA"
/db_xref="taxon:58031"
/sex="female"
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/vector="Org: Sporophyll with ovules detached.; Vector:
pBK-CMV; Site 1: Xho I; Site 2: Eco RI; Date: Completed
08/09/2002. Submitted to CSHL 08/21/2002. Sample: Young
emergent sporophyll with ovules detached (ovules used to
make a separate library). From New York Botanical Garden
Conservatory accession number 808/59 A. Collected
06/04/2002). Library: Made using Stratagene's ZAP Express
Vector Kit. Library was size fractionated for large
inserts."

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Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

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RESULT 1471
LOCUS DR063041 19 bp mRNA linear EST 06-JUN-2005
DEFINITION iq24h10.g1 Cycas ovule (NYBG) Cycas rumphii cDNA 3', mRNA sequence.
ACCESSION DR063041
VERSION DR063041.1 GI:66986609
KEYWORDS EST.
SOURCE Cycas rumphii
ORGANISM Cycas rumphii
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Cycadophyta; Cycadales; Cycadales; Cycas.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Cycas ovules (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Cycas rumphii"
/mol_type="mRNA"
/db_xref="taxon:58031"
/sex="female"
/clone_lib="Cycas ovule (NYBG)"
/vector="Org: Ovules; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

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FEATURES
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/organism="Cycas rumphii"
/mol_type="mRNA"
/db_xref="taxon:58031"
/sex="female"
/clone_lib="Cycas ovule (NYBG)"
/vector="Org: Ovules; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

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Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

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RESULT 1472
LOCUS DR063459/c 19 bp mRNA linear EST 06-JUN-2005

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```

DEFINITION ip65g04.g1 Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR063459
VERSION DR063459.1 GI:66987027
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo megasporophyll (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES             source
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    1..19
    /organism="Ginkgo biloba"
    /mol_type="mRNA"
    /db_xref="taxon:3311"
    /sex="Female"
    /clone_lib="Ginkgo megasporophyll (NYBG)"
    /note="Organ: megasporophyll; Vector: pBK-CMV, Site_1:
    XhoI; Site_2: Eco RI; Stratagene ZAP Express cDNA
    Synthesis Kit. The library was size-fractionated to enrich
    for large inserts."

Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1473
DR065256/c
LOCUS
DEFINITION ip92c10.g1 Ginkgo microsporophyll (NYBG) Ginkgo biloba cDNA 3',
mRNA sequence.
ACCESSION DR065256
VERSION DR065256.1 GI:66988824
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo microsporophyll (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES             source
    source
    1..19
    /organism="Ginkgo biloba"
    /mol_type="mRNA"
    /db_xref="taxon:3311"
    /sex="Female"
    /clone_lib="Ginkgo microsporophyll (NYBG)"
    /note="Organ: megasporophyll; Vector: pBK-CMV, Site_1:
    XhoI; Site_2: Eco RI; Stratagene ZAP Express cDNA
    Synthesis Kit. The library was size-fractionated to enrich
    for large inserts."

Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1473
DR065256/c
LOCUS
DEFINITION ip92c10.g1 Ginkgo microsporophyll (NYBG) Ginkgo biloba cDNA 3',
mRNA sequence.
ACCESSION DR065256
VERSION DR065256.1 GI:66988824
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo microsporophyll (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES             source
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    /note="Organ: megasporophyll; Vector: pBK-CMV, Site_1:
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    Synthesis Kit. The library was size-fractionated to enrich
    for large inserts."

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/mol_type="mRNA"
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Synthesis Kit. The library was size-fractionated to enrich
for large inserts."

Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1474
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LOCUS
DEFINITION ik86f08.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR073123
VERSION DR073123.1 GI:67050974
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES             source
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    /note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI;
    Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
    The library was size-fractionated to enrich for large
    inserts."

Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1475
DR074208
LOCUS
DEFINITION il53h03.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR074208
VERSION DR074208.1 GI:67052176
KEYWORDS EST.

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SOURCE
ORGANISM Ginkgo biloba (maidenhair tree)

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo. 1 (bases 1 to 19)

AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W., Benfey,P., Coruzzi,G. and Stevenson,D.

TITLE Expressed tag sequences from Ginkgo male leaf (NYBG)

JOURNAL Unpublished (2005)

COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES
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/sex="male"
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Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
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Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1476
AZ307313
LOCUS 19 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0008H20R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0008H20 R, genomic survey sequence.

ACCESSION AZ307313
VERSION AZ307313.1 GI:10346192
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: H column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
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Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1477
AZ310079/c
LOCUS 19 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0018K17R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0018K17 R, genomic survey sequence.

ACCESSION AZ310079
VERSION AZ310079.1 GI:10351709
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: K column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0018K17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
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Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1478
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LOCUS AZ310105 19 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0018E21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0018E21 R, genomic survey sequence.

ACCESSION AZ310105
VERSION AZ310105.1 GI:10351761
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: E column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
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/organism="Mus musculus"
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/clone="UUGC1M0018E21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1479
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LOCUS AZ317743 19 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0036B18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0036B18 R, genomic survey sequence.

ACCESSION AZ317743
VERSION AZ317743.1 GI:10366848
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0036 row: B column: 18
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adapted DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adapted mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

      Query Match          0.7%; Score 19; DB 1; Length 19;
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Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1480
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LOCUS
DEFINITION 1M0072H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0072H15 F, genomic survey sequence.
ACCESSION AZ340311
VERSION AZ340311.1 GI:10415441
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0072 row: H column: 15
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

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        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
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        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adapted DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adapted mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

      Query Match          0.7%; Score 19; DB 1; Length 19;
      Best Local Similarity 100.0%; Pred. No. 1.2e+03;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1480
AZ340311/c
LOCUS
DEFINITION 1M0072H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0072H15 F, genomic survey sequence.
ACCESSION AZ340311
VERSION AZ340311.1 GI:10415441
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0072 row: H column: 15
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1482
AZ364226
LOCUS
DEFINITION
1M0110B24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0110B24 F, genomic survey sequence.
ACCESSION
AZ364226
VERSION
GI:10477926
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0110 row: B column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
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Location/Qualifiers
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/organism="Mus musculus"
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1483
AZ365696
LOCUS
DEFINITION
1M0112A07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0112A07 R, genomic survey sequence.
ACCESSION
AZ365696
VERSION
GI:10479396
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0112 row: A column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1484

AZ374409
LOCUS AZ374409 19 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0127D10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0127D10 F, genomic survey sequence.
ACCESSION AZ374409
VERSION AZ374409.1 GI:10488109
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0127 row: D column: 10
Seq primer: CGTTGTAAACGACGCCGACGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0127D10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1485

AZ374619
LOCUS AZ374619 19 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0127F04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0127F04 R, genomic survey sequence.
ACCESSION AZ374619
VERSION AZ374619.1 GI:10488319
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0127 row: F column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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        /mol_type="genomic DNA"
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        /clone="UUGC1M0127F04"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

  Query Match      0.7%; Score 19; DB 1; Length 19;
  Best Local Similarity 100.0%; Pred. No. 1.2e+03;
  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 2709 AAAAAAAAAAAAAAAAAAAAA 2727
  Db 1 AAAAAAAAAAAAAAAAAAAAA 19

  RESULT 1486
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  LOCUS
  DEFINITION
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  accession
  version
  keywords
  source
  organism
  Mus musculus (house mouse)
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 19)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0144 row: L column: 10
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 19.

  Query Match      0.7%; Score 19; DB 1; Length 19;
  Best Local Similarity 100.0%; Pred. No. 1.2e+03;
  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 2709 AAAAAAAAAAAAAAAAAAAAA 2727
  Db 1 AAAAAAAAAAAAAAAAAAAAA 19

  RESULT 1487
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    AZ391509 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  accession
  version
  keywords
  source
  organism
  Mus musculus (house mouse)
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 19)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0153 row: K column: 08
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 19.

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FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0182P04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1489
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LOCUS
DEFINITION
1M0182P04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0182P04 F, genomic survey sequence.
ACCESSION
AZ414413
VERSION
AZ414413.1 GI:10534063
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0182 row: P column: 04
Seq primer: CGTTGTAAACACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0182P04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1489
AZ414413
LOCUS
DEFINITION
1M0182P04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0182P04 F, genomic survey sequence.
ACCESSION
AZ414413
VERSION
AZ414413.1 GI:10534063
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0182 row: P column: 04
Seq primer: CGTTGTAAACACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

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      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1490
AZ422604
LOCUS          19 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION    IM0201B21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone, UUGC1M0201B21 F, Genomic survey sequence.
ACCESSION     AZ422604
VERSION       AZ422604.1 GI:10546617
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 19)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0201 row: B column: 21
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES                                     Location/Qualifiers
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      /db_xref="taxon:10090"
      /clone="UUGC1M0188013"
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      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1490
AZ422604
LOCUS          19 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION    IM0201B21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone, UUGC1M0201B21 F, Genomic survey sequence.
ACCESSION     AZ422604
VERSION       AZ422604.1 GI:10546617
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 19)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0201 row: B column: 21
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0204020"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1492
AZ441329/c
LOCUS
DEFINITION 19 bp DNA linear GSS 03-OCT-2000
clone UUGC1M0233D01 F, genomic survey sequence.
ACCESSION AZ441329
VERSION AZ441329.1 GI:10565342
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: D column: 01
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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was blunt end-repaired with T4 DNA polymerase and T4
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
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and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1492
AZ441329/c
LOCUS
DEFINITION 19 bp DNA linear GSS 03-OCT-2000
clone UUGC1M0233D01 F, genomic survey sequence.
ACCESSION AZ441329
VERSION AZ441329.1 GI:10565342
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: D column: 01
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES
source

Location/Qualifiers

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0236C13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1494

AZ450180
LOCUS
1M0248K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0248K13 R, genomic survey sequence.

ACCESSION
AZ450180
VERSION
GSS.

KEYWORDS
AZ450180.1 GI:10604710

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0248 row: K column: 13

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAA 2725
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Db 1 CTAATAAAAAAAAAAAAAA 19

RESULT 1495

AZ453930/c

LOCUS

1M0255G11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0255G11 R, genomic survey sequence.

ACCESSION
AZ453930

VERSION
GSS.

KEYWORDS
AZ453930.1 GI:10612055

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0255 row: G column: 11

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

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                             /clone_lib="Mouse 10kb plasmid UUCG1M library"
                             /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1496
AZ460906      19 bp DNA linear GSS 04-OCT-2000
LOCUS      1M0266E03R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION  clone UUCG1M0266E03 R, genomic survey sequence.
ACCESSION  AZ460906
VERSION    AZ460906.1 GI:10619031
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0266 row: E column: 03
            Seq primer: CACACAGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.

FEATURES             Location/Qualifiers
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                             /clone_lib="Mouse 10kb plasmid UUCG1M library"
                             /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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ligated to the blunt ends in high molar excess. The
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1497
AZ471494/c    19 bp DNA linear GSS 04-OCT-2000
LOCUS      1M0286E11F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION  clone UUCG1M0286E11 F, genomic survey sequence.
ACCESSION  AZ471494
VERSION    AZ471494.1 GI:10629619
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0286 row: E column: 11
            Seq primer: CGTTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.

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FEATURES

source

Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0286E11"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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electrophoresis. Vector DNA was prepared from a derivative
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with adaptors complementary to the insert adaptors and
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Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
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Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1498

AZ476576/c

LOCUS 19 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0295F04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0295F04 R, genomic survey sequence.

ACCESSION AZ476576
VERSION AZ476576.1 GI:10634701
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0295 row: F column: 04
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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0.005 inch orifice at constant velocity. The sheared DNA
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with adaptors complementary to the insert adaptors and
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Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
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Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1499

AZ486786/c

LOCUS 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0315D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315D21 F, genomic survey sequence.

ACCESSION AZ486786
VERSION AZ486786.1 GI:10653902
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: D column: 21
Seq primer: CGTTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES
  source
    Location/Qualifiers
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        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUC1M0315D21"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
      Query Match          0.7%; Score 19; DB 1; Length 19;
      Best Local Similarity 100.0%; Pred. No. 1.2e+03;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1500
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    clone UUC1M0323E17 R, genomic survey sequence.
  ACCESSION
    AZ490652
  VERSION
    AZ490652.1 GI:10661595
  KEYWORDS
    GSS.
  SOURCE
    Mus musculus (house mouse)
  ORGANISM
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  REFERENCE
    1 (bases 1 to 19)
    AUTHORS
      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
      Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
      Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
      Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
  JOURNAL
    Unpublished (2000)
  COMMENT
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0323 row: E column: 17
    Seq primer: CACACAGGAACAGCTATGACC
    Class: plasmid ends
    High quality sequence stop: 19.

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        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
      Query Match          0.7%; Score 19; DB 1; Length 19;
      Best Local Similarity 100.0%; Pred. No. 1.2e+03;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1501
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    clone UUC1M0350B04 F, genomic survey sequence.
  ACCESSION
    AZ508040
  VERSION
    AZ508040.1 GI:10689356
  KEYWORDS
    GSS.
  SOURCE
    Mus musculus (house mouse)
  ORGANISM
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  REFERENCE
    1 (bases 1 to 19)
    AUTHORS
      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
      Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
      Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
      Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
  JOURNAL
    Unpublished (2000)
  COMMENT
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0350 row: B column: 04
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    Class: plasmid ends
    High quality sequence stop: 19.

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      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
DB 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1502
AZ579119
LOCUS      19 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION  clone UUGC1M0363M16 F, genomic survey sequence.
ACCESSION  AZ579119
VERSION    AZ579119.1 GI:11693580
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0363 row: M column: 16
            Seq primer: CGTTGTAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.

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      /mol_type="genomic DNA"
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      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
DB 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1502
AZ579119
LOCUS      19 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION  clone UUGC1M0363M16 F, genomic survey sequence.
ACCESSION  AZ579119
VERSION    AZ579119.1 GI:11693580
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0363 row: M column: 16
            Seq primer: CGTTGTAAACGACGCCAGT
            Class: plasmid ends
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		/clone_lib="Mouse 10kb plasmid UUGC1M library"	
		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
		Query Match 0.7%; Score 19; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	2709	AAAAAAAAAAAAAAAAAAAAA 2727	
Db	1	AAAAAAAAAAAAAAAAAAAAA 19	
RESULT 1504			
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DEFINITION			
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ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
<p>19 bp DNA linear GSS 13-DEC-2000</p> <p>1M0404C09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0404C09 R, genomic survey sequence.</p> <p>AZ593210.1 GI:11715400</p> <p>GSS.</p> <p>Mus musculus (house mouse)</p> <p>Mus musculus</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.</p> <p>1 (bases 1 to 19)</p> <p>Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.</p> <p>Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts</p> <p>Unpublished (2000)</p> <p>Contact: Robert B. Weiss</p> <p>University of Utah Genome Center</p> <p>University of Utah</p> <p>Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA</p> <p>Tel: 801 585 5606</p> <p>Fax: 801 585 7177</p> <p>Email: ddunn@genetics.utah.edu</p> <p>Insert Length: 10000 Std Error: 0.00</p> <p>Plate: 0404 row: C column: 09</p> <p>Seq primer: CACACGGAACAGCTATGACC</p> <p>Class: plasmid ends</p> <p>High quality sequence stop: 19.</p>			

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		/clone_lib="Mouse 10kb plasmid UUGC1M library"	
		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
		Query Match 0.7%; Score 19; DB 1; Length 19; Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	2709	AAAAAAAAAAAAAAAAAAAAA 2727	
Db	1	AAAAAAAAAAAAAAAAAAAAA 19	
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AZ585865			
LOCUS			
DEFINITION			
AZ585865			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
<p>19 bp DNA linear GSS 13-DEC-2000</p> <p>1M0391D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0391D21 F, genomic survey sequence.</p> <p>1 (bases 1 to 19)</p> <p>Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.</p> <p>Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts</p> <p>Unpublished (2000)</p> <p>Contact: Robert B. Weiss</p> <p>University of Utah Genome Center</p> <p>University of Utah</p> <p>Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA</p> <p>Tel: 801 585 5606</p> <p>Fax: 801 585 7177</p> <p>Email: ddunn@genetics.utah.edu</p> <p>Insert Length: 10000 Std Error: 0.00</p> <p>Plate: 0391 row: D column: 21</p> <p>Seq primer: CGTTGTAAACGACGCCAGT</p> <p>Class: plasmid ends</p> <p>High quality sequence stop: 19.</p>			

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Location/Qualifiers

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/organism="Mus musculus"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1506
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LOCUS 19 bp DNA linear GSS 13-DEC-2000
DEFINITION IM045P16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0445P16 R, genomic survey sequence.

ACCESSION AZ616154
VERSION AZ616154.1 GI:11738344
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0445 row: P column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers

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/strain="C57BL/6J"
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1507
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LOCUS 19 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0474J05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0474J05 F, genomic survey sequence.

ACCESSION AZ627844
VERSION AZ627844.1 GI:11750130
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: J column: 05
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

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		/clone_lib="Mouse 10kb plasmid UUGC1M library"	
		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
Query Match		0.7%;	Score 19; DB 1; Length 19;
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Matches		19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 1508			
AZ631701			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
<p>19 bp DNA linear GSS 13-DEC-2000</p> <p>1M0486E01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0486E01 F, genomic survey sequence.</p> <p>1 (bases 1 to 19)</p> <p>Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.</p> <p>Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts</p> <p>Unpublished (2000)</p> <p>Contact: Robert B. Weiss</p> <p>University of Utah Genome Center</p> <p>Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA</p> <p>Tel: 801 585 5606</p> <p>Fax: 801 585 7177</p> <p>Email: ddunne@genetics.utah.edu</p> <p>Insert Length: 10000 Std Error: 0.00</p> <p>Plate: 0486 row: E column: 01</p> <p>Seq primer: CGTTGTAACGACGCCAGT</p> <p>Class: plasmid ends</p> <p>High quality sequence stop: 19.</p>			

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        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1511
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  clone UUGC1M0508E17 R, genomic survey sequence.
ACCESSION
  AZ644698
VERSION
  AZ644698.1 GI:11773485
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 19)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0508 row: E column: 17
  Seq primer: CACACAGGAACGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 19.

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        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1510
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LOCUS
DEFINITION
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  clone UUGC1M0507D18 F, genomic survey sequence.
ACCESSION
  AZ643659
VERSION
  AZ643659.1 GI:11771446
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 19)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0507 row: D column: 18
  Seq primer: CGTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 19.

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/strain="C57BL/6J"
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/clone="UUGC1M0517L16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1512
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LOCUS                               19 bp DNA linear GSS 14-DEC-2000
DEFINITION
clone UUGC1M0517L16 F, genomic survey sequence.
ACCESSION
AZ648335
VERSION
AZ648335.1 GI:11780699
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0517 row: L column: 16
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES                               Location/Qualifiers
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/clone="UUGC1M0517L16"
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1512
AZ648335
LOCUS                               19 bp DNA linear GSS 14-DEC-2000
DEFINITION
clone UUGC1M0517L16 F, genomic survey sequence.
ACCESSION
AZ648335
VERSION
AZ648335.1 GI:11780699
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0517 row: L column: 16
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

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        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

  Query Match          0.7%; Score 19; DB 1; Length 19;
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  QY 2709 AAAAAAAAAAAAAAAAAA 2727
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  ACCESSION
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  VERSION
    AZ764497.1 GI:12879521
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  SOURCE
    Mus musculus (house mouse)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  REFERENCE
    1 (bases 1 to 19)
  AUTHORS
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
  JOURNAL
    Unpublished (2000)
  COMMENT
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0560 row: H column: 03
    Seq primer: CACACAGGAACAGCTATGACC
    Class: plasmid ends
    High quality sequence stop: 19.

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        /clone="UUGC1M0560H03"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

  Query Match          0.7%; Score 19; DB 1; Length 19;
  Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 2709 AAAAAAAAAAAAAAAAAA 2727
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  Db 1 AAAAAAAAAAAAAAAAAA 19

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    AZ764522
  VERSION
    AZ764522.1 GI:12879571
  KEYWORDS
    GSS.
  SOURCE
    Mus musculus (house mouse)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  REFERENCE
    1 (bases 1 to 19)
  AUTHORS
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
  JOURNAL
    Unpublished (2000)
  COMMENT
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0560 row: E column: 16
    Seq primer: CACACAGGAACAGCTATGACC
    Class: plasmid ends
    High quality sequence stop: 19.

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FEATURES                      Location/Qualifiers
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/mol_type="genomic DNA"
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/clone="UUGC1M0560P14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1516
A2764534
LOCUS
DEFINITION
  A2764534
  1M0560P14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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ACCESSION
  A2764534
VERSION
  A2764534.1 GI:12879595
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 19)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0560 row: P column: 14
  Seq primer: CACACAGGAAACAGCTATGACC
  Class: plasmid ends
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FEATURES                      Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560E16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1517
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LOCUS
DEFINITION
  A2770387
  1M0571L23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0571L23 R, genomic survey sequence.
ACCESSION
  A2770387
VERSION
  A2770387.1 GI:12891520
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 19)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0571 row: L column: 23
  Seq primer: CACACAGGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 19.

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/mol_type="genomic DNA"
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES
source

Location/Qualifiers
1. .19
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0014020"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1518
AZ778858

LOCUS
DEFINITION
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clone UUGC2M0014020 F, genomic survey sequence.

ACCESSION
AZ778858
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0014 row: 0 column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1519
AZ779901

LOCUS
DEFINITION
2M0016EL6R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M016EL6 R, genomic survey sequence.

ACCESSION
AZ779901
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: E column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		
	/clone_lib="Mouse 10kb plasmid UUGC1M library"		
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match		0.7%;	Score 19; DB 1; Length 19;
Best Local Similarity		100.0%;	Pred. No. 1.2e+03;
Matches		19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	2709	AAAAAAAAAAAAAAAAAAAAA 2727	
Db	1	AAAAAAAAAAAAAAAAAAAAA 19	
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LOCUS	2M0021003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0021003 R, genomic survey sequence.		
DEFINITION			
ACCESSION	AZ781876		
VERSION	AZ781876.1 GI:12915007		
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	1 (bases 1 to 19)		
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
	Unpublished (2000)		
TITLE	Contact: Robert B. Weiss		
	University of Utah		
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA		
	Tel: 801 585 5606		
	Fax: 801 585 7177		
JOURNAL	Email: ddunn@genetics.utah.edu		
	Insert Length: 10000		
	Plate: 0021		
	Seq primer: CACACAGAAACAGTGTATGACC		
	Class: plasmid ends		
High quality sequence stop: 19.			

FEATURES		Location/Qualifiers	
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	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		
	/clone_lib="Mouse 10kb plasmid UUGC1M library"		
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match		0.7%;	Score 19; DB 1; Length 19;
Best Local Similarity		100.0%;	Pred. No. 1.2e+03;
Matches		19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	2709	AAAAAAAAAAAAAAAAAAAAA 2727	
Db	1	AAAAAAAAAAAAAAAAAAAAA 19	
RESULT 1521			
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LOCUS	2M0034M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0034M12 F, genomic survey sequence.		
DEFINITION			
ACCESSION	AZ787634		
VERSION	AZ787634.1 GI:12926621		
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	1 (bases 1 to 19)		
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.		
	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
	Unpublished (2000)		
TITLE	Contact: Robert B. Weiss		
	University of Utah		
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA		
	Tel: 801 585 5606		
	Fax: 801 585 7177		
JOURNAL	Email: ddunn@genetics.utah.edu		
	Insert Length: 10000		
	Plate: 0034		
	Seq primer: CATTGTAAAACAGCGGCAGT		
	Class: plasmid ends		
High quality sequence stop: 19.			

FEATURES
source

Location/Qualifiers

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.78; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1522
AZ788058/c

LOCUS AZ788058 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0034I24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0034I24 R, genomic survey sequence.

ACCESSION AZ788058
VERSION AZ788058.1 GI:12927475
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: I column: 24
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note: Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
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Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1523
AZ789590/c

LOCUS AZ789590 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0037G06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0037G06 R, genomic survey sequence.

ACCESSION AZ789590
VERSION AZ789590.1 GI:12930573
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: G column: 06
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES             Location/Qualifiers
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                             /clone_lib="Mouse 10kb plasmid UUGC1M library"
                             /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709  AAAAAAAAAAAAAAAAAAAAAA 2727
Db  19  AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1524
AZ792713/c
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DEFINITION       2M0045C22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0045C22 F, genomic survey sequence.
ACCESSION        AZ792713
VERSION          AZ792713.1  GI:12936930
KEYWORDS         GSS.
SOURCE           Mus musculus (house mouse)
ORGANISM         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS         Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE           Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL          Unpublished (2000)
COMMENT         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: C column: 22
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES             Location/Qualifiers
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                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                             /clone_lib="Mouse 10kb plasmid UUGC1M library"
                             /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709  AAAAAAAAAAAAAAAAAAAAAA 2727
Db  19  AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1525
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DEFINITION       2M0049C12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0049C12 R, genomic survey sequence.
ACCESSION        AZ795403
VERSION          AZ795403.1  GI:12942392
KEYWORDS         GSS.
SOURCE           Mus musculus (house mouse)
ORGANISM         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS         Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE           Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL          Unpublished (2000)
COMMENT         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0049 row: C column: 12
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES

source

Location/Qualifiers
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/db_xref="taxon:10090"
/clone="UUGC2M0049C12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1526

AZ801970/c

LOCUS AZ801970 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0060112R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0060112 R, genomic survey sequence.

ACCESSION AZ801970
VERSION AZ801970.1 GI:12954293

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0060 row: 1 column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers
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/clone="UUGC2M0060112"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1527

AZ822225/c

LOCUS AZ822225 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0095E17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0095E17 F, genomic survey sequence.

ACCESSION AZ822225
VERSION AZ822225.1 GI:12992133

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0095 row: E column: 17
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES
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/clone="UUGC2M0139G08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1529
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LOCUS 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0139G08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0139G08 R, genomic survey sequence.
ACCESSION AZ841581
VERSION AZ841581.1 GI:13011489
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: G column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0139G08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1529
AZ841581
LOCUS 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0139G08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0139G08 R, genomic survey sequence.
ACCESSION AZ841581
VERSION AZ841581.1 GI:13011489
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: G column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES                                     Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db   1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1530
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DEFINITION 2M0168P10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION  AZ861896
VERSION    AZ861896.1  GI:13058674
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 19)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D. Weiss,R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
          Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0168 row: P column: 10
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 19.

FEATURES                                     Location/Qualifiers
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db   1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1531
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ACCESSION  AZ936798
VERSION    AZ936798.1  GI:13795379
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 19)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D. Weiss,R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
          Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0193 row: L column: 10
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          Class: plasmid ends
          High quality sequence stop: 19.

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FEATURES
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/clone_lib="Mouse 10kb plasmid UUGC2M library"
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Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1533
AZ985501 19 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0267821F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0267E21 F, genomic survey sequence.
ACCESSION AZ985501
VERSION AZ985501.1 GI:13856728
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0267 row: E column: 21
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
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/sex="Female"
/lab_hosts="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1533
AZ985501 19 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0267821F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0267E21 F, genomic survey sequence.
ACCESSION AZ985501
VERSION AZ985501.1 GI:13856728
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0267 row: E column: 21
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES
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/sex="Female"
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/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1534

CL680736 19 bp DNA linear GSS 09-JUL-2004
LOCUS PRI012a_H07_2 - PRI012a.BR (19) Note: Recurring String Mixed stage
pacificus genomic, genomic survey sequence.
DEFINITION

ACCESSION CL680736.1 GI:50187696
VERSION
KEYWORDS
SOURCE
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 19)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppADB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBLISHED Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT 14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source

Location/Qualifiers
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/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1535

CL685439 19 bp DNA linear GSS 09-JUL-2004
LOCUS PRI0141b_A04_2 - PRI0141b.BR (19) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
DEFINITION

ACCESSION CL685439.1 GI:50193696
VERSION
KEYWORDS
SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 19)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppADB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBLISHED Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT 14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source
Location/Qualifiers
1..19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1536

CL693186 19 bp DNA linear GSS 10-JUL-2004
LOCUS PRI0160c_B05_2 - PRI0160c.BR (19) Note: Recurring String Mixed
stage fosmid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.
DEFINITION

ACCESSION CL693186.1 GI:50215094
VERSION
KEYWORDS
GSS.

```

SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT 14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: r7
Class: fosmid ends.
Location/Qualifiers
1..19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

FEATURES
source
Location/Qualifiers
1..19
/mol_type="genomic DNA"
/organism="Homo sapiens"
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Ottewaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Ottewaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1537
LOCUS
DEFINITION DKFZp566D1846.r1.566 (synonym: hfkD2) Homo sapiens cDNA clone
ACCESSION AL038507
VERSION AL038507.1 GI:49682146
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Ottewaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Ottewaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAA 2726
Db 2 TAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1539
LOCUS
DEFINITION DKFZp566F0346.r1.566 (synonym: hfkD2) Homo sapiens cDNA clone
ACCESSION AL038576
VERSION AL038576
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Ottewaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Ottewaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1537
LOCUS
DEFINITION CL693191 19 bp DNA linear GSS 10-JUL-2004
PR10160C_H08.2 - PR10160C.BR (19) Note: Recurring String Mixed
stage fosmid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.
ACCESSION CL693191
VERSION CL693191.1 GI:50215099
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT 14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: r7
Class: fosmid ends.
Location/Qualifiers
1..19
/organism="Pristionchus pacificus"

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/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1538
LOCUS
DEFINITION DKFZp566D1846.r1.566 (synonym: hfkD2) Homo sapiens cDNA clone
ACCESSION AL038507
VERSION AL038507.1 GI:49682146
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Ottewaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Ottewaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAA 2726
Db 2 TAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1539
LOCUS
DEFINITION DKFZp566F0346.r1.566 (synonym: hfkD2) Homo sapiens cDNA clone
ACCESSION AL038576
VERSION AL038576
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Ottewaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Ottewaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1537
LOCUS
DEFINITION CL693191 19 bp DNA linear GSS 10-JUL-2004
PR10160C_H08.2 - PR10160C.BR (19) Note: Recurring String Mixed
stage fosmid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.
ACCESSION CL693191
VERSION CL693191.1 GI:50215099
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT 14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: r7
Class: fosmid ends.
Location/Qualifiers
1..19
/organism="Pristionchus pacificus"

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```

Wiemann,S.
EST (Ottenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKF2p566P0346"
        /tissue_type="kidney"
        /dev_stage="fetal"
        /lab_host="X1-2blue"
        /clone_lib="566 (synonym: hfkd2)"
        /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAA...AAAAAAAAA 2726
|||||
Db 2 TAAAAA...AAAAAAAAA 20

RESULT 1540
AL038754
LOCUS DKF2p566M1346.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
DEFINITION DKF2p566M1346, mRNA sequence.
ACCESSION AL038754
VERSION AL038754.1 GI:49682201
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
  Wiemann,S.
  TITLE EST (Ottenwaelder, et al.)
  JOURNAL Unpublished (1999)
  COMMENT Contact: MIPS
  MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKF2p566M1346"
        /tissue_type="kidney"
        /dev_stage="fetal"
        /lab_host="X1-2blue"
        /clone_lib="566 (synonym: hfkd2)"
        /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAA...AAAAAAAAA 2726
|||||
Db 2 TAAAAA...AAAAAAAAA 20

RESULT 1541
AL038845
LOCUS DKF2p566P1746_r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
DEFINITION

```

```

DKF2p566P1746, mRNA sequence.
ACCESSION AL038845
VERSION AL038845.1 GI:49682220
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
  AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
  Wiemann,S.
  TITLE EST (Ottenwaelder, et al.)
  JOURNAL Unpublished (1999)
  COMMENT Contact: MIPS
  MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKF2p566P1746"
        /tissue_type="kidney"
        /dev_stage="fetal"
        /lab_host="X1-2blue"
        /clone_lib="566 (synonym: hfkd2)"
        /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAA...AAAAAAAAA 2726
|||||
Db 2 TAAAAA...AAAAAAAAA 20

RESULT 1542
AL587759/c
LOCUS AL587759 BP Chicken Brain Library Gallus gallus cDNA clone
DEFINITION ROS061G06, mRNA sequence.
ACCESSION AL587759
VERSION AL587759.1 GI:13192793
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
  1 (bases 1 to 20)
  MURRAY,P.
  AUTHORS BP Chicken Brain Library
  TITLE Unpublished (2001)
  JOURNAL Contact: Frazer Murray
  COMMENT Dept. Genomics and Bioinformatics
  Roslin Institute
  Roslin, Midlothian, EH25 9PS, UK
  Tel: +44 (0)131 527 4200
  Fax: +44 (0)131 440 0434
  Email: frazer.murray@bbsrc.ac.uk
  GCGGCCGCTTTT...TTTTTTT 3', Poly A RNA purchased from Clontech
  (*6854-
  Seq primer: M13P.
  Location/Qualifiers
    1..20
      /organism="Gallus gallus"
      /mol_type="mRNA"
      /db_xref="taxon:9031"
      /clone="ROS061G06"
      /tissue_type="Brain"
      /dev_stage="Unknown"

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/lab_host="DH10B"
 /clone_lib="BP Chicken Brain Library"
 /note="Vector: pSFor1; Site_1: NotI; Site_2: SalI; Cloned
 unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
 5' TCGACTTCAG 3' ; 3' adaptor sequence: 5'
 GCGCGCGTTTCTTTTCTTTT 3' Poly A RNA purchased from
 Clontech (+6854-1)"

Query Match 0.7%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAA12AG12RM1 2726
 |||||

Db 20 TAAAAA12AG12RM1 2

RESULT 1543

CF318278/c

LOCUS HD--08-F13.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--08-F13, mRNA sequence.

ACCESSION

CF318278

VERSION

CF318278.1

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 20)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .20

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HD--08-F13"

/tissue_type="callus"

/dev_stages="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

line."

Query Match

Best Local Similarity

0.7%; Score 19; DB 1; Length 20;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAA12AG12RM1 2727

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Db 20 AAAAAA12AG12RM1 2

RESULT 1544

CN754148

LOCUS

CN754148

LOCUS

CN754148

LOCUS

CN754148

LOCUS

DEFINITION ID0AAA12AG12RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA12AG12
 5' mRNA sequence.

ACCESSION CN754148

VERSION CN754148.1

KEYWORDS GI:47519145

SOURCE EST.

ORGANISM Acyrthosiphon pisum (pea aphid)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE 1 (bases 1 to 20)

Hunt, D., Tagu, D. and Wincker, P.

Stern, D., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
 An expressed sequence tags database for the pea aphid Acyrthosiphon
 pisum

Unpublished (2004)

Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33 2 23 48 51 65

Fax: +33 2 23 48 51 50

Risk of contamination by bacterial sequences from obligatory
 (Buchner) or facultative endosymbionts. These sequences were
 obtained in the frame of the International Consortium of Aphid
 Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 12 row: G column: 12.

Location/Qualifiers

1. .20

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

/cultivar="developmentstage"

/db_xref="taxon:7029"

/clone="ID0AAA12AG12"

/tissue_type="whole insect"

/dev stage="nymphs and adults (parthenogenetic females)"

/lab_host="XLI-Blue"

/clone_lib="ApMS"

/note="Vector: pBS-SK minus, Site_1: EcoRI; Site_2: XhoI;
 Sample name: ID0AAA ; Plant growth place: Department of
 Ecology & Evolutionary Biology, Princeton University ;
 Soil conditions: Soil ; Sowing date: 01/06/1999 ;
 Harvesting date: 01/06/1999 ; Stress date: no stress ;
 Description: Aphids inoculated on one-week old Vicia faba
 under non-sterile conditions. All parthenogenetic stages
 and both winged and wingless adults were collected for
 library construction. ; experimental condition: long
 photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match

Best Local Similarity

0.7%; Score 19; DB 1; Length 20;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAA12AG12RM1 2728

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Db 1 AAAAAA12AG12RM1 20

RESULT 1545

DN955202

LOCUS DN955202

DEFINITION DN955202

it83f09.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
 sequence.

ACCESSION DN955202

VERSION DN955202.1

KEYWORDS GI:63027340

SOURCE EST.

ORGANISM Gnetum gnemon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
 1 (bases 1 to 20)

REFERENCE 1 (bases 1 to 20)

Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
 Gnetum gnemon

```

O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
FEATURES
    source
        1..20
            /organism="Gnetum gnemon"
            /mol_type="rRNA"
            /db_xref="taxon:3382"
            /sex="female"
            /clone_lib="Gnetum female cone (NYBG)"
            /notes="Organ: mature, unfertilized reproductive strobili;
            Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
            Completed 02/11/02, submitted for sequencing 02/12/02.
            Library: Stratagene ZAP Express cDNA Synthesis Kit. The
            library was size-fractionated to enrich for large inserts.
            Sample: NYBG accession number #436/84"
Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
      |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1546
AZ341237
LOCUS          AZ341237          20 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION    IM0073G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0073G03 R, genomic survey sequence.
ACCESSION     AZ341237
VERSION       AZ341237.1 GI:10417288
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     1 (bases 1 to 20)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0073 row: G column: 03
              Seq primer: CACACAGGAACGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 10.
              Location/Qualifiers
                  1..20
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                      /mol_type="genomic DNA"

O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
FEATURES
    source
        1..20
            /organism="Gnetum gnemon"
            /mol_type="rRNA"
            /db_xref="taxon:3382"
            /sex="female"
            /clone_lib="Gnetum female cone (NYBG)"
            /notes="Organ: mature, unfertilized reproductive strobili;
            Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
            Completed 02/11/02, submitted for sequencing 02/12/02.
            Library: Stratagene ZAP Express cDNA Synthesis Kit. The
            library was size-fractionated to enrich for large inserts.
            Sample: NYBG accession number #436/84"
Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
      |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1547
AZ579178
LOCUS          AZ579178          20 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION    IM0363F11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0363F11 F, genomic survey sequence.
ACCESSION     AZ579178
VERSION       AZ579178.1 GI:11693523
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     1 (bases 1 to 20)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0363 row: F column: 11
              Seq primer: CGTTGTAAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 20.
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/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.7%; Score 19; DB 1; Length 20;
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 2 AAAAAAAAAAAAAAAAAA 20

RESULT 1548
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LOCUS AZ638704 20 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0498E13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0498E13 R, genomic survey sequence.
ACCESSION AZ638704
VERSION AZ638704.1 GI:11760894
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0498 row: E column: 13
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"

FEATURES
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1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 2 AAAAAAAAAAAAAAAAAA 20

RESULT 1549
AZ849506
LOCUS AZ849506 20 bp DNA linear GSS 21-FEB-2001
DEFINITION ZM0150P21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0150P21 R, genomic survey sequence.
ACCESSION AZ849506
VERSION AZ849506.1 GI:13033596
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: P column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers 1. .20
/organism="Mus musculus"
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FEATURES
source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"

TITLE
Niederhauern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0017 row: N column: 14
Seq primer: CTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .23
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/strain="C57BL/6J"
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/clone="UUGC1M0017N14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source
1. .23
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Left Cardiac Ventricle (DOGES77)"
/note="Organ: Heart; Vector: pBluescript II SK; Site: 1: EcoRI; Site 2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.7%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 23 AAAAAAAAAAAAAAAAAA 5
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RESULT 1553
CX002873/c
LOCUS
DEFINITION
CX002873.1 23 bp mRNA linear EST 03-DEC-2004
iv34c07.b1 Left Cardiac Ventricle (DOGES77) Canis familiaris cDNA,
mRNA sequence.
ACCESSION
CX002873
VERSION
CX002873.1 GI:56274289
KEYWORDS
EST.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris

Query Match 0.7%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1
|||||

RESULT 1553
CX002873/c
LOCUS
DEFINITION
CX002873.1 23 bp mRNA linear EST 03-DEC-2004
iv34c07.b1 Left Cardiac Ventricle (DOGES77) Canis familiaris cDNA,
mRNA sequence.
ACCESSION
CX002873
VERSION
CX002873.1 GI:56274289
KEYWORDS
EST.
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris

REFERENCE
1 (bases 1 to 23)
AUTHORS
Balijs, V.S., Nascimento, L.U. and McCombie, M.R.
TITLE
ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL
Unpublished (2004)

COMMENT

Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org.

FEATURES

source
1. .23
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Left Cardiac Ventricle (DOGES77)"
/note="Organ: Heart; Vector: pBluescript II SK; Site: 1: EcoRI; Site 2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.7%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 23 AAAAAAAAAAAAAAAAAA 5
|||||

RESULT 1554
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LOCUS
DEFINITION
DX032218.1 23 bp DNA linear GSS 10-JAN-2005
KBRB029E14R KBRB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBRB029E14, genomic survey
sequence.
ACCESSION
DX032218
VERSION
DX032218.1 GI:84726515
KEYWORDS
GSS.
SOURCE
Brassica rapa subsp. pekinensis
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
1 (bases 1 to 23)
AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
TITLE
End sequence of Brassica rapa BamHI (KBRB) BAC clone
JOURNAL
Unpublished (2005)
COMMENT
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pheom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBRB029E14
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .23
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/sub_species="pekinensis"
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/clone="KBRB029E14"

/lab_host="E.coli DH10B"
 /clone_lib="KBrB, Brassica rapa BamHI BAC library"
 /notes="vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
 pekinensis var. Chifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 0.7%; Score 19; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1555
 AZ442146/c
 LOCUS 1M0234B16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0234B16 R, genomic survey sequence.

ACCESSION AZ442146
 VERSION AZ442146.1 GI:10566159
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Keilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0234 row: B column: 16
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends

High quality sequence stop: 22.
 Location/Qualifiers
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 /db_xref="taxon:10090"
 /clone="UUGC1M0234B16"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male); was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (GI/4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

FEATURES
 source

1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0234B16"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male); was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (GI/4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.7%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1.3e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
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 Db 22 AAAAAAAAAACACAAAAAAAAA 1

RESULT 1556
 CT017313/c

LOCUS KBrH128J11 genomic clone, KBrH (HindIII) BAC library Brassica rapa
 DEFINITION subsp. pekinensis, genomic survey sequence.

ACCESSION CT017313
 VERSION CT017313.1 GI:71471431
 KEYWORDS GSS.
 SOURCE Brassica rapa subsp. pekinensis
 ORGANISM Brassica rapa subsp. pekinensis

REFERENCE 1
 AUTHORS Viehoveer, P., Holtgraewe, D. and Weisshaar, B.
 TITLE BAC end sequences of Brassica rapa
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 22)
 AUTHORS Li, Y. and Weisshaar, B.

TITLE Direct Submission
 JOURNAL Submitted (09-AUG-2005) Weisshaar B., Bielefeld University,
 Institute for Genome Research, Universitaetstrasse 25, D-33594
 Bielefeld, Germany
 COMMENT Contact: Bernd Weisshaar
 Bielefeld University, Institute for Genome Research
 Universitaetstrasse 25, D-33594 Bielefeld, Germany Email:
 bernd.weisshaar@uni-bielefeld.de

BAC end sequences of Brassica rapa BAC clone KBrH128J11; generated
 as contribution to the 'Multinational Brassica rapa Sequencing
 Project' Seq primer: sp6B ATTAGGTGACACTATAG
 Class: BAC ends.
 Location/Qualifiers
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 /mol_type="genomic DNA"
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 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrH128J11"
 /clone_lib="KBrH, Brassica rapa HindIII BAC library
 GF-SCF-1002, Vector: pCUGIBAC1"
 /lab_host="E.coli DH10B"

FEATURES
 source

1..22
 /organism="Brassica rapa subsp. pekinensis"
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 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrH128J11"
 /clone_lib="KBrH, Brassica rapa HindIII BAC library
 GF-SCF-1002, Vector: pCUGIBAC1"
 /lab_host="E.coli DH10B"

Query Match 0.7%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1.3e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||
 Db 22 AAAAAAAAAACACAAAAAAAAA 1

RESULT 1557
 CF291486/c

LOCUS CF291486 23 bp mRNA linear EST 14-AUG-2003
 DEFINITION 14ROOT--01-021.b1 Rice root plasmid cDNA library (14ROOT) Oryza
 sativa (japonica cultivar-group) cDNA clone 14ROOT--01-021, mRNA


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VERSION AL587572.1 GI:13192606
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 20)
REFERENCE Murray, F.
AUTHORS BP Chicken Brain Library
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGCGCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13F.
Location/Qualifiers
1..20
/organism="Gallus gallus"
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/clone="ROS059B11"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Clon
undirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGCGCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
Clontech (-6854-1)"
Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY 2707 CTAAAAAAAAAAAAAAAAAA 2726
| | | | | | | | | | | | | | | | | | | | | |
DB 20 CCAAAAAAAAAAAAAAAAAA 1
RESULT 1561
CF299570/c
LOCUS CF299570
DEFINITION CF299570 20 bp mRNA linear EST 15-AUG-200
7LEAF--03-K09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K09, mRNA
sequence.
CF299570 20 bp mRNA linear EST 15-AUG-200
CF299570.1 GI:33671331
7LEAF--03-K09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K09, mRNA
sequence.
CF299570 20 bp mRNA linear EST 15-AUG-200
CF299570.1 GI:33671331
7LEAF--03-K09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K09, mRNA
sequence.
ACCESSION CF299570
VERSION CF299570.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
AUTHORS Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

```

```

source
1. .20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF-03-K09"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH108"
/clone_lib="rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2705 TACTAAAAA 2724
      |||||||
Db 20 TAGTAAAAA 1

RESULT 1562
CF308984/c
LOCUS
DEFINITION
CF308984 20 bp mRNA linear EST 15-AUG-2003
ABF--03-A01.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--03-A01, mRNA sequence.
CF308984
CF308984.1 GI:33680745
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF-03-A01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match          0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAA 2728
      |||||||

```

```

Db      20 AAAAAAAAAAAAAAAAACAAAAAA 1

RESULT 1563
CF316662/c
LOCUS
DEFINITION
HD--06-A20.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
Library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--06-A20, mRNA sequence.
CF316662
CF316662.1 GI:33688423
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--06-A20"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAAAAAAAAAAAAAAA 2726
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CCAAAAAAAAAAAAAAAAAA 1

RESULT 1564
DR073483
LOCUS
DEFINITION
ik86b11.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION
DR073483
VERSION
DR073483.1 GI:67051364
KEYWORDS
EST.
SOURCE
Ginkgo biloba (maidenhair tree)
Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Ginkgoales; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 20)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAAAAAAAAAAAAAA 2726
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CCAAAAAAAAAAAAAAAAAA 1

RESULT 1565
DR073483
LOCUS
DEFINITION
ik86b11.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION
DR073483
VERSION
DR073483.1 GI:67051364
KEYWORDS
EST.
SOURCE
Ginkgo biloba (maidenhair tree)
Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Ginkgoales; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 20)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)

JOURNAL COMMENT
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@csuhl.org
Original 3 prime EST has been reverse completed to be in 5 prime
direction
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..20
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2728
| | | | | | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 1565
AZ375620
LOCUS
DEFINITION
IM0129A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0129A08 F, genomic survey sequence.
ACCESSION
AZ375620
VERSION
AZ375620.1 GI:10489320
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: A column: 08
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0129A08"

JOURNAL COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: A column: 08
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0129A08"

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/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.78; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1566

AZ486787/c
 LOCUS 20 bp DNA linear GSS 05-OCT-2000
 DEFINITION 1M0315D23F Mouse 10kb plasmid UGCC1M library Mus musculus genomic clone UGCC1M0315D23 F, genomic survey sequence.

ACCESSION AZ486787
 VERSION AZ486787.1 GI:10653904
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0315 row: D column: 23

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0315D23"

FEATURES

source

1. .20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0363G19"

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.78; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 |||||
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1567

AZ579122
 LOCUS 20 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0363G19F Mouse 10kb plasmid UGCC1M library Mus musculus genomic clone UGCC1M0363G19 F, genomic survey sequence.

ACCESSION AZ579122
 VERSION AZ579122.1 GI:11693583
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0363 row: G column: 19

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

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/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0363G19"

```

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
      ||| ||||| ||||| |||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

```

RESULT 1568

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AZ645312/C
LOCUS
DEFINITION
  1M0510K11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0510K11 R, genomic survey sequence.

```

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ACCESSION
  AZ645312
VERSION
  AZ645312.1 GI:11774684
KEYWORDS
  GSS.
SOURCE
  Mus musculus
  Mus musculus (house mouse)

```

ORGANISM

```

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

```

```

REFERENCE
  1 (bases 1 to 20)

```

```

AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.

```

```

TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts

```

```

JOURNAL
  Unpublished (2000)

```

```

COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center

```

```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

```

```

Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: K column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

```

FEATURES

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source

```

```

1..20
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  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC1M0510K11"

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```

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
      ||| ||||| ||||| |||||
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT 1569

```

AZ821905
LOCUS
DEFINITION
  2M0094D20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0094D20 R, genomic survey sequence.

```

```

ACCESSION
  AZ821905
VERSION
  AZ821905.1 GI:12991813
KEYWORDS
  GSS.
SOURCE
  Mus musculus
  Mus musculus (house mouse)

```

ORGANISM

```

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

```

```

REFERENCE
  1 (bases 1 to 20)

```

```

AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.

```

```

TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts

```

```

JOURNAL
  Unpublished (2000)

```

```

COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center

```

```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

```

```

Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: D column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

```

FEATURES

```

source

```

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1..20
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  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC2M0094D20"

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Best Local Similarity 95.0%; Pred. No. 1.3e+03; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 ||||| ||||| ||||| |||||
 Db 20 AAAAAAAAAAGAGAAAAAAA 1

RESULT 1572
 DX071064/c
 LOCUS DX071064 20 bp DNA linear GSS 10-JAN-2006
 DEFINITION KBrB080L01F KBrB, Brassica rapa BamHI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBrB080L01, genomic survey
 sequence.

ACCESSION DX071064.1 GI:84765360
 VERSION DX071064.1
 KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis
 ORGANISM Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
 Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
 Hahn,J.H. and Park,B.S.
 End sequence of Brassica rapa BamHI (KBrB) BAC clone

TITLE Unpublished (2005)
 JOURNAL Contact: Beom-Seok Park
 COMMENT Brassica Genomics Team

National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea
 Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
 KBrB080L01
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1..20

/organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrB080L01"
 /lab_host="E.coli DH10B"
 /clone_lib="KBrB, Brassica rapa BamHI BAC library"
 /note="Vector: PCUGIBAC1; Site_1: BamHI; Brassica rapa ssp
 pekinensis var. Chiifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 0.7%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 ||||| ||||| ||||| |||||
 Db 20 AAAAAAAAAAGAGAAAAAAA 1

RESULT 1573
 DX071075
 LOCUS DX071075 20 bp DNA linear GSS 10-JAN-2006
 DEFINITION KBrB080L07F KBrB, Brassica rapa BamHI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBrB080L07, genomic survey
 sequence.

ACCESSION DX071075
 VERSION DX071075.1 GI:84765371
 KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis
 ORGANISM Brassica rapa subsp. pekinensis

REFERENCE
 AUTHORS

TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
 JOURNAL Unpublished (2005)
 COMMENT Contact: Beom-Seok Park

Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea
 Tel: +82-31-299-1670
 Fax: +82-31-299-1672

Email: pbeom@da.go.kr
 BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
 KBrB080L07
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1..20

/organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrB080L07"
 /lab_host="E.coli DH10B"
 /clone_lib="KBrB, Brassica rapa BamHI BAC library"
 /note="Vector: PCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
 pekinensis var. Chiifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 0.7%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 ||||| ||||| ||||| |||||
 Db 1 AAAAAAAAAAGAGAAAAA 20

RESULT 1574
 BX558161/c

LOCUS BX558161 21 bp mRNA linear EST 10-OCT-2003
 DEFINITION morsitans morsitans cDNA clone Tse37a05_plc, mRNA sequence.

ACCESSION BX558161
 VERSION BX558161.1 GI:33429302
 KEYWORDS EST.

SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
 morsitans morsitans and expression analysis of putative immune
 response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)
 PUBMED 14519198
 COMMENT Contact: Hall N

Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane
 Prof. M.J.Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.

FEATURES

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1     21      /organism="Glossina morsitans morsitans"
          /mol_type="mRNA"
          /sub_species="morsitans"
          /db_xref="taxon:37546"
          /clone="tse37a05_pic"
          /tissue_type="adult infected gut"
          /clone_lib="Glossina morsitans morsitans adult infected
gut"
          /notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

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Query Match 0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTATAAAAAAAAAAAAAAAAAA 2725
|| |||||
Db 21 ACAAAAAAAAAAAAAAAAAA 2

RESULT 1575
CF319625
LOCUS CF319625 21 bp mRNA linear EST 15-AUG-2003
DEFINITION HD-10-D06.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (Japonica cultivar-group) cDNA clone
HD-10-D06, mRNA sequence.

ACCESSION	CF319625	CF319625.1	GI:33691386
VERSION	EST.		
KEYWORDS			
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.		
TITLE	Large-scale Sequencing Analysis of Rice ESTs		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Gyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.		

```

FEATURES
source
1. .21
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39347"
/clone="HD--10-D06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E. coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

Query Match 0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy	2707	CTAAAAAAAAAAAAAAAAAA	2726
Dd			
	2	CTATAAAAAAAAAAAAAA	21

RESULT	1576
CF333393/c	
LOCUS	CF333393 21 bp mRNA linear EST 18-AUG-2003
DEFINITION	JMT--02-E09_b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) CDNA clone
	JMT--02-E09, mRNA sequence.
ACCESSION	CF333393
KEYWORDS	CF333393.1 GI:33815062
SOURCE	EST.
ORGANISM	Oryza sativa (japonica cultivar-group)
	Oryza sativa (japonica cultivar-group)
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
	clade; Ehrhartoidae; Orzyeae; Oryza.
REFERENCE	1 (bases 1 to 21)
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

FEATURES
source
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--02-E09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

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Query Match      0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy	2706	ACTAAAAAAAAAAAAAAAAA	2725
Db	20	ACCAAAAAAAAAAAAAAAAA	1

RESULT	1577
LOCUS	DU829016/c
DEFINITION	DU829016 21 bp DNA linear GSS 22-DEC-2005 KBRs004D04F KBRs, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBRs004D04, genomic survey sequence.
ACCESSION	DU829016
VERSION	DU829016.1
KEYWORDS	GI:83865612
SOURCE	GSS.
ORGANISM	Brassica rapa subsp. pekinensis Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 21)

REFERENCE
 Yang, T.-J., Kwon, S.-J., Kim, J. A., Kim, J. S., Lim, K. B., Jin, M.,
 AUTHORS

Park, J. Y., Lim, M. H., Kim, H. I., Choi, B. S., Seol, Y. J., Park, D. S.,
Hahn, J. H. and Park, B. S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS004D04
Seq primer: T7
Class: BAC ends.

FEATURES

source
1..21
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS004D04"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

Query Match 0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 20 TAAAAAAAAAAAAAAAAAAAA 1

RESULT 1578

AL048750
LOCUS
DEFINITION
DKFZp566L123.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
22 bp mRNA linear EST 04-SEP-2003
DKFZp566L123 mRNA sequence.
ACCESSION
AL048750
VERSION
AL048750.1 GI:4727821
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 22)
AUTHORS
Koehler, K., Beyer, A., Mewes, H. W., Gassenhuber, J. and Wiemann, S.
TITLE
EST (Koehler, et al.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source
1..22
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566L123"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
Query Match 0.7%; Score 18.4; DB 1; Length 22;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 3 TCAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1579

CT019890/c
LOCUS
DEFINITION
KBrH130A15 genomic clone, KBrH (HindIII) BAC library Brassica rapa
subsp. pekinensis, genomic survey sequence.
CT019890
ACCESSION
CT019890.1 GI:71468840
KEYWORDS
GSS.
SOURCE
Brassica rapa subsp. pekinensis

ORGANISM

Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 Vichoever, P., Holtgraewe, D. and Weisshaar, B.
AUTHORS
BAC end sequences of Brassica rapa
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 23)
AUTHORS
Li, Y. and Weisshaar, B.
TITLE
Direct Submission
JOURNAL
Submitted (09-AUG-2005) Weisshaar B., Bielefeld University.
Institute for Genome Research, Universitaetsstrasse 25, D-33594
Bielefeld, Germany
COMMENT
Contact: Bernd Weisshaar
Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany Email:
bernd.weisshaar@uni-bielefeld.de
BAC end sequences of Brassica rapa BAC clone KBrH130A15; generated
as contribution to the 'Multinational Brassica rapa Sequencing
Project' Seq primer: ml3f TGTAAGGACGCCAGT
Class: BAC ends.

FEATURES

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1..23
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/strain="Chiifu type 401-42"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrH130A15"
/clone_lib="KBrH, Brassica rapa HindIII BAC library
GF-SCF-1002, Vector: pCUGIBac1"
/lab_host="E.coli DH10B"

Query Match 0.7%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAA 4

RESULT 1580

AL038692
LOCUS
DEFINITION
DKFZp566J0846.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
18 bp mRNA linear EST 06-JUL-2004
DKFZp566J0846 mRNA sequence.

ACCESSION

AL038692
VERSION
AL038692.1 GI:49682190
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 18)

AUTHORS Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

TITLE EST (Ottenwaelder, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

FEATURES Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany.

source Location/Qualifiers

1. .18

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp566j0846"

/tissue_type="kidney"

/dev_stage="fetal"

/lab_host="X1-2blue"

/clone_lib="566 (synonym: hfkd2)"

/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1581

BO582676/c

LOCUS BO582676 18 bp mRNA linear EST 06-DEC-2002

DEFINITION E01281-024-007-P18-SP6 MP12-ADIS-024-inflorescence Beta vulgaris

ACCESSION BO582676

VERSION BO582676.1 GI:26112253

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.

AUTHORS 1 (bases 1 to 18)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

PUBLISHED 12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 18 Std Error: 0.00

Plate: 7 row: P column: 18

Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES Location/Qualifiers

source 1. .18

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db_xref="taxon:161934"

/clone="024-007-P18"

/tissue_type="inflorescence"

/lab_host="EMDH10B"

/clone_lib="MP12-ADIS-024-inflorescence"

/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

SP6-Sali-CCACGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

QY 2709 AAAAAAAAAAAAAAAAAA 2726

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1582

BO590027/c

LOCUS BO590027 18 bp mRNA linear EST 06-DEC-2002

DEFINITION E012844-024-019-E24-T7 MP12-ADIS-024-storage root Beta vulgaris

ACCESSION BO590027

VERSION BO590027.1 GI:26119610

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.

AUTHORS 1 (bases 1 to 18)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

PUBLISHED 12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 18 Std Error: 0.00

Plate: 19 row: E column: 24

Seq primer: T7; GTAATACGACTCCTACTATAGGC.

FEATURES Location/Qualifiers

source 1. .18

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db_xref="GABI:190095"

/db_xref="taxon:161934"

/clone="024-019-E24"

/tissue_type="storage root"

/lab_host="EMDH10B"

/clone_lib="MP12-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site_1: Sali; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

SP6-Sali-CCACGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RT-PCR."

Query Match 0.7%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
 |||||
 DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1586

CF299674/c
 LOCUS
 DEFINITION 18 bp mRNA linear EST 15-AUG-2003
 7LEAF--03-M14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--03-M14, mRNA
 sequence.

ACCESSION CF299674.1 GI:33671435

VERSION CF299674

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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 Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
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 DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1587

CF301151/c
 LOCUS
 DEFINITION 18 bp mRNA linear EST 15-AUG-2003
 7LEAF--05-005.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--05-005, mRNA
 sequence.

ACCESSION CF301151

VERSION CF301151.1 GI:33672912

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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 Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source
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 with oligoribonucleotides and then used as templates for
 RT-PCR."

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QY 2708 TAAAAAAAAAAAAAAAAA 2725
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 DB 18 TAAAAAAAAAAAAAAAAA 1

RESULT 1588

CF301325/c
 LOCUS
 DEFINITION 18 bp mRNA linear EST 15-AUG-2003
 7LEAF--06-Cl2.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--06-Cl2, mRNA
 sequence.

ACCESSION CF301325

VERSION CF301325.1 GI:33673086

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

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Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source
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/lab_host="E.coli DH10B"
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RT-PCR."

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  18 AAAAAAAAAAAAAAAAAA 1

RESULT 1589
CF302409/c
LOCUS      18 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION  7LEAF--06-L22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
          sativa (japonica cultivar-group) cDNA clone 7LEAF--06-L22, mRNA
          sequence.
ACCESSION  CF301760.1 GI:33673521
VERSION    CF301760
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
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   /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
   /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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   RT-PCR."

Query Match          0.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAA 2726
Db  18 AAAAAAAAAAAAAAAAAA 1

RESULT 1590
CF302409/c
LOCUS      18 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION  7LEAF--07-N19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
          sativa (japonica cultivar-group) cDNA clone 7LEAF--07-N19, mRNA
          sequence.
ACCESSION  CF302409
VERSION    CF302409
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
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           Fax: 82 31 321 6355
           Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

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   RT-PCR."

Query Match          0.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAA 2726
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RESULT 1590
CF302409/c
LOCUS      18 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION  7LEAF--07-N19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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ACCESSION  CF302409
VERSION    CF302409
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
           Oryza sativa (japonica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
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           Fax: 82 31 321 6355
           Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
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   RT-PCR."

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KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
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   /lab_host="E.coli DH10B"
   /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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Query Match          0.7%; Score 18; DB 1; Length 18;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2707 CTTAAAAAAAAAAAAAAAAA 2724
Db  18 CTTAAAAAAAAAAAAAAAAA 1

RESULT 1591
DE073142/c
LOCUS      18 bp      mRNA      linear      EST 08-JUN-2005
DEFINITION  qs66c01.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
          sequence.
ACCESSION  DR073142
VERSION    DR073142
KEYWORDS   EST.
SOURCE     Ginkgo biloba (maidenhair tree)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
           O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
           Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE     Expressed tag sequences from Ginkgo female leaf (NYBG)
JOURNAL   Unpublished (2005)
COMMENT   Contact: W. Richard McCombie
           Lita Annenberg Hazen Genome Sequencing Center
           Cold Spring Harbor Laboratory
           PO Box 100, Cold Spring Harbor, NY 11724, USA
           Tel: 516 367 8884
           Fax: 516 367 8874
           Email: mcombie@cshl.org
           Seq primer: -21M13UnivRev.

FEATURES             source
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   /mol_type="mRNA"
   /db_xref="taxon:3311"

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/sex="female"
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 Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
 The library was size-fractionated to enrich for large
 inserts."

Query Match 0.7%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
 |||||
 Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1592

DR074121/c 18 bp mRNA linear EST 08-JUN-2005
 LOCUS 1K98C05.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
 DEFINITION

ACCESSION

DR074121

VERSION

DR074121.1 GI:67052070

KEYWORDS

EST.

SOURCE

Ginkgo biloba (maidenhair tree)

ORGANISM

Ginkgo biloba

REFERENCE

1 (bases 1 to 18)

AUTHORS

Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,

O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,

Benfey,P., Coruzzi,G. and Stevenson,D.

Expressed tag sequences from Ginkgo male leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M3UnivRev.

FEATURES

Location/Qualifiers

1..18

/organism="Ginkgo biloba"

/mol_type="mRNA"

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/clone_lib="Ginkgo male leaf (NYBG)"

/notes="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI; Site_2:

Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The

library was size-fractionated to enrich for large

inserts."

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726

|||||

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1593

CF293167/c

LOCUS

CF293167

DEFINITION

30DGS--02-E02.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza

sativa (japonica cultivar-group) cDNA clone 30DGS--02-E02, mRNA

sequence.

ACCESSION

CF293167

VERSION

CF293167.1 GI:33662200

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

Location/Qualifiers

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/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

ORGANISM

Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1..19

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/cultivar="Nackdong"

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/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"

/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

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Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726

|||||

Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 1594

CF298396/c

LOCUS

CF298396

DEFINITION

7LEAF--01-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa (japonica cultivar-group) cDNA clone 7LEAF--01-M05, mRNA

sequence.

ACCESSION

CF298396

VERSION

CF298396.1 GI:33670157

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

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FEATURES
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/tissue_type="leaf"
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/lab_host="E.coli DH108"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match 0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
Db 19 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1598
CF331361/c
LOCUS
DEFINITION
NACL--07-H08.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--07-H08, mRNA
sequence.
CF331361
CF331361.1 GI:33810941
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
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/clone_host="E.coli DH108"
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RT-PCR."
Query Match 0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2726

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Db 19 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1599
CF335293/c
LOCUS
DEFINITION
JMT--04-017.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--04-017, mRNA sequence.
CF335293
CF335293.1 GI:33818938
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--04-017"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
Query Match 0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
Db 19 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1600
CN545923/c
LOCUS
DEFINITION
EST 17867 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CG00RL006D08 3', mRNA sequence.
CN545923
CN545923.1 GI:46910548
EST.
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 19)
Abbal,P., Agasse,A., Ageorges,A., Atanaseova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimpet,J.,
Hamdi,S., Romieu,C. and Terrier,N.

```

TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages

JOURNAL Unpublished (2002)

COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7

FEATURES

Location/Qualifiers

source

1..19
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006D08"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2726

Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 1601

CX002732/c

LOCUS CX002732 19 bp mRNA linear EST 03-DEC-2004
DEFINITION iv33e03.b1 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA, mRNA sequence.

ACCESSION CX002732

VERSION CX002732.1 GI:56274148

KEYWORDS EST.

SOURCE Canis familiaris (dog)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 19)

AUTHORS Baliya,V.S., Nascimento,L.U. and McCombie,W.R.

TITLE ESTs from Canis familiaris left cardiac ventricle (dog)

JOURNAL Unpublished (2004)

COMMENT Contact: W. Richard McCombie

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcmcbie@cshl.org.

Location/Qualifiers

FEATURES

source

1..19
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"

/clone_lib="Left Cardiac Ventricle (DOGEST7)"

/note="Organ: Heart; Vector: pBluescript II SK; Site_1: EcoRI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary

Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2726

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1602

AZ345795

LOCUS

DEFINITION IM0080H09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080H09 R, genomic survey sequence.

ACCESSION AZ345795

VERSION AZ345795.1 GI:10425032

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: H column: 09

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080H09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725
|||||
Db 2 TAAAAAAAAAAAAAAAAA 19

RESULT 1603

AZ650575 19 bp DNA linear GSS 14-DEC-2000
LOCUS
DEFINITION
clone UUGC1M0520P13 R, genomic survey sequence.

ACCESSION
AZ650575

VERSION
GSS.

KEYWORDS
Mus musculus (house mouse)

SOURCE
Mus musculus

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0520 row: P column: 13

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0520P13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725
|||||
Db 2 TAAAAAAAAAAAAAAAAA 19

RESULT 1604

AJ666275/c

LOCUS

DEFINITION

AJ666275 CSEQRAN09 Sus scrofa cDNA clone C0000033_B07, mRNA

sequence.

ACCESSION

AJ666275

VERSION

AJ666275.1

KEYWORDS

EST.

SOURCE

Sus scrofa

ORGANISM

Sus scrofa (pig)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

Sus.

REFERENCE

1 (bases 1 to 20)

AUTHORS

Anderson,S.I., Finlayson,H.A. and Archibald,A.L.

TITLE

Development of cDNA and EST resources for studying reproduction and

embryo development in pigs and cattle

JOURNAL

Unpublished (2004)

COMMENT

Contact: Anderson SI

Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred

v0.020425.c. Vector identified by crossmatch with the -minscore 20

and -mismatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:

ECORI R. Site 2: NotI Description: Normalised library constructed

from pooled tissue from day 30 placentas. Clones available from UK

Centre for Functional Genomics in Farm Animals, Roslin Institute,

Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

Location/Qualifiers

1..20

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="C0000033_B07"

/tissue_type="placenta"

/clone_lib="CSEQRAN09"

/note="Vector: pBlueScriptII(KS+); Site 1: EORI; Site 2:

NotI; Single pass sequencing. Normalised library

constructed from pooled tissue from day 30 placentas."

Query Match 0.7%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726

|||||

Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 1605

AL587727/c

LOCUS

DEFINITION

AL587727 BP Chicken Brain Library Gallus gallus cDNA clone

ROS061D01, mRNA sequence.

ACCESSION

AL587727

VERSION

AL587727.1

KEYWORDS

EST.

SOURCE

Gallus gallus (chicken)

ORGANISM

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 20)
Murray.F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTCTTTTCTTTTCTTTT 3', Poly A RNA purchased from Clontech
(*6854-

Seq primer: M13F.

FEATURES
source

Location/Qualifiers
1..20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS061D01"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH108"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dr. 5' adaptor sequence:
5' TCGACTCTGAG 3' ; 3' adaptor sequence: 5'
GCGGCCGCTTTTCTTTTCTTTTCTTTT 3', Poly A RNA purchased from
Clontech (*6854-1)"

Query Match 0.7%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 1606
CA853586/c
LOCUS

CA853586 20 bp mRNA linear EST 01-AUG-2003
B09H12.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
B09H12 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CA853586.1 GI:33390391
CA853586
EST.
Glycine max (soybean)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

1 (bases 1 to 20)
Alkharouf,N., Khan,R. and Matthews,B.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Genome 47 (2), 380-388 (2004)
15060591
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..20
/organism="Glycine max"
/mol_type="mRNA"

FEATURES
source

Location/Qualifiers
1..20
/organism="Glycine max"
/mol_type="mRNA"

/cultivar="Peking"
/db_xref="taxon:3847"
/clone="B09H12"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 12hr SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from roots of soybean cv. Peking 12 hrs after
infection by SCN race 3. These are cloned in pBluescript
SK- phagemid."

Query Match 0.7%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 1607
CF282002/c

LOCUS
DEFINITION
CF282002 20 bp mRNA linear EST 14-AUG-2003
14ETL--09-F01.bl Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F01,
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF282002.1 GI:33659389
EST.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gsbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source

Location/Qualifiers
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--09-F01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"

/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 1608
CF320843/c

LOCUS CF320843 20 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD-11-001.gi OsHDACL1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD-11-001, mRNA sequence.
 ACCESSION CF320843
 VERSION CF320843.1 GI:33692604
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD-11-001"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OsHDACL1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /notes="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.7%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAA 2726
 |||||
 Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 1609
 AZ345856/c
 LOCUS AZ345856 20 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0080G17R Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UUGCIM0080G17 R, genomic survey sequence.
 ACCESSION AZ345856
 VERSION AZ345856.1 GI:10425093
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D..Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: G column: 17
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES
 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIM0080G17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAA 2726
 |||||
 Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 1610
 AZ370699/c
 LOCUS AZ370699 20 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0121N17R Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UUGCIM0121N17 R, genomic survey sequence.
 ACCESSION AZ370699
 VERSION AZ370699.1 GI:10484399
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D..Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0121 row: N column: 17
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

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1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0121N17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42np; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid pL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

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Query Match      0.7%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT	1611
AL048772	
LOCUS	21 bp mRNA linear EST 04-SEP-2003
DEFINITION	DKFZP566N143_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION	DKFZP566N143, mRNA sequence.
VERSION	AL048772
KEYWORDS	AL048772.1 GI:4727843
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Homnidae; Homo.
REFERENCE	1 (bases 1 to 21)
AUTHORS	Koehrer K., Beyer A.,
TITLE	EST (Koehrer, et al.)
JOURNAL	Unpublished (1999)
COMMENT	Contact: MIPS
	MIPS
FEATURES	Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
	Location/Qualifiers
source	1. .21

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566N143"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="XL-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMPl; Site_1: NotI; Site_2: SalI"

Query Match      0.7%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2708 TAAAAAAAAAAAAAAA 2725
          |||||
Db       4 TAAAAAAAAAAAAAAA 21

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Query Match          0.7%;      Score 18;  DB 1;  Length 21;
Best Local Similarity 100.0%;  Pred. NO. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
      |||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 4
      |||||

```

RESULT	1613			
AZ610868/c				
LOCUS	AZ610868	21 bp	DNA	linear
DEFINITION	1M0436G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0436G12 F, genomic survey sequence.			GSS 13-DEC-2000

```

ACCESSION      AZ610868
VERSION        AZ610868.1  GI:11733058
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0436 row: G column: 12
               Seq primer: CGTTGTAACACGCGCCAGT
               Class: plasmid ends
               High quality sequence stop: 21.
               Location/Qualifiers
               1..21
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC1M0436G12"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /notes="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."

Query Match      0.7%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2708 TAAAAA
Db   18 TAAAAA

RESULT 1614
AZ764492
LOCUS      21 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION IM0560D04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560D04 R, genomic survey sequence.

```

```

ACCESSION      AZ764492
VERSION        AZ764492.1  GI:12879511
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0560 row: D column: 04
               Seq primer: CACACAGGAACAGCTATGACC
               Class: plasmid ends
               High quality sequence stop: 21.
               Location/Qualifiers
               1..21
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
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               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /notes="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."

Query Match      0.7%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2708 TAAAAA
Db   4 TAAAAA

RESULT 1615
CF328832/c
LOCUS      22 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--03-020.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--03-020, mRNA

```

```

sequence.
ACCESSION CF328832
VERSION CF328832.1 GI:33805905
KEYWORDS EST.
SOURCE Oriza sativa (japonica cultivar-group)
ORGANISM Oriza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzeae; Oriza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
CONTACT: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongui University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     1..22
     /organism="Oriza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
     /culivar="Nackdong"
     /db_xref="taxon:39947"
     /clone="NACL--03-020"
     /tissue_type="callus"
     /dev_stage="proliferated callus on 2N6 media for 30 days"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice callus plasmid cDNA library (NACL)"
     /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
           with oligoribonucleotides and then used as templates for
           RT-PCR."
Query Match      0.7%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1616
AZ843648
LOCUS 2M0142807R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0142807 R, genomic survey sequence.
ACCESSION AZ843648
VERSION AZ843648.1 GI:13013556
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Bescorn,T., Duval,B., Hamill,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
CONTACT: Robert B. Weiss
          University of Utah Genome Center
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177

```

```

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0142 row: B column: 07
Seq primer: CACACAGAAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
     1..22
     /organism="Mus musculus"
     /mol_type="genomic DNA"
     /strain="C57BL/6J"
     /db_xref="taxon:10090"
     /clone="UUGC2M0142B07"
     /sex="Male"
     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
     /clone_lib="Mouse 10kb plasmid UUGC1M library"
     /note="Vector: PWD42nv; Purified genomic DNA from M.
           musculus C57BL/6J (male) was obtained from the Jackson
           Laboratory Mouse DNA Resource
           (http://www.jax.org/resources/documents/dnares/). The DNA
           was hydrodynamically sheared by repeated passage through a
           0.005 inch orifice at constant velocity. The sheared DNA
           was blunt end-repaired with T4 DNA polymerase and T4
           polynucleotide kinase. Adaptor oligonucleotides were
           ligated to the blunt ends in high molar excess. The
           adapted DNA was purified and size-selected for a 9.5 to
           10.5 kb range using preparative agarose gel
           electrophoresis. Vector DNA was prepared from a derivative
           of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
           inducible derivative of plasmid R1. The vector was ligated
           with adaptors complementary to the insert adaptors and
           purified. The sheared, adapted mouse DNA was annealed to
           adapted vector DNA, and transformed into
           chemically-competent E. coli XL10-Gold (Stratagene) cells
           and selected for ampicillin resistance."
Query Match      0.7%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
Db 1 AAAAAAAAAAAAAAAAAAAAAA 18

RESULT 1617
TA231E08Q
LOCUS T. brucei sheared genomic DNA clone 231e08, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL480935
VERSION AL480935.1 GI:11846704
KEYWORDS GSS.
SOURCE Trypanosoma brucei
          Trypanosoma brucei
          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
          Trypanosoma
          1 (bases 1 to 22)
REFERENCE Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
          Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
          Melville,S.E., Rajandream,M.A. and Barrell,B.G.
          Direct Submission
          Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
          project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
          Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
          nh@sanger.ac.uk
          Constructed at the Institute for Genomic Research (TIGR),
          Rockville, MD. Genomic DNA isolated from a cloned population of
          Trypanosoma brucei (TREU27/4 GUTat 10.1) was mechanically sheared
          to give a tight size distribution (
          4 kb). The v + i method used for the library construction is
          described in detail in Smith, H. and Venter, J.C. (Making small
          insert libraries for whole genome shotgun sequencing projects. In

```


COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-06-Cl2"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2703 TGTACTAAAAAAAAAAAAA 2723

Db 21 TGTATATAAAAAAAAAAAAAA 1
|||||

RESULT 1621

AW248782/c
LOCUS 2821017.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821017 3',
DEFINITION mRNA sequence.

ACCESSION AW248782

VERSION AW248782.1 GI:6591775

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

1 (bases 1 to 21)

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Other ESTs: 2821017.5prime

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTF DNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 21
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: trace file contained 21 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.

Plate: LLCM5 row: L column: 10

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Homo sapiens"

FEATURES

source

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821017"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site.1: XhoI; Site.2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.6%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 1.4e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2729

Db 21 AAAAAAAAAATTAATAAAAAA 1
|||||

RESULT 1622

DV751812

LOCUS

DEFINITION DV751812 21 bp mRNA linear EST 21-NOV-2005
ID0AAH9BD052M1 ID0AAH Acyrthosiphon pisum cDNA clone ID0AAH9BD05
5', mRNA sequence.

ACCESSION DV751812

VERSION DV751812.1 GI:82580156

KEYWORDS EST.

SOURCE Acyrthosiphon pisum (pea aphid)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 21)

REFERENCE Stern,D.L., Wincker,P. and Tagu,D.

TITLE Large-scale gene discovery in the pea aphid Acyrthosiphon pisum

JOURNAL Unpublished (2005)

COMMENT Contact: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

PCR Primers

FORWARD: TCCGAGATCTGGACGAC

Plate: 9B row: D column: 5.

Location/Qualifiers

1..21

source

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

/db_xref="taxon:7029"

/clone="ID0AAH9BD05"

/tissue_type="salivary gland"

/dev_stage="adult parthenogenetic females"

/lab_host="E. coli BM25.8"

/clone_lib="ID0AAH"

/note="Vector: pTriplex2; Site.1: SfiIA; Site.2: SfiIB;

Sample name: ID0AAH Plant growth place: 9 Gerad REECK

Soil conditions: none Sowing date: 01/07/2004 Harvesting

date: 01/08/2004 Description: Small description of

dissection protocole and RNA extraction: Aphid heads were

obtained by a cut between head and thorax. A second cut

was made along the top of the heads. Brain and salivary

glands were gently pushed out of the heads and salivary

principal gland and, usually, an accompanying accessory

gland). Total RNA was isolated using the Micro RNA

isolation kit from Stratagene (La Jolla, CA). experimental

condition: see description"

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Query Match      0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2700 GTTTGTACTAAAAA 2720
Db 1 GTTTGTACTAAAAA 21

RESULT 1623
AZ597932/c
LOCUS
DEFINITION
IM0412D33F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0412D23 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
MUS musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0412 row: D column: 23
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0412D23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

QY 2709 AAAAAAAAAAAAAAAAAA 2729
Db 21 AAAAAAAAAAGAAAAA 1

RESULT 1624
AZ627840/c
LOCUS
DEFINITION
1M0474B05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474B05 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
MUS musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: B column: 05
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474B05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Query Match 0.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
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 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1625
 AZ647578/c
 LOCUS 21 bp DNA linear GSS 14-DEC-2000
 DEFINITION LM0514117F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 Clone UUGC1M0514117 F, genomic survey sequence.

ACCESSION AZ647578
 VERSION
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Murioidea; Muridae; Murinae; Mus.
 1 (bases 1 to 21)

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0514 row: I column: 17
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.

Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0514117"
 /sex="Male"

FEATURES
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 1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0514117"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 ||||| ||||| ||||| ||||| |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1626
 CL693188

LOCUS 21 bp DNA linear GSS 10-JUL-2004
 DEFINITION PRI0160c.F06.2 - PRI0160c.BR (21) Note: Recurring String Mixed
 stage fosmid library of P. pacificus var. California Pristionchus
 pacificus genomic, genomic survey sequence.

ACCESSION CL693188
 VERSION
 KEYWORDS GSS.
 SOURCE
 ORGANISM Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
 Neodiplogasteridae; Pristionchus.

REFERENCE
 AUTHORS Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
 AppADB: an AcedB database for the nematode satellite organism
 Pristionchus pacificus
 Nucleic Acids Res. 32 (1), D421-D422 (2004)

JOURNAL
 PUBMED 14681447
 COMMENT Contact: Sommer RJ

Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371

Fax: 00497071601498
 Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end
 sequenced at Vancouver, Canada.
 Seq primer: T7
 Class: fosmid ends.

Location/Qualifiers
 1..21
 /organism="Pristionchus pacificus"
 /mol_type="genomic DNA"
 /strain="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus
 var. California"
 /note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 ||||| ||||| ||||| ||||| |||||
 Db 1 AAAAAAAAAAACACAAAAAA 21

RESULT 1627

LOCUS

DEFINITION KBXS013K03F KBRs, Brassica rapa Sau3AI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBRs013K03, genomic survey
 sequence.

ACCESSION
 VERSION
 KEYWORDS GSS.
 SOURCE
 ORGANISM Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

```

REFERENCE
AUTHORS      1 (bases 1 to 21)
              Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
              Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
              Hahn,J. H. and Park,B.S.
TITLE
JOURNAL      End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
COMMENT      Unpublished (2005)
              Contact: Beom-Seok Park
              Brassica Genomics Team
              National Institute of Agricultural Biotechnology
              225 Seodun-Dong, Suwon, 441-707, Korea
              Tel: +82-31-299-1670
              Fax: +82-31-299-1672
              Email: pbeom@da.go.kr
              BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
              KBrS013K03
              Seq primer: T7
              Class: BAC ends.
              Location/Qualifiers
                source
                  1..21
                    /organism="Brassica rapa subsp. pekinensis"
                    /mol_type="genomic DNA"
                    /cultivar="Chiifu"
                    /sub_species="pekinensis"
                    /db_xref="taxon:51351"
                    /clone="KBrS013K03"
                    /lab_host="E. coli DH10B"
                    /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                    /notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                    ssp pekinensis var. Chiifu BAC-library (KBrS BAC) is
                    available at NIAB."

Query Match      0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db      ||||| ||||| ||||| ||||| |||||
        1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1628
DU831616/c      22 bp DNA linear GSS 22-DEC-2005
LOCUS      KBrS008L22F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
DEFINITION      subsp. pekinensis genomic clone KBrS008L22, genomic survey
                sequence.
ACCESSION      DU831616.1 GI:83868212
VERSION      GSS.
KEYWORDS      Brassica rapa subsp. pekinensis
SOURCE      Brassica rapa subsp. pekinensis
ORGANISM      Brassica rapa subsp. pekinensis
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 22)
AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
                Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
                Hahn,J. H. and Park,B.S.
TITLE      End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
                Brassica Genomics Team
                National Institute of Agricultural Biotechnology
                225 Seodun-Dong, Suwon, 441-707, Korea
                Tel: +82-31-299-1670
                Fax: +82-31-299-1672
                Email: pbeom@da.go.kr
                BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                KBrS013D12
                Seq primer: T7
                Class: BAC ends.
                Location/Qualifiers
                  source
                    1..22
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                      /cultivar="Chiifu"
                      /sub_species="pekinensis"
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                      /clone="KBrS013D12"
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                      /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                      /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                      ssp pekinensis var. Chiifu BAC-library (KBrS BAC) is
                      available at NIAB."

Query Match      0.6%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2706 ACTAAAAAAAAAAAAAAAAAAAAA 2726
Db      ||||| ||||| ||||| ||||| |||||
        21 ACACAAAAAAAAAAAAAAAAAAAA 1

RESULT 1629
DU833993/c      22 bp DNA linear GSS 22-DEC-2005
LOCUS      KBrS013D12F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
DEFINITION      subsp. pekinensis genomic clone KBrS013D12, genomic survey
                sequence.
ACCESSION      DU833993.1 GI:83870589
VERSION      GSS.
KEYWORDS      Brassica rapa subsp. pekinensis
SOURCE      Brassica rapa subsp. pekinensis
ORGANISM      Brassica rapa subsp. pekinensis
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 22)
AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
                Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
                Hahn,J. H. and Park,B.S.
TITLE      End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
                Brassica Genomics Team
                National Institute of Agricultural Biotechnology
                225 Seodun-Dong, Suwon, 441-707, Korea
                Tel: +82-31-299-1670
                Fax: +82-31-299-1672
                Email: pbeom@da.go.kr
                BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
                KBrS013D12
                Seq primer: T7
                Class: BAC ends.
                Location/Qualifiers
                  source
                    1..22
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                      /cultivar="Chiifu"
                      /sub_species="pekinensis"
                      /db_xref="taxon:51351"
                      /clone="KBrS013D12"
                      /lab_host="E. coli DH10B"
                      /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                      /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                      ssp pekinensis var. Chiifu BAC-library (KBrS BAC) is
                      available at NIAB."

Query Match      0.6%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db      ||||| ||||| ||||| ||||| |||||
        22 AAAAAAAAAAAAAAAAAAGCAAAA 2

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RESULT 1630
CF291665/cLOCUS
DEFINITION

CF291665 19 bp mRNA linear EST 14-AUG-2003
 sativa (japonica cultivar-group) cDNA clone 14ROOT--02-D01, mRNA
 sequence.

ACCESSION

CF291665.1 GI:33660698

VERSION

EST.

KEYWORDS

SOURCE

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

REFERENCE

1 (bases 1 to 19)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..19
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ROOT--02-D01"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match

Best Local Similarity 0.6%; Score 17.4; DB 1; Length 19;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

2708 TAAAAAATAAAAA 2726

19 TCATAAAAAA 1

DB

RESULT 1631

CF291899/c

LOCUS

DEFINITION

CF291899 19 bp mRNA linear EST 14-AUG-2003
 sativa (japonica cultivar-group) cDNA clone 14ROOT--02-I08, mRNA
 sequence.

ACCESSION

CF291899

VERSION

EST.

KEYWORDS

SOURCE

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

REFERENCE

1 (bases 1 to 19)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..19
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

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/clone="14ROOT--02-I08"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match

Best Local Similarity 0.6%; Score 17.4; DB 1; Length 19;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

2709 AAAAAAATAAAAA 2727

19 AAAAAAATAAAAA 1

DB

RESULT 1632

CF292072/c

LOCUS

DEFINITION

CF292072 19 bp mRNA linear EST 14-AUG-2003
 sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M03, mRNA
 sequence.

ACCESSION

CF292072

VERSION

EST.

KEYWORDS

SOURCE

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

REFERENCE

1 (bases 1 to 19)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..19
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ROOT--02-M03"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match

Best Local Similarity 0.6%; Score 17.4; DB 1; Length 19;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1633
CF329144/c
LOCUS   19 bp mRNA linear EST 14-AUG-2003
DEFINITION
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-N17, mRNA
sequence.
ACCESSION
CF329144.1 GI:33661177
VERSION
CF329144.1
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--05-H18"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db      1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1635
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LOCUS   19 bp mRNA linear EST 18-AUG-2003
DEFINITION
sativa (japonica cultivar-group) cDNA clone NACL--04-F15, mRNA
sequence.
ACCESSION
CF329136.1 GI:33806509
VERSION
CF329136.1
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1634
CF310688
LOCUS   19 bp mRNA linear EST 15-AUG-2003
DEFINITION
ABF--05-H18.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-H18, mRNA sequence.
ACCESSION
CF310688
VERSION
CF310688.1 GI:33682449
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

```

```

TITLE
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..19
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/cultivar="Nackdong"
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/clone="ABF--05-H18"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db      1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1635
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LOCUS   19 bp mRNA linear EST 18-AUG-2003
DEFINITION
sativa (japonica cultivar-group) cDNA clone NACL--04-F15, mRNA
sequence.
ACCESSION
CF329136.1 GI:33806509
VERSION
CF329136.1
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"

```


Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0109 row: I column: 13
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 High quality sequence stop: 19.
 Location/Qualifiers
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 /strain="C57BL/6J"
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 /clone="UGGCM0109113"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
 source

Query Match 0.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1639
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 LOCUS
 DEFINITION
 1M0360E13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 clone UUGCIM0360E13 F, genomic survey sequence.
 ACCESSION
 AZ513919
 VERSION
 AZ513919.1 GI:10695235
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 DUNN,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
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 Location/Qualifiers
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 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
 source

Query Match 0.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
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 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1640
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 LOCUS
 DEFINITION
 1M0511G04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 clone UUGCIM0511G04 R, genomic survey sequence.
 ACCESSION
 AZ645841
 VERSION
 AZ645841.1 GI:11775726
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 DUNN,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.,
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
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 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0511 row: G column: 04
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

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 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
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 Db 19 AAAAAAAAAAGAAAAAAAAA 1

RESULT 1641

AZ650252
 LOCUS AZ650252 19 bp DNA linear GSS 14-DEC-2000
 DEFINITION IM0520N17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0520N17 F, genomic survey sequence.
 ACCESSION AZ650252
 VERSION AZ650252.1 GI:11784550
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.,
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0520 row: N column: 17
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
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 Db 1 AAAAAAAAAAGAAAAAAAAA 19

RESULT 1642

AZ654747/c
 LOCUS AZ654747 19 bp DNA linear GSS 14-DEC-2000
 DEFINITION IM0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0529F08 F, genomic survey sequence.
 ACCESSION AZ654747
 VERSION AZ654747.1 GI:11791893
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weises,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0529 row: F column: 08
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

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 /clone="UUGC1M0529F08"
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 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1643

CL693177 19 bp DNA linear GSS 10-JUL-2004
 LOCUS PRI0160b.G03.2 - PRI0160b.BR (19) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL693177.1 GI:50215085
 VERSION GSS.
 KEYWORDS Pristionchus pacificus

ORGANISM Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

TITLE AppaDB: an AcedB database for the nematode satellite organism
 JOURNAL Pristionchus pacificus
 PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)
 COMMENT 14681447
 Contact: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: ralf.sommer@tuebingen.mpg.de
 This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
 Seq primer: T7
 Class: fosmid ends.

FEATURES

source
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Query Match 0.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1644

CF319428/c 20 bp mRNA linear EST 15-AUG-2003
 LOCUS HD--09-O20.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 DEFINITION HD--09-O20, mRNA sequence.

ACCESSION CF319428
 VERSION CF319428.1 GI:33691189
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongsin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1. .20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /clone="HD--09-O20"
 /tissue_type="callus"
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 /lab_host="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAGAAAAA 2725
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Db 20 CTAAGAAAAA 2

RESULT 1645
CF333052/c

LOCUS
DEFINITION JMT--01-M17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--01-M17, mRNA sequence.
CF333052 GI:33814360

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..20
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAA 2727
|||
Db 20 AAAAAA 2

RESULT 1646
DY228778/c

LOCUS
DEFINITION ID0AAK5YC02CM1 AphL3SD Acyrthosiphon pisum cDNA clone ID0AAK5YC02 5', mRNA sequence.

ACCESSION
VERSION
DY228778.1 GI:86462906

KEYWORDS
SOURCE
ORGANISM

Acyrthosiphon pisum (pea aphid)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Psocodea; Psocoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

REFERENCE
AUTHORS
TITLE

1 (bases 1 to 20)
Stern,D.L., Wincker,P. and Tagu,D.
Large-scale gene discovery in the pea aphid Acyrthosiphon pisum (Hemiptera)
Unpublished (2005)
Contact: D. Tagu

JOURNAL
COMMENT
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50

PCR Primers
FORWARD: GCCGATACTTCGTATAGCA
Plate: 5Y row: C column: 2.

FEATURES
source
1..20
Location/Qualifiers

/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="yr2"
/db_xref="taxon:7029"
/clone="ID0AAK5YC02"
/tissue_type="head"
/dev_stage="third instar nymph (L3)"
/lab_host="TOP10"
/clone_lib="AphL3SD"
/note="Vector: pDNR-LIB; Site 1: SfiI; Site 2: SfiI; Sample name: AphL3SD ; Plant growth place: INRA-Rennes, UMR BIO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil conditions: peat ; Sowing date: 20/03/2003 ; Harvesting date: 10/04/2003 ; Stress date: no stress ; Description: aphids inoculated on one-week old Vicia faba germinations under non sterile conditions. ; experimental condition: short photoperiod (12-hr light/12-hr dark at 18 c)"

Query Match 0.6%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAA 2727
|||
Db 19 AAAAAA 1

RESULT 1647
AZ308846/c

LOCUS
DEFINITION AZ308846 Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0012H15 F, genomic survey sequence.

ACCESSION
VERSION
AZ308846.1 GI:10349246

KEYWORDS
SOURCE
Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0012 row: H column: 15
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0012H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 21 AAAAAAAAAACAAAAA 3

RESULT 1648
BQ590128/c
LOCUS BQ590128 17 bp mRNA linear EST 06-DEC-2002
DEFINITION E012843-024-019-E19-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-019-E19 3-PRIME, mRNA sequence.

ACCESSION BQ590128
VERSION BQ590128.1 GI:26119711
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany

FEATURES
source
1. .17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:189986"
/db_xref="taxon:161934"
/clone="024-019-E19"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCWSFORT6; Site:1: Sali; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2708 TAAAAAAAAAAAAAAAAA 2724
|||||
Db 17 TAAAAAAAAAAAAAAAAA 1

RESULT 1649
BQ590687
LOCUS BQ590687 17 bp mRNA linear EST 06-DEC-2002
DEFINITION S013717-024-018-B24-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-018-B24 3-PRIME, mRNA sequence.

ACCESSION BQ590687
VERSION BQ590687.1 GI:26120270
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany

FEATURES
source
1. .17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db_xref="GABI:189432"
 /db_xref="taxon:161934"
 /clone="024-018-B24"
 /tissue_type="storage root"
 /lab_host="EMDH108"
 /clone_lib="MP1Z-ADIS-024-storage root"
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet. library provided by KWS
 Kleinfanzlebeher Saatzzucht AG Binbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 1650

BQ591177/c

LOCUS

DEFINITION E012715-024-017-B22-T7 MP1Z-ADIS-024-storage root Beta vulgaris

cDNA clone 024-017-B22 3-PRIME, mRNA sequence.

ACCESSION BQ591177

VERSION BQ591177.1

KEYWORDS BQ591177.1 GI:26120760

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 17)

REFERENCE Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpi-z-koeln.mpg.de

Insert Length: 17 Std Error: 0.00

Plate: 17 row: B column: 22

Seq primer: T7; GTAATACGACTCACTATAGGCG.

Location/Qualifiers

1..17

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/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding

line)"

/db_xref="GABI:188948"

/db_xref="taxon:161934"

/clone="024-017-B22"

/tissue_type="storage root"

/lab_host="EMDH108"

/clone_lib="MP1Z-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfanzlebeher Saatzzucht AG Binbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:

SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1651

CF290854/c

LOCUS

DEFINITION 14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
 sativa (japonica cultivar-group) cDNA clone 14ROOT--01-A21, mRNA
 sequence.

ACCESSION CF290854

VERSION CF290854.1

KEYWORDS GI:33659887

SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

1 (bases 1 to 17)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..17

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ROOT--01-A21"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1652

CF294668/c

LOCUS

DEFINITION 30DGS--04-El7.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
 sativa (japonica cultivar-group) cDNA clone 30DGS--04-El7, mRNA
 sequence.

ACCESSION CF294668

VERSION CF294668.1

GI:33663701

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KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAAAAAAA 2724
|||||
Db 17 TAAAAAATAAAAAAAAAA 1

RESULT 1653
CF295988/c
LOCUS 30DGS--06-C17.1 17 bp mRNA linear EST 14-AUG-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--06-C17, mRNA
sequence.
ACCESSION CF295988
VERSION CF295988.1 GI:33665021
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="30DGS--06-C17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAAAAAAA 2724
|||||
Db 17 TAAAAAATAAAAAAAAAA 1

RESULT 1653
CF295988/c
LOCUS 30DGS--06-C17.1 17 bp mRNA linear EST 14-AUG-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--06-C17, mRNA
sequence.
ACCESSION CF295988
VERSION CF295988.1 GI:33665021
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"

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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAAAAAAA 2724
|||||
Db 17 TAAAAAATAAAAAAAAAA 1

RESULT 1654
CF298589/c
LOCUS 7LEAF--02-A18.b1 17 bp mRNA linear EST 15-AUG-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A18, mRNA
sequence.
ACCESSION CF298589
VERSION CF298589.1 GI:33670350
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
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/tissue_type="leaf"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAATAAAAAAAAAA 2725
|||||
Db 17 AAAAAAATAAAAAAAAAA 1

RESULT 1655
CF310219/c
LOCUS ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION ABF3-overexpressing transgenic rice plasmid cDNA

```



```

library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--04-M02, mRNA sequence.
CF310219 GI:33681980
EST.
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--04-M02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1656
CF334566/c
LOCUS
DEFINITION
JMT--03-O13.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--03-O13, mRNA sequence.
CF334566
CF334566.1 GI:33817460
EST.
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

```

```

Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="JMT--03-O13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1657
CF336950/c
LOCUS
DEFINITION
JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--07-D04, mRNA sequence.
CF336950
CF336950.1 GI:33822280
EST.
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAA 2724
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 Db 17 TAAAAAAAAAAAAAAAAA 1

RESULT 1658
 CX309551/c
 LOCUS
 DEFINITION 17 bp mRNA linear EST 03-JAN-2005
 Drosophila melanogaster Embryo Larva Pupa Adult
 Drosophila melanogaster cDNA clone AM02384 3, mRNA sequence.

ACCESSION CX309551
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBLISHED
 COMMENT

1 (bases 1 to 17)
 Yandell,M., Bailey,A.M., Misra,S., Shu,S., Witel,C., Evans-Holm,M.,
 Celniker,S.E. and Rubin,G.M.
 A computational and experimental approach to validating annotations
 and gene predictions in the Drosophila melanogaster genome
 Proc. Natl. Acad. Sci. U.S.A. 102 (5), 1566-1571 (2005)
 Other ESTs: AM02384.5prime
 15668397
 Contact: Stapleton, M.
 BDGP

Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
 Plate: AM.23 row: G column: 12
 High quality sequence stop: 17.

FEATURES
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 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:7227"
 /clone="AM02384"
 /sex="male and female"
 /dev_stage="0 to 24 hours mixed stage embryonic, late
 third instar larvae, mixed stage pupae, mixed age adults"
 /clone_lib="AM Drosophila melanogaster Embryo Larva Pupa
 Adult"
 /note="RT-PCR products were amplified with pairs of
 gene-specific primers from template RNA representing
 pooled Drosophila stages. Products were directly
 sequenced from both ends with the same oligos used to
 prime PCR."

Query Match 0.6%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1659
 CF301057/c
 LOCUS
 DEFINITION 18 bp mRNA linear EST 15-AUG-2003
 7LEAF--05-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--05-M05, mRNA
 sequence.

ACCESSION CF301057
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

1 (bases 1 to 18)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..18
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--05-M05"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1660
 CF320046/c
 LOCUS
 DEFINITION 18 bp mRNA linear EST 15-AUG-2003
 HD--10-M11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--10-M11, mRNA sequence.

ACCESSION CF320046
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

1 (bases 1 to 18)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..18
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
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 /tissue_type="callus"

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 18)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
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 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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 1..18
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--05-M05"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2725
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 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1660
 CF320046/c
 LOCUS
 DEFINITION 18 bp mRNA linear EST 15-AUG-2003
 HD--10-M11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--10-M11, mRNA sequence.

ACCESSION CF320046
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

1 (bases 1 to 18)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..18
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--10-M11"
 /tissue_type="callus"

/dev stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.6%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAA...AAAAA 2724

Db 17 TAAAAA...AAAAA 1

RESULT 1661

CF320418/c

LOCUS

DEFINITION HD-11-E22.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

JOURNAL

COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1..18

source

/organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD-11-E22"
 /tissue_type="callus"
 /dev stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match

0.6%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAA...AAAAA 2725

Db 18 AAAAAA...AAAAA 2

RESULT 1662

AZ853220

LOCUS

DEFINITION 2M0156J15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0156J15 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: gdunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0156 row: J column: 15

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1..19

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0156J15"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (GII4732114)gb(AFI29072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match

0.6%; Score 17; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAA...AAAAA 2725

Db 3 AAAAAA...AAAAA 19

RESULT 1663

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CF298207      20 bp      mRNA      linear      EST 15-AUG-2003
LOCUS      7LEAF--01-H23.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa (japonica cultivar-group) cDNA clone 7LEAF--01-H23, mRNA
sequence.
ACCESSION      CF298207.1 GI:33669968
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 20)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--01-H23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match      0.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAA 2725
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Db      1 AAAAAAAAAAAAAAAAAA 17

RESULT 1664
AZ818055
LOCUS      2M0087B23R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION      clone UGCG2M0087B23 R, genomic survey sequence.
ACCESSION      AZ818055
VERSION
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhauser,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center

CF298207      20 bp      mRNA      linear      EST 15-AUG-2003
LOCUS      7LEAF--01-H23.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa (japonica cultivar-group) cDNA clone 7LEAF--01-H23, mRNA
sequence.
ACCESSION      CF298207.1 GI:33669968
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 20)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--01-H23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match      0.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAA 2725
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Db      1 AAAAAAAAAAAAAAAAAA 17

RESULT 1664
AZ818055
LOCUS      2M0087B23R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION      clone UGCG2M0087B23 R, genomic survey sequence.
ACCESSION      AZ818055
VERSION
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhauser,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center

```

```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000      Std Error: 0.00
Plate: 0087 row: B column: 23
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0087B23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match      0.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAA 2725
      |||
Db      4 AAAAAAAAAAAAAAAAAA 20

RESULT 1665
DR065210/c
LOCUS      iD91f09.g1 Ginkgo microsporophyll (NYBG) Ginkgo biloba cDNA 3',
DEFINITION      mRNA sequence.
ACCESSION      DR065210
VERSION      DR065210.1 GI:66988778
KEYWORDS      EST.
SOURCE      Ginkgo biloba (maidenhair tree)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 21)
AUTHORS      Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martensen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE      Expressed tag sequences from Ginkgo microsporophyll (NYBG)
JOURNAL      Unpublished (2005)
COMMENT      Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874

```

Email: mcombie@cshl.org
 Seq primer: -21M13UnivRev.
 Location/Qualifiers
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 /organism="Ginkgo biloba"
 /mol_type="mRNA"
 /db_xref="taxon:3311"
 /sex="male"
 /clone_lib="Ginkgo microsporophyll (NYBG)"
 /note="Organ: microsporophyll; Vector: pBK-CMV; Site_1:
 XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA
 Synthesis Kit. The library was size-fractionated to enrich
 for large inserts."

Query Match 0.6%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 21 AAAAAAAAAAAAAAAAAA 5

RESULT 1666
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 LOCUS AZ943299 21 bp DNA linear GSS 26-APR-2001
 DEFINITION 2M0203K21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0203K21 R, genomic survey sequence.

ACCESSION AZ943299
 VERSION AZ943299.1 GI:13807290
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Bescorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0203 row: K column: 21
 Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0203K21"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: FW42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 21 AAAAAAAAAAAAAAAAAA 5

RESULT 1667
 CF298018/c

LOCUS CF298018 20 bp mRNA linear EST 15-AUG-2003
 DEFINITION CF298018 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-D19, mRNA sequence.

ACCESSION CF298018
 VERSION CF298018.1 GI:33669779
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
 source

1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
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 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.6%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAA 2725
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 Db 20 AATCAAAAAAAAAAAAAAAAAA 1

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RESULT 1668
CF300961/c
LOCUS
DEFINITION
  CF300961
  7LEAF--05-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
  sativa (japonica cultivar-group) cDNA clone 7LEAF--05-K03, mRNA
  sequence.
ACCESSION
  CF300961
VERSION
  CF300961.1 GI:33672722
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1. (bases 1 to 20)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
  source
    1..20
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="7LEAF--05-K03"
    /tissue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
  Query Match      0.6%; Score 16.8; DB 1; Length 20;
  Best Local Similarity 90.0%; Pred. No. 1.6e+03;
  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
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  Db 20 AAGAGAAAAAAAAAAAAAAAAAAA 1

  RESULT 1670
  AW333777/c
  LOCUS
  DEFINITION
    AW333777
    S25H10 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
  ACCESSION
    AW333777
  VERSION
    AW333777.1 GI:6830134
  KEYWORDS
    EST.
  SOURCE
    Pneumocystis carinii
    ORGANISM
    Pneumocystis carinii
    Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
    Pneumocystidaceae; Pneumocystis.
  REFERENCE
    1. (bases 1 to 20)
    Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
    Edman,J.C., Kovacs,J. and Cushion,M.
    Expressed sequence tags from Pneumocystis carinii
    Unpublished (2000)
    Contact: Staben C
    School of Biological Sciences
    University of Kentucky
    101 Morgan Building, University of Kentucky, Lexington, KY
    40506-0225, USA
    Tel: 606 257 2161
    Fax: 606 257 1717
    Email: staben@pop.uky.edu.
  FEATURES
    source
      1..20
      /organism="Pneumocystis carinii"
      /mol_type="mRNA"
      /db_xref="taxon:4754"
      /lab_host="E. coli"
      /clone_lib="AGS-1"
      /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
      P. carinii organisms (3x10e9) from a single rat (99-1-6,
      sacrificed on 3/17/99) at Cincinnati VA facilities.
      Trizol extracted RNA. Oligo dt priming, standard
      conditions described by vendor, Stratagene. Further
      details see www.uky.edu/Project/Pneumocystis/"
  Query Match      0.6%; Score 16.8; DB 1; Length 20;
  Best Local Similarity 90.0%; Pred. No. 1.6e+03;
  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 2705 TACTAAAAAAAAAAAAAAAAAA 2724
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  Db 20 TAATATAAAAAAAAAAAAAAAAAA 1

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RESULT 1669
CF301101/c
LOCUS
DEFINITION
  CF301101
  7LEAF--05-N04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
  sativa (japonica cultivar-group) cDNA clone 7LEAF--05-N04, mRNA
  sequence.
ACCESSION
  CF301101
VERSION
  CF301101.1 GI:33672862
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1. (bases 1 to 20)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea

```

RESULT 1671
 DYZ23532
 LOCUS ID0AA110YJ11RM1 ID0AEE Acyrthosiphon pisum cDNA clone ID0AA110YJ11
 DEFINITION 5', mRNA sequence.
 ACCESSION DYZ23532 20 bp mRNA linear EST 03-FEB-2006
 VERSION DYZ23532
 KEYWORDS DYZ23532.1 GI:86457660
 SOURCE EST.
 ORGANISM Acyrthosiphon pisum (pea aphid)
 Acyrthosiphon pisum
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
 1 (bases 1 to 20)
 REFERENCE Stern, D.L., Wincker, P. and Tagu, D.
 AUTHORS Large-scale gene discovery in the pea aphid *Acyrthosiphon pisum*
 TITLE (Hemiptera)
 JOURNAL Unpublished (2005)
 COMMENT Contact: D. Tagu
 INRA Rennes
 UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
 Tel: +33.2.23.48.51.65
 Fax: +33.2.23.48.51.50
 PCR Primers
 FORWARD: CAGGAACAGCTATGACC
 Plate: 10Y row: J column: 11.
 Location/Qualifiers
 1..20
 /organism="Acyrthosiphon pisum"
 /mol_type="mRNA"
 /cultivar="yr2"
 /db_xref="taxon:7029"
 /clone="ID0AA110YJ11"
 /tissue_type="antennae"
 /dev_stage="L3"
 /lab_host="Xl1-Blue"
 /clone_lib="ID0AEE"
 /note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
 Sample name: ID0AEE ; Plant growth place: INRA Rennes, UMR
 BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil
 conditions: Soil ; Sowing date: 15/04/2004 ; Harvesting
 date: 15/04/2004 ; Description: Aphids inoculated on
 one-week old *Vicia faba* under non-sterile conditions. A.
 pisum YR2 is holocyclic, i.e. able to change its
 reproductive mode under short photoperiods (sexual) versus
 long photoperiods (clonal). experimental condition: long
 photoperiod (16-hr light/8-hr dark at 18 degC)"

FEATURES

source
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0077E20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 Kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2701 TTTGTACTAAAAA 2720
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 Db 1 TTTTAAATAAAAA 20

RESULT 1672
 AZ343730/c
 LOCUS AZ343730 20 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0077220F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0077220 F, genomic survey sequence.

ACCESSION AZ343730
 VERSION AZ343730
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 AUTHORS

TITLE

JOURNAL

COMMENT

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.,
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0077 row: E column: 20
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 Kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0077E20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 Kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 2728
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 Db 20 AGAAAAA 1

RESULT 1673

AZ368518
 LOCUS AZ368518 20 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0118G09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0118G09 R, genomic survey sequence.

ACCESSION AZ368518
 VERSION AZ368518
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 AUTHORS


```

AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
  source
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      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
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      /clone="HD-09-107"
      /tissue_type="callus"
      /dev_stage="proliferated callus on 2N6 media for 2 weeks"
      /lab_host="E.coli DH10B"
      /clone_lib="OSHDA1-overexpressing transgenic rice plasmid
      cDNA library (HD)"
      /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
      treated with ABA(20um) for 1hr_ Oligo-capped mRNA was
      reverse transcribed and then used for PCR. mRNA was
      derived from rice Histone Deacetylase overexpression
      line."

  Query Match      0.6%; Score 16.8; DB 1; Length 21;
  Best Local Similarity 90.0%; Pred. No. 1.6e+03;
  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2706 ACTAATAAAAAAAAAAAAAAAAAA 2725
Db 20 ACGAATAAAAAAAAAAATAAAA 1

RESULT 1676
AJ725584
LOCUS      AJ725584 riken1 Gallus gallus cDNA clone 2c16r4, mRNA sequence.
DEFINITION
ACCESSION  AJ725584
VERSION     AJ725584.1 GI:53890998
KEYWORDS   EST.
SOURCE     Gallus gallus (chicken)
ORGANISM   Gallus gallus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.

REFERENCE   1 (bases 1 to 18)
AUTHORS    Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezubov,Y., Zaim,J.,
            Fiedler,P., Kutter,S., Blagodatski,A., Kostovska,D., Kotter,M.,
            Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M.
TITLE      Full-length cDNAs from chicken bursal lymphocytes to facilitate
            gene function analysis
JOURNAL    Genome Biol. 6 (1), R6 (2005)
PUBMED    15642098
COMMENT    Contact: Caldwell RB
            GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie
            Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.

FEATURES
  source
    1..18
      /organism="Gallus gallus"
      /mol_type="mRNA"
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      /clone="2c16r4"
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      /dev_stage="2-3 weeks old"
      /clone_lib="riken1"
      /note="CB inbred strain"

  Query Match      0.6%; Score 16.4; DB 1; Length 18;
  Best Local Similarity 94.4%; Pred. No. 1.6e+03;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2708 TAAAAAATAAAAAAAAAA 2725
Db 1 TCAAAAAAAAAAAAAAAAAA 18

RESULT 1678
BM658677/c
LOCUS      BM658677 L2V602768363.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
DEFINITION
ACCESSION  BM658677
VERSION     BM658677.1 GI:18958998
KEYWORDS   EST.
SOURCE     Sus scrofa (pig)
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.

REFERENCE   1 (bases 1 to 18)
AUTHORS    Adelson,D.L. and Gail,C.A.
TITLE      Porcine ESTs
JOURNAL    Unpublished (2002)
COMMENT    Contact: David L. Adelson
            Animal Breeding and Genetics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798452616
            Fax: 9798456970

```

```

Email: david.adelson@tamu.edu.
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  /organism="Sus scrofa"
  /mol_type="mRNA"
  /db_xref="taxon:9823"
  /clone_lib="CSEQFXL37 pig adrenal"
  /notes="Organ: adrenal gland; Vector: pBluescript SK+;
  Site 1: NotI; Site 2: EcoRI; sequence 5' of the insert
  (5'-NNN...NNNinsert)
  GCGAATTGAGCTCCACCGCGTGGCGGCGGCTCGAG. Sequence 3' of
  the inserts (AAGAATTCGATATCAAGCTTATCGATACCTCGACCTCGAG.
  non-normalized library, sequenced 3' with M13R primer."

Query Match      0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
Db 18 AAAAAAAAAAGAAAAAAAAA 1

RESULT 1679
CF300456/c
LOCUS
DEFINITION
  CF300456 18 bp mRNA linear EST 15-AUG-2003
  7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
  sativa (japonica cultivar-group) cDNA clone 7LEAF--04-N23, mRNA
  sequence.
ACCESSION
  CF300456
VERSION
  CF300456.1 GI:33672217
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 18)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
    1. .18
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="ABF--03-I19"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH108"
    /clone_lib="ABF3-overexpressing transgenic rice plasmid
    cDNA library (ABF)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
    for 2hrs. Oligo-capped mRNA was reverse transcribed and
    then used for PCR. mRNA was prepared from ABA-responsive
    element binding transcription factor 3 overexpression
    line."

REFERENCE
AUTHORS
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
  Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
  Unpublished (2003)
COMMENT
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
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    /mol_type="mRNA"
    /cultivar="Nackdong"
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    /clone="7LEAF--04-N23"
    /tissue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH108"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."

Query Match      0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
Db 18 AGAAAAAAAAAAAAAAAAA 1

RESULT 1680
CF309376/c
LOCUS
DEFINITION
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  ABF--03-I19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
  library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
  ABF--03-I19, mRNA sequence.
ACCESSION
  CF309376
VERSION
  CF309376.1 GI:33681137
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 18)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
    1. .18
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
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    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH108"
    /clone_lib="ABF3-overexpressing transgenic rice plasmid
    cDNA library (ABF)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
    for 2hrs. Oligo-capped mRNA was reverse transcribed and
    then used for PCR. mRNA was prepared from ABA-responsive
    element binding transcription factor 3 overexpression
    line."

Query Match      0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAA 2723
Db 18 AGTAAAAAAAAAAAAAAAAA 1

RESULT 1681
CF329285/c
LOCUS
DEFINITION
  CF329285 18 bp mRNA linear EST 18-AUG-2003
  NACL--04-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza
  sativa (japonica cultivar-group) cDNA clone NACL--04-I22, mRNA
  sequence.
ACCESSION
  CF329285
VERSION
  CF329285.1 GI:33806806
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 18)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/note="Rice callus plasmid cDNA library (NACL)"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725
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Db 18 TAGAAAAAAAAAAAAAAAAA 1

RESULT 1682

CF329484/c
LOCUS CF329484 18 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-N06.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION CF329484
VERSION CF329484.1 GI:33807207
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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/db_xref="taxon:39947"
/clone="NACL--04-N06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2706 ACTAAAAAAAAAAAAAAAAA 2723
|
Db 18 AGTAAAAAAAAAAAAAAAAA 1

RESULT 1683

CF329485
LOCUS CF329485 18 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-N06.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION CF329485
VERSION CF329485.1 GI:33807209
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAA 2723
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Db 1 AGTAAAAAAAAAAAAAAAAA 18

RESULT 1684

CR786637
LOCUS CR786637 18 bp mRNA linear EST 01-OCT-2004
DEFINITION DKFZp468J2331.r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone DKFZp468J2331-5', mRNA sequence.
ACCESSION CR786637
VERSION CR786637.1 GI:53705634
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Pongo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Oeanger, A., Fobo, G., Han, M. and Wiemann, S.

TITLE Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
 JOURNAL Unpublished (2004)
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKF2);
 Email s.wiemann@dkfz-heidelberg.de; mfoerschung GmbH in Berlin,
 Germany. Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468J2331
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.

FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9600"
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 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="468 (synonym: phrt1)"
 /note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"
 Query Match 0.6%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
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 Db 1 AAAAAAAAAAAAAAAAAA 18
 RESULT 1685
 AJ666205/c 19 bp mRNA linear EST 28-JUN-2004
 LOCUS AJ666205 CSEQRAN09 Sus scrofa cDNA clone C0000033_E15, mRNA
 DEFINITION sequence.
 ACCESSION AJ666205
 VERSION AJ666205.1 GI:49350656
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.
 1 (bases 1 to 19)
 Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
 Development of cDNA and EST resources for studying reproduction and
 embryo development in pigs and cattle
 Unpublished (2004)
 JOURNAL Contact: Anderson SI
 COMMENT Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred
 v0.020425.c. Vector identified by cross match with the -minscore 20.
 and -mismatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
 EcoRI R. Site 2: NotI Description: Normalised library constructed
 from pooled tissue from day 30 placentas. Clones available from UK
 Centre for Functional Genomics in Farm Animals, Roslin Institute,
 Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
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 1..19
 /organism="Sus scrofa"
 /mol_type="mRNA"
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 constructed from pooled tissue from day 30 placentas."

Query Match 0.6%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
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 Db 19 AAAAAAAAAAGAAAAA 2

RESULT 1686
 CF298472/c 19 bp mRNA linear EST 15-AUG-2003
 LOCUS CF298472 sativa (japonica cultivar-group) cDNA clone 7LEAF--01-001, mRNA
 DEFINITION sequence.

ACCESSION CF298472
 VERSION CF298472.1 GI:33670233
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 JOURNAL Contact: Nahm B.H.
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..19
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /tissue_type="leaf"
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 RT-PCR."

Query Match 0.6%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAA 2725
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 Db 18 TATAA 1

RESULT 1687
 CF326845 19 bp mRNA linear EST 18-AUG-2003
 LOCUS CF326845 NACL--01-B12.g1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--01-B12, mRNA
 sequence.

ACCESSION CF326845
 VERSION CF326845.1 GI:33801944
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2725
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 Db 1 TCAAAAAAAAAAAAAAAAAAAAAA 18

RESULT 1690
 AZ360314
 LOCUS 19 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0103G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0103G03 R, genomic survey sequence.
 ACCESSION AZ360314
 VERSION AZ360314.1 GI:10474014
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0103 row: G column: 03
 Seq primer: CACACAGGAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
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 /clone="UUGC1M0103G03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
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 Db 2 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1691
 AZ447251/c
 LOCUS 19 bp DNA linear GSS 04-OCT-2000
 DEFINITION 1M0244J19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0244J19 F, genomic survey sequence.
 ACCESSION AZ447251
 VERSION AZ447251.1 GI:10599050
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0244 row: J column: 19
 Seq primer: CGTTGTAAACGACGCCGACGT
 Class: plasmid ends
 High quality sequence stop: 19.

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 /strain="C57BL/6J"
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 /sex="Male"
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

[illegible]

and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
PUBMED
COMMENT

TITLE
JOURNAL
PUBMED
COMMENT

Contact: Weissshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 28 row: F column: 08
Seq primer: SP6r; ATTTAGGTGACACTATAGAGA.
Location/Qualifiers
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line)"
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 1695
BQ592965/c
LOCUS
DEFINITION
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cDNA clone 024-028-A01 3-PRIME, mRNA sequence.
ACCESSION
BQ592965
VERSION
BQ592965.1 GI:26122548
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
Herwig, R., Schulz, B., Weissshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
PUBMED
COMMENT

Contact: Weissshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de

TITLE
JOURNAL
PUBMED
COMMENT

Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
PUBMED
COMMENT

Contact: Weissshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de

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Location/Qualifiers
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 1696
BQ595369/c
LOCUS
DEFINITION
S013317-024-022-P02-T7 MPIZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION
BQ595369
VERSION
BQ595369.1 GI:26124952
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
Herwig, R., Schulz, B., Weissshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
PUBMED
COMMENT

Contact: Weissshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
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Location/Qualifiers
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FEATURES
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 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 16 TAAAAAAAAAAAAAAAAA 1

RESULT 1697

BQ595717
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 DEFINITION E012692-024-022-H07-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
 cDNA clone 024-022-H07 5-PRIME, mRNA sequence.

ACCESSION BQ595717
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 16)
 AUTHORS Herwig,R.; Schulz,B.; Weishaar,B.; Hennig,S.; Steinfath,M.;
 Drungowski,M.; Stahl,D.; Wruck,W.; Menze,A.; O'Brien,J.; Lehrach,H.
 and Radelof,U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
 PUBMED 12472698
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mp1z-koeln.mpg.de
 Insert Length: 16 Std Error: 0.00
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 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
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QY 2709 AAAAAAAAAAAAAAAAAA 2724
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 Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 1698

CF279325/c
 LOCUS
 DEFINITION 14ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-J09,
 mRNA sequence.

ACCESSION CF279325
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE 1 (bases 1 to 16)
 AUTHORS Kim,J.S.; Jun,K.M.; Cheong,P.J.; Kim,M.J.; Lee,T.H.; Shin,Y.C.;
 Song,S.I.; Kim,Y.-K.; Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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 Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 1699

CF296130/c
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 sativa (japonica cultivar-group) cDNA clone 30DGS--06-F22, mRNA
 sequence.

ACCESSION CF296130
 VERSION
 KEYWORDS
 CF296130.1 GI:33665163

Query Match 0.6%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
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QY 2709 AAAAAAAAAAAAAAAAAA 2724
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 Db 16 AAAAAAAAAAAAAAAAAA 1

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SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
               Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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   /lab_host="E.coli DH10B"
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   with oligoribonucleotides and then used as templates for
   RT-PCR."

Query Match      0.6%; Score 16; DB 1; Length 16;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAA
Db 16 TAAAAA

RESULT 1700
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                 HD--06-C03, mRNA sequence.
ACCESSION
VERSION         CF311057.1 GI:33682818
KEYWORDS
SOURCE
ORGANISM        Oryza sativa (japonica cultivar-group)
                 Oryza sativa (japonica cultivar-group)
                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
                 clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS         Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE           Large-scale Sequencing Analysis of Rice ESTs
JOURNAL         Unpublished (2003)
COMMENT         Contact: Nahm B.H.
                 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                 of Bioscience and Bioinformatics, Myongji University
                 Yongin, Kyeonggi, Korea
                 Tel: 82 31 330 6193
                 Fax: 82 31 321 6355
                 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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   with oligoribonucleotides and then used as templates for
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16 TAAAAA

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LOCUS
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                 ABF--06-C03, mRNA sequence.
ACCESSION
VERSION         CF311057.1 GI:33682818
KEYWORDS
SOURCE
ORGANISM        Oryza sativa (japonica cultivar-group)
                 Oryza sativa (japonica cultivar-group)
                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
                 clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS         Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE           Large-scale Sequencing Analysis of Rice ESTs
JOURNAL         Unpublished (2003)
COMMENT         Contact: Nahm B.H.
                 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                 of Bioscience and Bioinformatics, Myongji University
                 Yongin, Kyeonggi, Korea
                 Tel: 82 31 330 6193
                 Fax: 82 31 321 6355
                 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAA
Db 16 AAAAAA

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                 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
                 HD--02-G01, mRNA sequence.
ACCESSION
VERSION         CF314013.1 GI:33685774
KEYWORDS
SOURCE
ORGANISM        Oryza sativa (japonica cultivar-group)
                 Oryza sativa (japonica cultivar-group)
                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
                 clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS         Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE           Large-scale Sequencing Analysis of Rice ESTs
JOURNAL         Unpublished (2003)
COMMENT         Contact: Nahm B.H.
                 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                 of Bioscience and Bioinformatics, Myongji University
                 Yongin, Kyeonggi, Korea
                 Tel: 82 31 330 6193
                 Fax: 82 31 321 6355
                 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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cDNA library (HD)"
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAA
Db 16 TAAAAA

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RESULT 1702
CF314377/c
LOCUS
DEFINITION
HD--02-001.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--02-001, mRNA sequence.
ACCESSION
CF314377
VERSION
CF314377.1 GI:33686138
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
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cDNA library (HD)"
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derived from rice Histone Deacetylase overexpression
line."
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAA 2724
Db 16 AAAAAAAAAAAAAA 1
RESULT 1703
CF315789/c
LOCUS
DEFINITION
HD--04-N10.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--04-N10, mRNA sequence.
ACCESSION
CF315789
VERSION
CF315789.1 GI:33687550
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)

```

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match 0.6%; Score 16; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAA 2724

Db 16 AAAAAAAAAAAAAA 1

RESULT 1704

CF316056/c

LOCUS

DEFINITION HD--05-D07.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--05-D07, mRNA sequence.

ACCESSION

VERSION

CF316056

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was

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treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16 AAAAAAAAAAAAAAA 1

RESULT 1705
CF317718/c
LOCUS
DEFINITION
HD--07-105-g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--07-105, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAA 2724
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Db 16 AAAAAAAAAAAAAAA 1

RESULT 1706
CF320356/c
LOCUS
DEFINITION
HD--11-D14_b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--11-D14, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa (japonica cultivar-group)"
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Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAA 2724
|||||
Db 16 AAAAAAAAAAAAAAA 1

RESULT 1707
CF327722/c
LOCUS
DEFINITION
NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-F06, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

```

FEATURES
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 TAAAAAATAAAAAAAAAA 2724
Db 16 TAAAAAATAAAAAAAAAA 1

RESULT 1708
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DEFINITION NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-J17, mRNA
sequence.
ACCESSION CF329320
VERSION CF329320.1 GI:33806877
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1..16
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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16 TAAAAAATAAAAAAAAAA 1

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    with oligoribonucleotides and then used as templates for
    RT-PCR."

Query Match      0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 16 TAAAAAATAAAAAAAAAA 1

FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 TAAAAAATAAAAAAAAAA 2724
Db 16 TAAAAAATAAAAAAAAAA 16

RESULT 1710
LOCUS CR786853 16 bp mRNA linear EST 01-OCT-2004
DEFINITION DKFP468E2231_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone
sequence.
ACCESSION CR786853
VERSION CR786853.1 GI:53705850
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Suarchontoglires; Primates; Catarrhini;
Hominoidea; Pongo.
1 (bases 1 to 16)
Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
Pongo pygmaeus mRNA (Koehler,K., Beyer,A., Mewes,H.W., et al.)
Unpublished (2004)
Contact: MIPS
MIPS

RESULT 1709
LOCUS CF333386 16 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-E05, mRNA sequence.
ACCESSION CF333386
VERSION CF333386.1 GI:33815044
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1..16
/organism="Oryza sativa (japonica cultivar-group)"
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Query Match      0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 TAAAAAATAAAAAAAAAA 2724
Db 1 TAAAAAATAAAAAAAAAA 16

```


Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; mforschung GmbH in Berlin,
Germany. Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468E2231>
Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

Location/Qualifiers
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/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAA 2724
Db 1 AAAAAAAAAAAAAA 16

RESULT 1711

DT498583
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DEFINITION WS0115_BR M08 PT-P-FL-A-2 Populus trichocarpa cDNA clone WS0115_M08
5', mRNA sequence.
ACCESSION DT498583
VERSION DT498583.1 GI:73895845
KEYWORDS EST.
SOURCE Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
ORGANISM Populus trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.

REFERENCE 1 (bases 1 to 16)
Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y.,
Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G.,
Babakiaff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A.,
Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A.,
Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and
Bohlmann, J.

The poplar transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries

Unpublished (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282

Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS0115 row: M column: 08
High quality sequence stop: 122
POLYA=Yes.

FEATURES

Location/Qualifiers
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/mol_type="mRNA"
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/sex="Female"
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/clone_lib="PT-P-FL-A-2"

/note="Vector: pBluescript II SK (+) XR; Site_1: SstI (5' end of cDNA); Site_2: XhoI (3' end of cDNA); Phloem and cambium from 8 year old trees harvested within the Boise Cascade region of Washington state on May 15th, 2001. cDNA was prepared from 20 micrograms of mRNA according to the full-length cDNA library construction method described by Carninci P. et al. (2000), Genome Research 10(10):1617-1630 and directionally ligated into the pBluescript II SK (+) XR vector digested with SstI (5' end) and XhoI (3'). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAA 2724
Db 1 AAAAAAAAAAAAAA 16

RESULT 1712

BQ591181/c
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DEFINITION BQ591181 024-017-H16-T7 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-H16 3-PRIME, mRNA sequence.

ACCESSION BQ591181
VERSION BQ591181.1 GI:26120764
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 17)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H.
and Radloff, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

12472698

Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

Email: weisshaar@piz-koeln.mpg.de

Insert Length: 17 Std Error: 0.00

Plate: 17 row: H column: 16

Seq primer: T7: GTAATACGACTCACTATAGGCG.

FEATURES

Location/Qualifiers
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/db_xref="GABI:188932"
/db_xref="taxon:161934"
/clone="024-017-H16"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: Sali; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

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Query Match      0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAA 2723
Db 16 TAAAAAATAAAAA 1

RESULT 1713
CF295807/c
LOCUS CF295807 17 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--05-012.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
          sativa (japonica cultivar-group) cDNA clone 30DGS--05-012, mRNA
          sequence.
ACCESSION CF295807
VERSION CF295807.1 GI:33664840
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
          Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
          source
          1..17
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          /mol_type="mRNA"
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          /lab_host="E.coli DH10B"
          /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAATAAAAA 2724
Db 16 AAAAAAATAAAAA 1

RESULT 1714
CF295807/c
LOCUS CF295807 17 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
          sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P11, mRNA
          sequence.
ACCESSION CF302447
VERSION CF302447.1 GI:33674208
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
          Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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          /organism="Oryza sativa (japonica cultivar-group)"
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          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

Query Match      0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAATAAAAA 2724
Db 16 AAAAAAATAAAAA 1

RESULT 1714
CF295807/c
LOCUS CF295807 17 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
          sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L20, mRNA
          sequence.
ACCESSION CF295807
VERSION CF295807.1 GI:33671400
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
          Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
          source
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          /dev_stage="7 days after germination"
          /lab_host="E.coli DH10B"
          /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
          /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
          with oligoribonucleotides and then used as templates for
          RT-PCR."

Query Match      0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAATAAAAA 2724
Db 16 AAAAAAATAAAAA 1

RESULT 1715
CF302447/c
LOCUS CF302447 17 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
          sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P11, mRNA
          sequence.
ACCESSION CF302447
VERSION CF302447.1 GI:33674208
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
          Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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          1..17
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/lab host="E.coli DH10B"
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/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAA 2724
Db 16 AAAAAAAAAAAAAA 1

RESULT 1716
CF311499/c
LOCUS
DEFINITION
ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-L20, mRNA sequence.
CF311499
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--06-L20"
/tissue_type="leaf"
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cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

FEATURES
source
Query Match          0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAA 2724
Db 16 AAAAAAAAAAAAAA 1

RESULT 1718
CF319075/c
LOCUS
DEFINITION
HD--09-H06.g1 OshDAC1-overexpressing transgenic rice plasmid
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-H06, mRNA sequence.
CF319075
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..17
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/mol_type="mRNA"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match          0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAA 2723
Db 16 TAAAAAAAAAAAAA 1

RESULT 1717
CF313013/c
LOCUS
DEFINITION
ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--08-P19, mRNA sequence.
CF313013
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="ABF--08-P19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

ABF--08-P19, mRNA sequence.
CF313013
CF313013.1 GI:33684774
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE AUTHORS TITLE JOURNAL COMMENT

1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES source

1..17
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/mol_type="mRNA"
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cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAA 2724
Db 16 AAAAAAAAAAAAAA 1

RESULT 1718 CF319075/c LOCUS

DEFINITION

HD--09-H06.g1 OshDAC1-overexpressing transgenic rice plasmid
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-H06, mRNA sequence.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

CF319075
17 bp mRNA linear EST 15-AUG-2003
Library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-H06, mRNA sequence.
CF319075
CF319075.1 GI:33690836
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE AUTHORS TITLE JOURNAL COMMENT

1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bnhahmeggbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2708 TAAAAA... 2723

Db 16 TAAAAA... 1

RESULT 1719

CF298591/c
LOCUS
DEFINITION
18 bp mRNA linear EST 15-AUG-2003
7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A20, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 18)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahmeggbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
1..18
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/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2708 TAAAAA... 2723

Db 16 TAAAAA... 1

RESULT 1720

CF278272/c
LOCUS
DEFINITION
19 bp mRNA linear EST 14-AUG-2003
14ETL--04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-C01, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahmeggbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2708 TAAAAA... 2723

Db 16 TAAAAA... 1

RESULT 1721

CF308042/c
LOCUS
DEFINITION
19 bp mRNA linear EST 15-AUG-2003
ABF--01-L07.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--01-L07, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
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/lab_host="E.coli DH108"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAATAAAAAAAAAA 2723
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Db 16 TAAATAAAAAAAAAA 1

RESULT 1722
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LOCUS
DEFINITION 19 bp mRNA linear EST 15-AUG-2003
ABF-07-A05.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF-07-A05, mRNA sequence.

ACCESSION CF311668
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="ABF3-overexpressing transgenic rice plasmid

CDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

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Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2724
|||||
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 1723
AZ764517
LOCUS
DEFINITION 19 bp DNA linear GSS 16-FEB-2001
1M0560L07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560L07 R, genomic survey sequence.

ACCESSION AZ764517
VERSION AZ764517
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: L column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560L07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2724

Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 1724

LOCUS AJ663023 19 bp mRNA linear EST 28-JUN-2004
DEFINITION AJ663023 CSEQPAN09 Sus scrofa CDNA clone C0000024_H21, mRNA sequence.

ACCESSION AJ663023

VERSION AJ663023.1 GI:49347146

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM

REFERENCE 1 (bases 1 to 19)

AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.

TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle

JOURNAL Unpublished (2004)

COMMENT Contact: Anderson SI

Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:

EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

source

1..19

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="C0000024_H21"

/tissue_type="placenta"

/clone_lib="CSEQPAN09"

/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match 0.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.8e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2727

Db 1 AAACCAAAAAAAAAAAAAAAAA 19

RESULT 1725

LOCUS CF298134 19 bp mRNA linear EST 15-AUG-2003
DEFINITION CF298134 7LEAF--01-G09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-G09, mRNA sequence.

ACCESSION

CF298134

CF298134.1 GI:33669895

EST.

KEYWORDS Oryza sativa (japonica cultivar-group)

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-G09"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.8e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2727

Db 1 AAGGAAAAAAAAAAAAAAAA 19

RESULT 1726

CF300236/c

LOCUS CF300236

DEFINITION 7LEAF--04-124.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-124, mRNA sequence.

ACCESSION CF300236

VERSION CF300236.1 GI:33671997

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

[illegible]

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.mvongui.ac.kr.

FEATURES

```

1. 13
source
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 89.5%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2709 AAAAAAAAAAAAAAAAAA 2727
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Db 1 AAAGATAAAAAAAAAAAA 19

RESULT 1730
AZ345499/C

LOCUS AZ345499 19 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0080F08F Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0080F06 F, genomic survey sequence.
ACCESSION AZ345499
VERSION AZ345499
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Rally,M., Rose,M., Stokes,R., Tinge,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
 COMMENT
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: F column: 06
 Seq primer: CGTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
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/strain="C57BL/6J"
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/clone="UUGC1M0080F06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

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/clone lib="Mouse 10kb plasmid UUGC1M library"
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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PW42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Query Match          0.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2709 AAAAAAAAAAAAAAAAAA 2727
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 Db 19 AAAAAAAAAAGAGAAAAA 1

RESULT 1731

AZ509929	AZ509929	19 bp	DNA	linear	GSS 05-OCT-2000
LOCUS	1M0354A07F	Mouse 10kb	plasmid	U9GCM1	library
DEFINITION	Clone U9GCM10354A07 F,	genomic	survey	sequence.	musculus
ACCESSION	AZ509929				
VERSION	AZ509929.1	GI:10691245			
KEYWORDS	GSS.				
SOURCE	Mus musculus	(house mouse)			

REFERENCE
AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kbp plasmid inserts

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kbp
 plasmid inserts

**JOURNAL
COMMENT**

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0354 row: A column: 07

Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends

	High quality sequence stop: 19.
FEATURES	Location/Qualifiers

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/sex="Male"  
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/clone lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 1 AAAAAAAAAAAAAAAAAATTAA 19

RESULT 1732

AZ611602/c
 LOCUS
 DEFINITION 1M0438G03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0438G03 F, genomic survey sequence.

ACCESSION AZ611602.1 GI:11733792
 VERSION
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

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Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0438G03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 1 AAAAAAAAAAAAAAAAACCAAAAA 1

RESULT 1733

AZ786336/c
 LOCUS
 DEFINITION 2M0031H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0031H17 R, genomic survey sequence.

ACCESSION AZ786336
 VERSION
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0031 row: H column: 17

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

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/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0031H17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAA 2727
 Db 19 AAAAAAAAAAGAGAAAAA 1

Search completed: November 7, 2006, 10:40:22
 Job time : 108 secs